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(21) International Application Number: PCT/US97/20313 (22) International Filing Date: 5 November 1997 (05.11.97) (30) Priority Data: 60/030,455 6 November 1996 (06.11.96) US (71) Applicant (for all designated States except US): WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH [US/US]; Nine Cambridge Center, Cambridge, MA 02142 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): LANDER, Eric, S. [US/US]; 151 Bishop Allen Drive, Cambridge, MA 02138, (US). WANG, David [CN/US]; Apartment 314, 276 Mass- achusetts Avenue, Arlington, MA 02173 (US). HUDSON, Thomas [CA/US]; 361 Metcalfe Avenue, Westmount, Quebec H3Z 2J2 (CA). (74) Agents: GRANAHAN, Patricia et al.; Hamilton, Brook, Smith & Reynolds, Two Militia Drive, Lexington, MA 02173 (US).		(81) Designated States: JP, US, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). Published <i>Without international search report and to be republished upon receipt of that report.</i>
(54) Title: BIALLELIC MARKERS (57) Abstract The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.		

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BIALLELIC MARKERS

RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996, the entire teachings of which are incorporated herein by reference.

BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution, generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism (RFLP) is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

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RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; WO90/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., WO 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include β -globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater

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frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a
5 polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays
10 employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for
15 their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to
20 both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table, column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.

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DETAILED DESCRIPTION OF THE INVENTION

DEFINITIONS

- An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.
- Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.
- Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).

- As used herein, the term primer refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and an agent for

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polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 5 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

10 The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with 15 the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same 20 chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site 25 is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include 30 restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

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and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

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conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's (sequence tag sites)); <http://shgc.stanford.edu> (Stanford STS's); and <http://ww.tigr.org/> (TIGR STS's). The Web sites also list primers for amplification of the fragments,

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and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference
5 in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being
10 assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table
15 lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the
20 complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are
25 replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

II. Analysis of Polymorphisms.

A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid
30 from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue

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samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988), transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,

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sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

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hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference

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sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

3. Allele-Specific Primers

5 An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in
10 conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows
15 a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of
20 the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

4. Direct-Sequencing

The direct analysis of the sequence of polymorphisms of
25 the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,
30 1988)).

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5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

10 6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

25 III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

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A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See
5 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in
10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

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match of suspect and crime scene sample would occur by chance.

$p(ID)$ is the probability that two random individuals have the same polymorphic or allelic form at a given

- 5 polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies x and y , the probability of each genotype in a diploid organism is (see WO 95/12607):

- 10 Homozygote: $p(AA) = x^2$
 Homozygote: $p(BB) = y^2 = (1-x)^2$
 Single Heterozygote: $p(AB) = p(BA) = xy = x(1-x)$
 Both Heterozygotes: $p(AB+BA) = 2xy = 2x(1-x)$

- The probability of identity at one locus (i.e., the
 15 probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(ID) = (x^2)^2 + (2xy)^2 + (y^2)^2.$$

- These calculations can be extended for any number of
 20 polymorphic forms at a given locus. For example, the probability of identity $p(ID)$ for a 3-allele system where the alleles have the frequencies in the population of x , y and z , respectively, is equal to the sum of the squares of the genotype frequencies:

- 25 $p(ID) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$

In a locus of n alleles, the appropriate binomial expansion is used to calculate $p(ID)$ and $p(exc)$.

- The cumulative probability of identity ($cum p(ID)$) for each of multiple unlinked loci is determined by multiplying
 30 the probabilities provided by each locus.

$$cum p(ID) = p(ID_1)p(ID_2)p(ID_3) \dots p(ID_n)$$

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The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(\text{ID}).$$

- 5 If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10 B. Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.

- 15 Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

- 20 If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child
- 25 attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

- The probability of parentage exclusion (representing
- 30 the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

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incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$), where x, y and z are the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

$$p(\text{non-exc}) = 1 - p(\text{exc})$$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3}) \dots$$

$$p(\text{non-excn})$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the

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circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance

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(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of
5 individuals who have been tested for the presence or absence of a phenotypic trait of interest and for polymorphic markers sets. To perform such analysis, the presence or absence of a set of polymorphisms (i.e. a polymorphic set) is determined for a set of the
10 individuals, some of whom exhibit a particular trait, and some of which exhibit lack of the trait. The alleles of each polymorphism of the set are then reviewed to determine whether the presence or absence of a particular allele is associated with the trait of interest. Correlation can be
15 performed by standard statistical methods such as a χ -squared test and statistically significant correlations between polymorphic form(s) and phenotypic characteristics are noted. For example, it might be found that the presence of allele A1 at polymorphism A correlates with
20 heart disease. As a further example, it might be found that the combined presence of allele A1 at polymorphism A and allele B1 at polymorphism B correlates with increased milk production of a farm animal.

Such correlations can be exploited in several ways. In
25 the case of a strong correlation between a set of one or more polymorphic forms and a disease for which treatment is available, detection of the polymorphic form set in a human or animal patient may justify immediate administration of treatment, or at least the institution of regular
30 monitoring of the patient. Detection of a polymorphic form correlated with serious disease in a couple contemplating a family may also be valuable to the couple in their reproductive decisions. For example, the female partner

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might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where Y_{ijkpn} is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record; μ is an overall mean; YS_i is the effect common to all cows calving in year-season; X_k is the effect common to cows in either the high or average selection line; β_1 to β_{17} are the binomial regressions of production record on mtDNA

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D-loop sequence polymorphisms; PE_n is permanent environmental effect common to all records of cow n ; a_n is effect of animal n and is composed of the additive genetic contribution of sire and dam breeding values and a Mendelian sampling effect; and e_p is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next generation of the herd.

D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized

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for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-

5 segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the
10 odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction θ , versus the situation in which the two are not linked, and thus segregating independently (Thompson &
15 Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions (θ),
20 ranging from $\theta = 0.0$ (coincident loci) to $\theta = 0.50$ (unlinked). Thus, the likelihood at a given value of θ is: probability of data if loci linked at θ to probability of data if loci unlinked. The computed likelihoods are usually expressed as the \log_{10} of this ratio (i.e., a lod
25 score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod
30 scores for differing values of θ (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See

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Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of θ at which the lod score is the highest is considered to be the best estimate of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of θ) than the possibility that the two loci are unlinked. By convention, a combined lod score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared. Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

IV. Modified Polypeptides and Gene Sequences

The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component) except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

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corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or
5 other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate
10 promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host
15 sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include
20 fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as
25 *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing
30 includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

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The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby,

- 5 *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is
- 10 secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

- The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene
- 15 and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating
- 20 the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292
- 25 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

- 30 In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate

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the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and
5 antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to
10 corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide-fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A*
15 *Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of
20 immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

V. Kits

25 The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific
30 oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,

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100 or all of the polymorphisms shown in the Table.

Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means
5 used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

10 The following Examples are offered for the purpose of illustrating the present invention and are not to be construed to limit the scope of this invention. The teachings of all references cited herein are hereby incorporated herein by reference.

15 EXAMPLES

The polymorphisms shown in the Table were identified by resequencing of target sequences from three to ten unrelated individuals of diverse ethnic and geographic backgrounds by hybridization to probes immobilized to
20 microfabricated arrays or conventional sequencing. The strategy and principles for design and use of such arrays are generally described in WO 95/11995. The strategy provides arrays of probes for analysis of target sequences showing a high degree of sequence identity to the reference
25 sequences of the fragments shown in the Table, column 1. The reference sequences were sequence-tagged sites (STSs) developed in the course of the Human Genome Project (see, e.g., *Science* 270, 1945-1954 (1995); *Nature* 380, 152-154, (1996)). Most STS's ranged from 100 bp to 300 bp in size.

30 A typical probe array used in this analysis has two groups of four sets of probes that respectively tile both strands of a reference sequence. A first probe set

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comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence.

5 That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three

10 additional probe sets. Thus, there are four probes corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in

15 the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different reference sequences were included

20 on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or

25 after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of label bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For

30 example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The

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corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). The existence of a polymorphism is also manifested by

5 differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a

10 difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined *a priori*, such

15 that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a

20 reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the

25 diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament

30 for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

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All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and
5 individually indicated to be so incorporated by reference.

1	2	3	4	5	6	7
						TGTGAACTCCACTTGAAGCCAAAGAAAGAACTCACACTTAAACACACATGCCAGTTGGGAAGGCTCT
						GAAACTCAGTGCATAATAGGAACACTTGAGACTAATGAAAGAGAGAGTTGAGACCAATCTTTATTTT
						GTACTGGCCAAATACTGAATAACAGTTGAAGGAAAGACATTGGAAAAAGCTTTTGAGGATAATGT
WI-7070	226	C	T	TACTAGACTTTATGCCATGGTGCTTTC/TJAGTTTAAATGCTGTCTCTGTCAG
						AAGCCATTGACGTAACATCTCAGAGGTTATTTGCATGGATTGACTCCTGGGACAAAGGAC/GCJAA
						AAACACTCTTCTGTGGATATCTGTCAGATAGATGACCCAAAGATCAGATGCTACCCAGATGTGTTTT
						GATAATACATAAGCCCTAGGATTTAGATACAATCTTGAAGAAACTGAGACAGATAATTCTGAATT
WI-10744	61	G	C	AAATGAGGTAAAGTTTCAGGCACTCA
						GGGCAATTACCAGCAAAAGTCAAAATACCAGCATCAAGTCAGGTGCAAAAGGAGGTAGAACAA
						TTACAGTAACATATGTCAATCTTTTGTATATTAGTATTATCTGCCAATGCCATAGATA/CJTAGTG
						GGTCCCTAATAGTTATTAGTCCCTTTTCTCCCTCTTCTCATCTCTGAATTTATTTTATACTTAA
WI-9975	126	C	T	GGGATTAGTTACCACCAAAATGTGTATGTATCAATTTGATCTTACTGAA
						GCTAGGTTTGTCTGTGGCTGCTTCACATAGACTTGAGATGACTTGATTACAGTAATCCCTATGT
						GATGTAACATAGCTAGACCTCCCTTCTCCGCAATCCAGCTCCAGGTTTCAGAAAGTATGCCACAC
						TCAACCCCTCTCTCCAGTTCATCCTGTATTAAATTTCTCCCATATTAAATCAAGGGAGTGGACAGGT
WI-8010	247	G	T	CCCTGGCTGAAAGAAATAAAGAGATCCCAAGTGGTGGG/GTCTT
						GCCGGCCTATCTTTTAAATTTAACTTGTATCTTTGGTGTCTCCATCCTAGGATCTGCCTTAAAT
						CTTTGCCTGTCTGA/GCJATTACCTGATCTACTTTTGATACACAAGGCTGATGGCTCACAATGT
						AGTAGGCCAATCTTCAGGTCTCTTTGAATTTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA
WI-5222b	85	G	C	TCTCGACTCTATAACAACCTCCACAGAA
						GCCCGGCCTATCTTTTAAATTTAACTTGTATCTTTGGTGTCTCCATCCTA/GCJGATTCTGCCTTAT
						AATCTTTGTCCTGTCTGTAGATTACCTGATCTACTTTTGATACACAAGGCTGATGGCTCACAATGT
						AGTAGGCCAATCTTCAGGTCTCTTTGAATTTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA
WI-5222	52	G	C	TCTCGACTCTATAACAACCTCCACAGAA
						TATGCACCTCCACAAAGCGATATAATTTAAAGTTTTTTTTCATTAGAAATAATGTATAAAAAATAA
						ATATGTTATTATAGGCAATTTATTACTAATATAGTCTCTTGGAAAGGACACCCCAACCAATACTT
						ATAAAGTACATGTAAATTTATAGTAACATAATTTACTATACATATGGAATAATCATATTTCTACA
WI-8007	242	C	A	GAAAGCTGAACAGACATTCACCAGGATACGACTGTGGAC/CJAGCTGCTG
						TCAGTTGCAAAAAATTGCTGCCATAAACATGCTTTGCTTATCTCTGTGCATATGTATGTTTGTAG
						TCTATATTCACACATATGAGTGAAATTTCTCTGGGGCATGGGAAATACATCTTTATGAGACATTGA
						ACTGCTCACCACATCATAGTATCCATTTAAACAGACCCCAACATGTATAAGAAATCCCTTTGTTTTAC
WI-9823	97	C	T	ATGCTTTCCAAATCTGATTTGTATGACTATTGTATGCACAGTTGGATCACC

WI-9651b	105	A	T	---	---	---	TCTACATCTATGGACAACCTCCATGCCCTTGCACATGCTGATCCCTCCTCCTGGAATCCCTTCCCT ACCTGTGCTCATGTACAATTTCTGCTGCTCTCAJATGGGGCAGCTTGCAGGCTCCCTTTAGAC ACCTGTACAGGTACAGCCAGCACTGCCCTACCTCCATGCCACTGCCAGGGAGCCCTTATAGGCCTCTG CTTTAAACCTGTAAATGGTATATTAATCCTTGGTGTGAATGTCTCTC
WI-9651	139	T	C	---	---	---	TCTACATCTATGGACAACCTCCATGCCCTTGCACATGCTGATCCCTCCTCCTGGAATCCCTTCCCT ACTTGTCTCATGTACAATTTCTGCTGCTCTCAAGGGCAGCTTGCAGGCTCCCTTTAGACACCT CT/JACAGGTACAGCCAGCACTGCCCTACCTCCATGCCACTGCCAGGGAGCCCTTATAGGCCTCTGT CTTTAAACCTGTAAATGGTATATTAATCCTTGGTGTGAATGTCTCTC
WI-7676b	309	A	C	---	---	---	GTGACCTTCTGCAGCGTGGAGATGGACATCCTTGTCTGGGACTTGGCCCTGCTATTTATTTTG TATTTATGTCTTAATCTTCCACTGATGCATCCTCAAGGTAGATGGGAGGCTGTGTGAAGGG GCCGCTTCTTGGTGCCTGCTGGTTCAGGGGCAGGAAGCGTGTGGACTGCAGCTTCTGCTGTGTC TCCCCCGTCTCCTGGAGCGATATAGGAGAGAGCAAGGATTGAGT
WI-7676	139	C	T	---	---	---	GTGACCTTCTGCAGCGTGGAGATGGACATCCTTGTCTGGGACTTGGCCCTGCTATTTATTTTG TATTTATGTCTTAATCTTCCACTGATGCATCCTCAAGGTAGATGGGAGGCTGTGTGAAGGG GC/JTGGCTTCTTGGTGCCTGCTGGTTCAGGGGCAGGAAGCGTGTGGACTGCAGCTTCTGCTG GTGCTCCCCCGTCTCCTGGAGCGATATAGGAGAGAGCAAGGATTGAGT
WI-10072	105	G	A	---	---	---	CATTATCTTGTCTTGGTCTGTTCAATCACTTCTCTCTCCAAATGAAGAGGATATTTAAGCATCAT CATCTGGCCCTTTTGGTGTGAATATTTTGTG/JATGACTCTCATGCACATGATAAAATTTGTTA TGCTGTCTTATCTATCTTTTGTATAGGAGTTTGGCCATGACCTTTATGAGGAGAAAGGGA TCACCCCTTTTGGCTCTACAACCTTATAGATATTTAAATATCTTT
WI-9986	42	T	C	---	---	---	TTGGTGTGAACCTCAGAAATATAGGAAAAATAGACAAATTTGAAT/A,CJGTACCCAGGAAACAAGAG CCCTGCACCTTGAACCTCAAAAGGAGTTCTATTTATCTGGCTGTTCAGACTTTATGTATCTTGAGAA GAGAACTGTTTCCCTCTAAATCAGTTTCATCATCTGTATCCAGGTAGTACTCACAAGAACATGTCA ATATCAATAGCATGCATAGGGGTGTGGATCTTAGAACTTATTGCAATT
WI-7041	174	C	A	---	---	---	GTCTATTGCAGGAGAAACGTCCCTTGGCACTCCCACTCTCATCAGGCCAAGTGGAGGACTGGCCAGA GGGCTGCACATGCAAACTCCAGTCCCTGCTTCAGAGAGCTGAAAGGGTCCCTCGGCTCTTTATTT CAGGGCTTGCATGCGCTCTATTCCCTCTGCTCTC/JACCACCTTCTTTGGAGCAAGGAGATGC AGCTGTATTGTGAACAAGCTCATTTGTACAGTGTCTGTATGAATAA
WI-7224	134	T	C	---	---	---	ATAACCCCTTGTGTATGATATCACCCCACTCACTAATATCAACTTATGTGCTATCAGATATCCTCTCT ACCTCAGCTTATTTGAAGAAAAATCCTAAACATCAAACTATCTTCAATCCATAAAAAATGTCAGCATTT /CJATTTAAAAACAATAACTTTTAAAGAAAAATAAGGACACATTTTCAAAATTAATAAAAAATAAG GCATTTAAGGATGGCTGTGATATCTTGGGAAGCAGAGTATCTATGCTAG

WI-10826	132 A C ---	---	---	TCCTATTGCAATTCACAGTAGCCCCATGAAGTAGGTATAACCAGCCTCTATTTTAACTGAGAAGAT GGAGGCCCTTTCCAAATGGACTAAGTAATGTGTCTCAGGTTTTCTTAATAGCAAAGACCTGCA/A/C JCCTGGCTTCTGACTCCAAAGCTTATCCGTTCTCATGCTGTGTCAGCCAGGACCCCATGCCGA GAAAGCCAGCCCTCTCCATCCCCAC
TIGR- A004S25	145 GA ---	---	---	AGATCTGCCATTAGTATTATTCCTTTGAAGATACITTTGGAGATTCAITTTCTTGAGTGGCACTGCAT GCTCAATCAGTGAAGAACTTTGGGGTATAGAAATGGAATGGAGATTTCAAACAGCTTTGCTGAAAC TGACTTTGG[G/A]CTCCAGACTTCACTGCTCTAGGCATTGAAACCATCACCTGGTTTGCATTCCTC ATGACTGAGGTTAACTTAAATGACTGAGGTTAACTTAAAC
WI-1021	24 A T --	---	---	AAACACACAGAATCATCAAGCAC[A/T]ATCTGTGTTTGAGATAAATGATAGTCTGAGTCAOCTATG TAAGAAGTAACCTGAAATAGTAGGATAGTATTATCATTTCTGTAAATAGATTCACCTCTCAGCAAT TGGTCTGTTTTCATTTCTATGGAACCTCTCCGTAAGTAAATTTTCTATGGAACCTCCCCATACTGT AATTGGACAGTTTGGTTCCAC
WI-4687	121 GT ---	---	---	TAGTATGTCACCTGCCATGGTAAGGACCTTTGATCAGTGGAAATAGAACACTTTGAATGGTCTTGTC TTTCAATAAAGAGTGACATGATTGAACATGTGTTTAGATAAAGGGCACCTT[G/T]GCAGGAGTGT TTAGGATGAAGAGAGAGAGATTAAAGGAAGATCAGGAAGAAAGTAGCAATGGGAATGAAATAAG GAGGCCCTGAGATCCACTGGATAATCTAAACCAAGAGAAAGAACTTGAT
WI-4719b	107 TG ---	---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTTAGGCTAGTGTCTTGGGTGTGAGCGGATT ATGCTGACGCCATGGGTGTTTCAATAGTGACTTGAGAGT[G/G]ACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTCAATTCACAAATCTGCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATTCACACTTGTCACACTTATCCTTAAGACATTTTTCACAGGA
WI-4719	70 GA ---	---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTTAGGCTAGTGTCTTGGGTGTGAGCGGATT AT[G/A]CTGACGCCATGGGTGTTTCAATAGTGACTTGAGAGTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTCAATTCACAAATCTGCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATTCACACTTGTCACACTTATCCTTAAGACATTTTTCACAGGA
WI-9484b	216 GC ---	---	---	TCAACACGCTTTTATTGOCACCTCTGGCTCCCTCGTCCAGCAAGATTCTACCTCTTACCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGTGTACCACCTCTCTGACACTGCCAAGT TAAAGAAAACCTGCTTGTGAGAGGGAGGGCCAGACAGGAGGAATTCAGGGCATGTATGGCTC AGTCCCACCTTCT[G/C]ACTGCAGAGTATAGGACCCAGGGTTCCAACTTT
WI-9484	178 G A ---	---	---	TCAACAGCTTTTATTGCCACTTCTGGCTCCCTCGTCCAGCAAGATTCTACCTCTTACCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGTGTACCACCTTCTCTGACACTGCCAAGT TAAAGAAAACCTGCTTGTGAGAGGGAGGGCCAGACAGG[G/A]AGGAATTCAGGGCATGTATG GCTCAGTCCCACTTCTGACTGCAGAGTATAGGACCCAGGGTTCCAACTTT

WI-7330	207 C T	AGGATGGAAGGAGACACGGGGGAGGAGAACTCTCTTCTGCTAAATCGATAGGAGTCAGTTTTGTCT TAAATGCTGACTACAGCCACTGACATGGTTGGCTGGAATTTCTCTTTAAATGTGGCATATAGGTTT GTGACACAAGAAAGTCATCTTTGGTGGCTAAGTTTACTAAGGAAAAATACTGAAAGATTAAAAG TGAGAG[C/T]TGAAAGAGAAATGATAATGCTTCCAACTGTAGCTGTCACAG
WI-9443	211 G A	TTAAAACAGTTTCAGGTTGTGAAGCAGAAAGGATGTGATTACAAATTTAAATGAATCAGTCACATT GCACAAATTAATCCTCTTGGCATCATACAAACTGGGTTTAAATGGCAAATGATGACATCATAGCATGA CCAACTCATGGAAGGAGTCTAGAGTCCATCAGCTCACACCTGAGGGGAAGGCACTGCAACCCA CTGACGAGAC[G/A]CAGAGACCTTGGACTACAGATGACACCATGCCCACTT
WI-7166	59 C T	TCCTCAAAAGAGAAAAACAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA[C/T]GGAT CATCAACAAGATTTCCCTGTGCAAAATATTTGACTATCTGTATCTTTTCATCCTTGACTAAATTCGTG ATTTCAAGCAGCATCTCTGGTTTAACTTGTGCTGTGAACAATGTGAAAGAGTCTTCCAAT TAATGCTTTTATATCTAGGCTACCTGTTGGTTAGATTCAAGGCCCGAG
WI-7259b	189 T C	GCTCTTCCCAGGAAGCGGGGTCTTGGCTGGAACTTCCAGAGAGGCGGGAGCAATTTTAGGC CCACCTGCTCCCATCTGCCCTGCAACAGCTGAGGCTGCTCTCTCTCTGAGTCTCTCTGGGCT GCGCAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTTAACCTGGCCACAGT[C/T]GGGGGAGCAG AGCCAGCAGGTGGACAGGTGTTTGCAGGGGCCCAACTTCCCCTGGAGCTC
WI-7259	188 G T	GCTCTTCCCAGGAAGCGGGGTCTTGGCTGGAACTTCCAGAGAGGCGGGAGCAATTTTAGGC CCACCTGCTCCCATCTGCCCTGCAACAGCTGAGGCTGCTCTCTCTCTGAGTCTCTCTGGGCT GCGCAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTTAACCTGGCCACAG[C/C,T]TGGGGGAGCA GAGCAGCAGGTGGACAGGTGTTTGCAGGGGCCCAACTTCCCCTGGAGC
WI-7322	275 A G	GTACTTTAGGCTGTGAGGGTGGGCATTTAGTGTGACCCCTTGACCCAGGGTTTCTAACAGATGAC CCTGTGAATCATAATTTAACTGCATATATTTATAGCCAGTCACATTTGCCCTCTCACCCCTATATG GCCATAACTGCCTAAGCACTCAGGCCTCCCACTCATCAACCCCTTTGACCAGAGAAAGCACTC TGGTTCTCTATCCCCTTGTACATAGAGATTTGTATGGGCTCTGGCTG
WI-7685	46 T C	TCAGTTCTAGTCTCTGGGGCCACACAGAACTCTTTTGGGCT[C/T]TCTTCTCCCTCTGGATCA AAGTAGGCAGGACCATGGGACCAGGCTTGGAGCTGAGCCTCTCACCTGACTCTCCGAAAAATCCT CTTCTCTGAGGCTGGATCCTAGCCTTATCCTCTGATCTCCATGGCTTCTCTCCCTCTGCCGACTC CTGGGTTGAGCTGTTGCTCAGTCCGCCAACAGATGCTTTTCTGCTC
WI-563	87 G A	TGTGACCAATTTTATTTAGAGGGTTTAAACATGGCCTGACTATCACCTGATGGTGGCCAGAAATTC CTGGGGAGGGCCTCCCT[G/A]CCCTGATCATGTCTACCTAACTGCCTACTCTAACAACTACTACTCC TGTGGTATGGGATCCTAAGCCAAAAAGCTGAAATGAACATGTTCTAGCACTACAGAAATCCCACT GCCCTCAGTAAGGCAATTTTAAATCTCTTTGGATAACCCAGGGCAGAT

WI-931c	191	C A	---				GACCAGGGCACCAGAAAGCCACGGAGCCACAGCCACTAGCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCTCCCTATCCCTACCAACACCTTCCAGTGCTTATTCTGCTGTGTCAAAATGATCCTCT GTTGCTGCACTGTCACTACTGTTGTATGGATTATAATTATGTCCTCAAAAAGCC[C/A]CGAGCCTGG TACAGAAAGGCATGGGAAAGATGTGCAGA
WI-931b	81	A G	---				GACCAGGGCACCAGAAAGCCACGGAGCCACAGCCACTAGCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCTCCCT[A/G]TCCCTCACCAACACCTTCCAGTGCTTATTCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCACTACTGTTGTATGGATTATAATTATGTCCTCAAAAAGCCCGAGCCTGG TACAGAAAGGCATGGGAAAGATGTGCAGA
WI-931	31	A G	---				GACCAGGGCACCAGAAAGCCACGGAGCCAC[A/G]GCCACTAGCCCTGAACCTTGCACACCCCTGGA GTTTCTCTCCCTCCCTATCCCTCACCAACACCTTCCAGTGCTTATTCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCACTACTGTTGTATGGATTATAATTATGTCCTCAAAAAGCCCGAGCCTGG TACAGAAAGGCATGGGAAAGATGTGCAGA
WI-10870b	91	C T	---				GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAACAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGG[C/T]ACCTACTTAGAGCAGTGGAGTACCTGAGTACGACCCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGACCTGTACTCTGTATACAAAATAGGACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCACTTAAATACGTTGCCCCCC
WI-10870	103	G A	---				GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAACAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGGACCTACTTAG[A/G]ACGTGGAGTACCTGAGTACGACCCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGACCTGTACTCTGTATACAAAATAGGACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCACTTAAATACGTTGCCCCCC
WI-7719b	281	T C	---				AGTTTATCTTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGCAATGGTCTGGCCAAAGTCTACAATGTCCCAATATCAAGGACAACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCCATTAGATCAAGACTACACGGTCTATGAGCAATAATGTG ATTCTGGACATTGCCCATGTATAATCCTCACTGATTTCAAGCTAAAGCAA
WI-7719	163	A G	---				AGTTTATCTTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGCAATGGTCTGGCCAAAGTCTACAATGTCCCAATATCAAGGACAACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCC[A/G]TTAGATCAAGACTACACGGTCTATGAGCAATAAT GTGATTTCTGGACATTGCCCATGTATAATCCTCACTGATTTCAAGCTAAA
WI-10396	72	C A	---				GCCTTGGAGTATATCTAACTGGCCTCCACTTTCATTTTCTTGAACATTTGCTATCAACTGGGAA GAGT[C/A]TGTGACTTTATGCCAGTTTCCCTCTCAGATTTTATGACGGTTGTTTTCTTTTGTTA TGCCATTTGAGGGATTGATTTCTTAAACTATGAAGTACTTGGCTGTCTCTCTCCATTGCTGTTACGG TTAACAGCCACCATTTGTAAACACTTTGT

WI-10673	94	C G	---	---	TCCCTTTATGCACCCAGAGATATTTATTAACACCAATTACGTAGCAGGCCATGGCTCATGGGACC CACCCCGTGGCACTCATGGAGGGG[C/G]TCAGGTTGGAACATATGCACTGCTGCCGCCACACA TCCTGCTGGGCCCTACCTGCCCAATTCAATCTCTGCCAATAATCTGCTTATTGTTCATCCTCG GAGAA TTGAAGGAGGTCAAGTTGTTTGTCATGATTTGTCAGAGAACCT
WI-7842	57	T C	---	---	CACAGCCATGCCCTTGAGGAGCGGGCCACAGATGCTGAATCCCTATCCCATCTGT[C/G]GTATGAG TCCCATTTGCCTTGCAATTAGCATCTGTCTCCCCCAAAAAGAAATGCTGCTATGAAGCTTTCTTTCT ACACACTCTGAGTCTCTGAATGAAGCTGAAGGCTTAGTACCAGAGCTAGTTTCAGCTGCTCAGAAT TCATCTGAAGAGAGACTTAAGATGAAAGCAAAATGATTCAGCTCCCTTATA
WI-7721	145	A C	---	---	CTGCTCATCAGCCACTGGAGTCCACACTTGAATTTGGGAGCTACCACGGTCTGCCATGCTCTGG AGGACAAGGGGCCACATCCCCACCCAGCTGTTACCAAGCCCGGGCAGGTGCAGCCCTTCTCTCC TGCTCTG[C/A/C]TCTGACTCTCTTTGAGGTCCTGTATGCTACCTCTGACTTCTGTGTGCCCTCTG TGCTGCTCTCATCCATCTCTTACTGGGGCTGGGGCTAGCCCCAA
WI-4767b	173	C A	---	---	TTTCAGTCTGTTTTATCCTTTTCATTGTCAAAAAGATGCTCTTAGACTGAAATTCATAAAGAGTTCCCT CAGGTCGGGTAAATCCTAGATCTTCTATATCCATTGAGTGTGATGGAGTTGGAGAGGGTATGTTT CTTGCTTGAGAAAATCCTAGAAAGCACAGGGATGACA[C/A]AAATCACTAAGGAAATCCCACTAAGA CTCTCTAACCCAGAGATTTTAACT
WI-4767	50	A G	---	---	TTTCAGTCTGTTTTATCCTTTTCATTGTCAAAAAGATGCTCTTAGACTGA[C/A]ATTCAAAAGATT CCTCAGGTCTGGTAATCCTAGATCTTCTATATCCATTGAGTGTGATGGAGTTGGAGAGGGTATG TTTCTTGCTTGAGAAATCCTAGAAAGCACAGGGATGACAAAATCACTAAGGAAATCCCACTAAGAC TCCTTAACCCAGAGATTTTAACT
WI-7718f	222	C T	---	---	ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAGTG ACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAGAA[C/T]CATGCAAGGAAGGAAAACTATGTATTAAAT
WI-7718e	60	T C	---	---	ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGAT[C/G]CAA GGATTACAGAAACTGATGCCAAGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718d	31	G A	---	---	ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAA GGATTACAGAAACTGATGCCAAGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT

WI-7718c	91 C G ---	---	ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGG[C/G]TGAGTGAGTTCAACTACATGTTCTGGGGCCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718b	248 A G ---	---	ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCCGGAGATAG ACTTTCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATT[G/A]T
WI-7718a	42 A T ---	---	ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGC[A/C, T]GTTACTCCCTACACTGATGC AAGGATTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCCGGAGAT AGATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAG TCAAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAA
WI-7227d	99 G C ---	---	AGGGAATTGTGTTGCTCTCTGGAGGAAGCCAGGCGCATCTAAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTCACTTTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGCTT TTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAGGGACTGAGCTAAACA GTGTTATTATGGGAAGGAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227c	291 G A ---	---	AGGGAATTGTGTTGCTCTCTGGAGGAAGCCAGGCGCATCTAAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTCACTTTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGCTT GGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAGGGACTGAGCTAAACAGTG TTATTATGGGAAGGAATGGCATTGCTGCTTTCAACCAGCGACTAATGCAAT
WI-7227b	93 G T ---	---	AGGGAATTGTGTTGCTCTCTGGAGGAAGCCAGGCGCATCTAAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTCACTTTTCAGACAAG[C/G]CTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAGGGACTGAGCTAAACA GTGTTATTATGGGAAGGAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227a	24 A G ---	---	AGGGAATTGTGTTGCTCTCTGGAGGAAGCCAGGCGCATCTAAACAAGCCAGTAGGTACCTGGC TCCGTGGACCAATTCACTTTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAGGGACTGAGCTAAACA GTGTTATTATGGGAAGGAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7310b	234 A C ---	---	CCCAATGCCTCTCCACGATGTCAAGGACTCCTGTCTGCTGAGGTGGGAGACAAGGAACCTCCG AAGAGGAAGCAAGAAAGCCGCTACTGTCTATGTTGTGATCCTTTCATCGAACAACTGATGCGAAAACT TGAATCTGTTACTGAAATGAGGAGAGAAGGACATGTGCTATTGAACTGAGCCAAACACACTGTAAT ATCCACAGACTCCCTCCCTGCCCCCATCCCA[A/C]ATGATCTTGAGATTTC

WI-7310a	64 T A ---	---	CCACAATGCCTCTCCACGATGTCAAGGACTCCTGTGTCTCTGGAGTGGGAGACAAAGGAACCTT/A JCCGAAGAGGAAGCAAGAAAGCCGTACTGTCTATGTGTGATCCTTCATCGAACAACCTGATGCGAA AACTTGAATCTGTTACTGAAATGAGGAGAGAGGACATGTGCTATTGAACCTGAGCCAAACACACTGT AAATATCCACAGACTCCCTCCCTGCCCCATCCCAATGATCTTGAGATTTC
WI-7878b	162 A G ---	---	CCAGCAACACCTACACCTTGTACCTGCCTGGGACTCCTATGATGGCTGTGGTTGATAATAATCA GATCATGCCCAAGACGGCCTCCTGATAATCGTCTTGGCATGATTGCAATGGAGGGCAAAATCGGTCC CTGAGGAGAAAATCTGGAGGAGCTGAG/GGTGTGATGAAGGTGTATTTGGGAGGGAGCACAGTGT CTGTGGGAGGCCAGGAAGCTCTACCCAAGATTGGTGAGGAAACTA
WI-7878a	51 C G ---	---	CCAGCAACACCTACACCTTGTACCTGCCTGGGACTCCTATGATGGCTGTGGTTGATAATAA TCAGATCATGCCCAAGACGGCCTCCTGATAATCGTCTTGGCATGATTGCAATGGAGGGCAAAATGC GTCCCTGAGGAGAAAATCTGGAGGAGCTGATGTGATGAAGGTGTATTTGGGAGGGAGCACAGTG TCTGTGGGAGGCCAGGAAGCTGCTACCCAAGATTGGTGAGGAAACTA
WI-7381c	213 C T ---	---	CTCCACATTCACAGGCCTTGAGCAGAAATTTCTGAGACTGAAGGGAAATCCCCCTTTCTTTCTACC AGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTTCTGCTATGGTGAGATC AGATGTGCCAAGGAAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAGACA AAACGGCCTCTGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381b	54 C G ---	---	CTCCACATTCACAGGCCTTGAGCAGAAATTTCTGAGACTGAAGGGAAATCCC/C/GJCTTTCTTTCT ACCAGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTTCTGCTATGGTGAG ATCAGATGTGCCAAGGAAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAAACGGCCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381a	53 C G ---	---	CTCCACATTCACAGGCCTTGAGCAGAAATTTCTGAGACTGAAGGGAAATCCC/C/GJCTTTCTTTCT ACCAGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTTCTGCTATGGTGAG ATCAGATGTGCCAAGGAAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAAACGGCCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-1017b	93 G A ---	---	AAATTGCTCTATTTCGGACCTCATATTAAATAAGAGCAATGAGAGCGGAGGAAATTTGAACCTCTCTC AGGTACTGACTGTGGACCCAGACAAAG/GA/GATGTAGATTGTACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTTCTCCCATTTTACAAATAAGGAGACAAAAATTTAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGTGAGGTTTGTCCC
WI-1017a	92 G A ---	---	AAATTGCTCTATTTCGGACCTCATATTAAATAAGAGCAATGAGAGCGGAGGAAATTTGAACCTCTCTC AGGTACTGACTGTGGACCCAGACAAAG/GA/GATGTAGATTGTACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTTCTCCCATTTTACAAATAAGGAGACAAAAATTTAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGTGAGGTTTGTCCC

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WI-1795b	130 T C ---	---	---	GAAGCAACCAGAAAGTATCTTTATCCCATCTAGATTATGCTGGTTCTTCAGACTCCTACGATTA AATTGTATGCATGTGAACAACACTGATGAGGTACTTAGATCTCAGTCTGCTTTGCAGAAAGAAAGT/CJC GTCTACCATTTTCAACAAAATTCGTAGTACAAATTTAAGTATCTCTGTTATCTCCCTTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATTT
WI-1795a	47 T C ---	---	---	GAAGCAACCAGAAAGTATCTTTATCCCATCTAGATTATGCTGGTT/CJCTTCCAGACTCCTACGA TTAAATTGTATGCATGTGAACAACACTGATGAGGTACTTAGATCTCAGTCTGCTTTGCAGAAAGAAAGTC GTCTACCATTTTCAACAAAATTCGTAGTACAAATTTAAGTATCTCTGTTATCTCCCTTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATTT
WI-10616d	136 GA ---	---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCCGGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCCTGGTCTCTCTATCACATTGCCA C/GAJTAGCCCTCCCTTCCCTTCCCTTACAGGCCCTCTTACGGGCCCGGAGTCCCTCTGAGACTCCC ATGGATCATTCCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTTTGT
WI-10616c	136 GA ---	---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCCGGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCCTGGTCTCTCTATCACATTGCCA C/GAJTAGCCCTCCCTTCCCTTCCCTTACAGGCCCTCTTACGGGCCCGGAGTCCCTCTGAGACTCCC ATGGATCATTCCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTTTGT
WI-10616b	141 C T ---	---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCCGGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCCTGGTCTCTCTATCACATTGCCA CGTAGC/CJCTCCCTTCCCTTCCCTTACAGGCCCTCTTACGGGCCCGGAGTCCCTCTGAGACTCCC ATGGATCATTCCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTTTGT
WI-10616a	116 GC ---	---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCCGGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCCTGGTCTCTCTATCACATTG CCACGTAGCCCTCCCTTCCCTTCCCTTACAGGCCCTCTTACGGGCCCGGAGTCCCTCTGAGACTCCC ATGGATCATTCCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTTTGT
WI-1126c	52 GA ---	---	---	CTCTTATTTCTCTGGGCACTGCTTTCTTTGGGGCAAACTTCCAGTATCACTG/AJATACTAATAA AAACCCCTGTAAGTCTGCTTGCATTTTCAAGATTCAATATATATCCAGATTGTTTTCCAGCAAGAA AATTTTATTTCTCAAGATATAAAAAATAAATATTTAATTCAGTTTCTCAAAAGGAATATGAAATT TGTTAAATGCAATCCAGCTGTAACTTTTTTGGACTTGCTTTATTTCTT
WI-1126b	230 T C ---	---	---	CTCTTATTTCTCTGGGCACTGCTTTCTTTGGGGCAAACTTCCAGTATCACTGATCACTAATAAAAA CCCTGTAAGTCTGCTTGCATTTTCAAGATTCAATATATATCCAGATTGTTTTCCAGCAAGAAATTT TTATTTCTCAAGATATAAAAAATAAATATTTAATTCAGTTTCTCAAAAGGAATATGAAATTTGTT AAAATGCAATCCAGCTGTAACTTTTTT/CJGGACTTGCTTTATTTCTT

WI-1126a	97 T C ---			CTCTATTCTCTGGGCACTGCTTTCTTTGGGGGCAAACTCCAGTATCACTGATCACTAATAATAAAAA CCCTGTAAGTCTGCTTGCATTTTCAAGATT/CJCAATATATATCCAGATTGTTTTCCCGCAAGAAAA ATTTATTTCTCAAGATATAAAAAATAAATAATTAATTTAGTTTCCCTCAAAAGGAATATGAAATTT GTTAAATGCAATCCAGCTGTAACTTTTGGACTTGCTTTTATTCTT
WI-11183c	124 C T ---			TAGTGCTAATTTTGGAAAAAGTTTGCTGATTTTAAAAATCTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTG/CJACTAACA TTATGACATACAAATGACCAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAATATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-11183b	192 T C ---			TAGTGCTAATTTTGGAAAAAGTTTGCTGATTTTAAAAATCTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGCTCACTAACATTT ATGACATACAAATGACCAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAAT/CJATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-11183a	118 C T ---			TAGTGCTAATTTTGGAAAAAGTTTGCTGATTTTAAAAATCTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGCTCACTAACACA TTATGACATACAAATGACCAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAATATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-10770b	174 G A ---			GCTTGGTTGCTTAGTCTTATTGTCTCAGTCTTGAGTTCTCCCTTTCTG/CJCTGGCCCTTTTGATTT TCACCCATACCTCTATGCCTGCTCAGACCAATTCCTCTATCTGGAGCGCTCTTCTTGACTTTCTC CTGTTCAACCAACCTTCTTTTATTCTTCAGGACACTCAGTTACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTTCTGTGTCCTTTCCC
WI-10770a	49 G T ---			GATGACAACTTCTGCTGTGACCCCTTAGTCTTGCTCATGACACTTTCAATCTCTGCCCTGTATCATGG TTATCACTGGACA/CJTAGCCACCTCCCAGCAGGCTTAGAACTCATGAGTAAGGACCCCTGTCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAACTTGCAITCT
WI-9667b	82 C T ---			GATGACAACTTCTGCTGTGACCCCTTAGTCTTGCTCATGACACTTTTCAATCTCTGCCCTGTATCATG G/CJTATCACTGGACACACCCACCTCCCAGCAGGCTTAGAACTCCATGAGTAAGGACCCCTGTCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAACTTGCAITCT
WI-9667a	68 G C ---			GATGACAACTTCTGCTGTGACCCCTTAGTCTTGCTCATGACACTTTTCAATCTCTGCCCTGTATCATG G/CJTATCACTGGACACACCCACCTCCCAGCAGGCTTAGAACTCCATGAGTAAGGACCCCTGTCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAACTTGCAITCT

WI-10400d	189 A G	ACATTTTATTAGCAAAACAAATCAGCAAAATAATAAATAGAAAGTAATTGCATTTTCAGACATCTGCTG GTTAACTGTTATAAGATGTTTAGCACACATGTAAAGCACTTACTAACACAATATTTTATTCTAAATTT TCCTTCCCTTACCTTTACTCTCCCAACCAAAATACGTAAGTACCTATGTC[AG]TGCCATGTAG TTTTTGGTTCATTTACTTGCAAATATTCAAAGGCGTTAATGCATTATG
WI-10400c	168 A C	ACATTTTATTAGCAAAACAAATCAGCAAAATAATAAATAGAAAGTAATTGCATTTTCAGACATCTGCTG GTTAACTGTTATAAGATGTTTAGCACACATGTAAAGCACTTACTAACACAATATTTTATTCTAAATTT TCCTTCCCTTACCTTTACTCTCCCAACCAAAATACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCATTTACTTGCAAATATTCAAAGGCGTTAATGCATTATG
WI-10400b	165 A G	ACATTTTATTAGCAAAACAAATCAGCAAAATAATAAATAGAAAGTAATTGCATTTTCAGACATCTGCTG GTTAACTGTTATAAGATGTTTAGCACACATGTAAAGCACTTACTAACACAATATTTTATTCTAAATTT TCCTTCCCTTACCTTTACTCTCCCAACCAAAATACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCATTTACTTGCAAATATTCAAAGGCGTTAATGCATTATG
WI-10400a	46 T C	ACATTTTATTAGCAAAACAAATCAGCAAAATAATAAATAGAAAGTAATTGCATTTTCAGACATCT GCTGGTTAACTGTTATAAGATGTTTAGCACACATGTAAAGCACTTACTAACACAATATTTTATTCTA ATTTTCTTTCCCTTACCTTTACTCTCCCAACCAAAATACGTAAGTACCTATGTCATGCCATGT AGTTTTTGGTTCATTTACTTGCAAATATTCAAAGGCGTTAATGCATTATG
WI-10809b	78 C T	AAAGGGCTACAAACTAAGGCCAAAACCATGAACGGTATAAGGAGGGTAAATGCAAGGGGAGACCC CACCTCTCACCA[CT]TAGAAAAGGGCATTTCAAGCACATTCATGAGGCTTCATATACTGGTTAG CAACAAATGGAATGATTAGCCCAAGGCAGGGTATGGACCAAAAGTGCCAGTGATGAGGCCACA GTGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-10809a	33 C T	AAAGGGCTACAAACTAAGGCCAAAACCATGA[CT]GGTATAAGGAGGGTAAATGCAAGGGGAGAG CCCCACCTCTCACCACTTAGAAAAGGGCATTTCAAGCACATTCATGAGGCTTCATATACTGGTTAGC AAACAAATGGAATGATTAGCCCAAGGCAGGGTATGGACCAAAAGTGCCAGTGATGAGGCCACAG TGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-7038c	266 T C	CGAGCTTGGGATAAAGCAAGGGGACCTTGGGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAAATCTGAGATGCTGGGCTGTCTCTCCCTCCAGGATGCTGGGCCCCAGCCTGGCCAGAC AAGAAGACTGTCAGGAAGGGTCGGAGTCTGTAACCAGCATACAGTTTGGCTTTTTCACATTGAT CATTTTATATGAAATAAAAGATCCTGCATTTATGGTGTAGTTCTGAGTCC
WI-7038b	140 A C	CGAGCTTGGGATAAAGCAAGGGGACCTTGGGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAAATCTGAGATGCTGGGCTGTCTCTCCCTCCAGGATGCTGGGCCCCAGCCTGGCCAGAC AAG[AC]GACTGTCAGGAAGGGTCGGAGTCTGTAACCAGCATACAGTTTGGCTTTTTCACATT GATCATTTTATATGAAATAAAAGATCCTGCATTTATGGTGTAGTTCTGA

WI-7038a	31	G A	---	---	CGAGCTTGGGATAAAGCAAGGGGACCTTGGC[G/A]CTCTCAGCTTCCCTGCCACATCCAGCTTGTG TCCCAATGAAATACGTAGATGCTGGGCTGTCTCCCTTCCAGGAATCTGGCCCCCAGCCTGGCCA GACAAGAAGACTGTCAGGAAGGTCGGAGTCTGTAACACAGCATACAGTTTGGCTTTTTCACATT GATCATTTTATATGAATAAAAGATCCTGCAATTTATGGTGTAGTTCTGA
WI-3429b	64	G T	---	---	ATACGCTTCTGTCTGCCACAGTGAACCAAGCAGCACCAGTGGCCAGGGTCGGGCTCCACACA[G/T] CCCTCAGCCCCCTTCACTTTGCAATGTGTCATCGGTGACTCAGCACAGAGTTTCCAACCTCATGTGA CAAAATACAGATCCCAAGTCTCCTCTCCTGGATTGGATCTAGCAAGACCAGACGAGCGTCCCTAGAA TCCTGACTGTTAAACAAGCACTCCAGGCAATCTTAAGACCAAGCACGGAGC
WI-3429a	62	C T	---	---	ATACGCTTCTGTCTGCCACAGTGAACCAAGCAGCACCAGTGGCCAGGGTCGGGCTCCACACA[C/T]AG CCCTCAGCCCCCTTCACTTTGCAATGTGTCATCGGTGACTCAGCACAGAGTTTCCAACCTCATGTGA CAAAATACAGATCCCAAGTCTCCTCTCCTGGATTGGATCTAGCAAGACCAGACGAGCGTCCCTAGAA TCCTGACTGTTAAACAAGCACTCCAGGCAATCTTAAGACCAAGCACGGAGC
WI-6786c	151	G A	---	---	ATTTAGGACAGTGAAAAAGGGATTATAAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAAAGGATAAAGAGTGAGTGACGGTGACCT GTAGCCCCATCTCT[G/A]TGGGATAAGGTGCCATTTGTTCTTGGAGGTGAAATGCCACATTG TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6786b	111	A T	---	---	ATTTAGGACAGTGAAAAAGGGATTATAAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAAAGGAT[AT]AAGAAAGTGAGTGACGGTGA CCTGTAGCCCCATCTCTGTGGGATAAGGTGCCATTTGTTCTTGGAGGTGAAATGCCACATTG TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6786a	106	A T	---	---	ATTTAGGACAGTGAAAAAGGGATTATAAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAA[AT]GGATAAAGAGTGAGTGACGGTGA CCTGTAGCCCCATCTCTGTGGGATAAGGTGCCATTTGTTCTTGGAGGTGAAATGCCACATTG TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6711b	226	G T	---	---	GGCTATTTGTAATGCTTGGTTATTGACTCCAAAATTGAATAGTATGGGGAAGAAATCCCTCACCT ACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCCCTAAACCTTCACTTCACTCTGAAT TTCATATACCTCCATTATAATCAATACATCATTCGAGAGAAAGAACACGGTGCCAACTGGGTT TGTTGGTGGCTGCACACCCACA[G/T]TGGCAACTAAGTGAATCTCTAAA
WI-6711a	36	T C	---	---	GGCTATTTGTAATGCTTGGTTATTGACTCCAAA[AT]TGAATAGTATGGGGAAGAAATCCCTC ACCTACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCCCTAAACCTTCACTTCACTCT GAATTCATATACCTCCATTATAATCAATACATCATTCGAGAGAAAGAACACGGTGCCAACTG GGTTGGTGGTGGCTGCACACCCACAGTGCGCAACTAAGTGAATCTCTAAA

WI-10613b	172 A C ...			ATTGATGCCAAATCATAATACCCCTGCATTCTAGAAACATACAGTGTAAATAGAAATTTTGAGCCATA TGGTGAAAAATTTAGAAAGTATTATCTCTATATGTATATCTAGCTTTAACATCAATGAATGTGATTT TTTGCAACTTTTGACAAGGCCAGGCAATTTTATTTG[A/C]GCCCTAGGAGGTTACTATAATTTAGA AAGGCTCTTACCTTCCACTCTATAATTTAAGTCTCGGACTTAGGATGTAG
WI-10613a	44 G A ...			ATTGATGCCAAATCATAATACCCCTGCATTCTAGAAACATACA[G/A]GTAAATAGAAATTTTGAGCC ATATGGTGAAAAATTTAGAAATTTATCTCTATATGTATATCTAGCTTTAACATCAATGAATGTG ATTTTGTCAACTTTTGACAAGGCCAGGCAATTTTATTTAGCCCTAGGAGGTTACTATAATTTAG AAAGGCTCTTACCTTCCACTCTATAATTTAAGTCTCGGACTTAGGATGTAG
WI-7587c	133 A T ...			GCTCTAGTGGGAAACCTCAGGTAGTCTCCGAAGATCTGTCTTTCCAAAGTGACTACCCCTTGAAAGC ACATCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAA[A/V] TJGGAATGAACCACTCCCTGCCATTCCTATAAGAAATATCCAAAGACCCAGGCAATTTTGCCCTCT TTCCACATGCCCCCATATGTCTGAGCCAAACTGCACCTGGGGCTGCCCTC
WI-7587b	81 G A ...			GCTCTAGTGGGAAACCTCAGGTAGTCTCCGAAGATCTGTCTTTCCAAAGTGACTACCCCTTGAAAGC ACATCCCTTCTG[G/A]ATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAA AGGAATGAACCACTCCCTGCCATTCCTATAAGAAATATCCAAAGACCCAGGCAATTTTGCCCTCTT TCCACATGCCCCCATATGTCTGAGCCAAACTGCACCTGGGGCTGCCCTC
WI-7587a	28 C T ...			GCTCTAGTGGGAAACCTCAGGTAGTCTCCGAAGATCTGTCTTTCCAAAGTGACTACCCCTTGAA AGCAGATCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAA AGGAATGAACCACTCCCTGCCATTCCTATAAGAAATATCCAAAGACCCAGGCAATTTTGCCCTCTT TCCACATGCCCCCATATGTCTGAGCCAAACTGCACCTGGGGCTGCCCTC
WI-10681b	103 T A ...			ATGACTCAGGTGACAAAAGAGCATGTCTAGACCCCATTGACTACGCAAACTCAATCAGCCAACC ACAGAAAAGCTAAAGACATCCTTTTAAAAAGCC[T/A]AAAGACAGCCATTTTAACTCTAATTCG TAGTTTATGATTTTCTCAAAATTTCCCAACACACAGAAAAGAACTTCAAGGTAGGTTCTAATGTTA CCATTGCTAACACTATTGTCTTTGGAGAAGGAGGAGTGACGCTCTGTAAAAG
WI-10681a	41 A T ...			ATGACTCAGGTGACAAAAGAGCATGTCTAGACCCCATTG[A/T]CTTACGCAAACTCAATCAGCCA ACCACAGAAAAGCTAAAGACATCCTTTTAAAAAGCCCTAAAGACAGCCATTTTAACTCTAATTCG TAGTTTATGATTTTCTCAAAATTTCCCAACACACAGAAAAGAACTTCAAGGTAGGTTCTAATGTTA CCATTGCTAACACTATTGTCTTTGGAGAAGGAGGAGTGACGCTCTGTAAAAG
WI-7222c	126 G T ...			GCCTCTCCTCAACTGTCTGGACCCCAAGGCTAGGAAAGGCTGCTTGAATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCCGAGTGAGCTCAGGTGTACCCCTGTTCTCAAGTTGGGGGATGGG[G/T]AATAA AGGAGGGGAATTCCTTGAACAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGAAGTTGTATTTCAAAGACTCGAATTCATTTT

WI-7222b	255	G A	---			GCCTCTCTCAACTGTCTGGACCCAAAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTACCCCTGTTCTCAAGTTGGGGATGGGAATAAAGG AGGGGAATTCCCTTGAACAAGAAGAACTGGGGATAGTTATATTCACCTGCCCTTGAAGCTTTAA GACAGTGATTTTGTGAAGTTGTATTTCAAGACTCGAATTCATTTCTCA
WI-7222a	126	G T	---			GCCTCTCTCAACTGTCTGGACCCAAAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTACCCCTGTTCTCAAGTTGGGGATGGG[G/TAATAA AGGAGGGGAATCCCTTGAACAAGAAGAACTGGGGATAGTTATATTCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGAAGTTGTATTTCAAGACTCGAATTCATTT
WI-8054d	41	C A	---			AAAGATGACACTTAGAACTGGATGACCTTGGCCCTTCTCTTC/AJTATCTCTCTCCAGTTCAAAATG CTTGATCTTTTAATAGCCAGCATTCCTTAGATCTGCAGTTGGCTCAACGCACCTCAAGCCTTAGCA CAATCTCTTTGTAGTTTTCAGCTTTTCCGGAAATCGGCTTAGTTGCCCACCATAGCCACTCTGCT TCCTGTCAACGCCGCTTCCCTGGCGTACAGAGAAATCCTTGCCCTT
WI-8054c	237	G T	---			AAAGATGACACTTAGAACTGGATGACCTTGGCCCTTCTCTTCATCTCTCTCCAGTTCAAAATGCTT GCATCTTTTAATAGCCAGCATTCCTTAGATCTGCAGTTGGCTCAACGCACCTCAAGCCTTAGCAAA TCTCTTTGTAGTTTTCAGCTTTTCCGGAAATCGGCTTAGTTGCCCACCATAGCCACTCTGCTCC TGTATAACGCCGCTTCCCTGGCGTACAGA[G/TAATCCTTGCCCTT
WI-8054b	148	T C	---			AAAGATGACACTTAGAACTGGATGACCTTGGCCCTTCTCTTCATCTCTCTCCAGTTCAAAATGCTT GCATCTTTTAATAGCCAGCATTCCTTAGATCTGCAGTTGGCTCAACGCACCTCAAGCCTTAGCAAA TCTCTTTGTAGTTTTCAGCTTTTCCGGAAATCGGCTTAGTTGCCCACCATAGCCACTCTGCT TCCTGTCAACGCCGCTTCCCTGGCGTACAGAGAAATCCTTGCCCTT
WI-8054a	131	C G	---			AAAGATGACACTTAGAACTGGATGACCTTGGCCCTTCTCTTCATCTCTCTCCAGTTCAAAATGCTT GCATCTTTTAATAGCCAGCATTCCTTAGATCTGCAGTTGGCTCAACGCACCTCAAGCCTTAGC/GJA CAATCTCTTTGTAGTTTTCAGCTTTTCCGGAAATCGGCTTAGTTGCCCACCATAGCCACTCTGCT TCCTGTCAACGCCGCTTCCCTGGCGTACAGAGAAATCCTTGCCCTT
WI-10854b	152	G T	---			TTCCACAAAACCTCCCTGGCCGGGTGACTAAGATGAGAAAGTGGGAGAACTGGATAGTTTAATAA ATGTTTATATTTACTTTAAAGCGAAGTTGAACACGAGACGATAGTTAACGCTCTGGTAAGTTTAT ACGGTGTGCGAGGCAACA[G/JGGAGAGGTACGGGAATAGTTCTACTTCTGTTTATTTCTTG TTTTAGACACAGGGTCTGCTGTG
WI-10854a	102	C T	---			TTCCACAAAACCTCCCTGGCCGGGTGACTAAGATGAGAAAGTGGGAGAACTGGATAGTTTAATAA ATGTTTATATTTACTTTAAAGCGAAGTTGAACA[C/JTGAAGACGATAGTTAACGCTCTGGTAAGTT TATACGGTGTGCGAGGCAACAAGGAGAGGTACGGGAATAGTTCTACTTCTGTTTATTTCTTG TTTTAGACACAGGGTCTGCTGTG

WI-9826b	127	G A	AATTTATATGGAAGGTTAGCAAACATATGGCCACAGGCCCATCTAGCCATGCTATTTTTGTG TGCCTGATGGCTGTTGGTGTGTCACGCAGTTGAGCCATTGTGACAGAGGCTGTTATGAJGCCTT CAAAGCCAAAAAATAATTTACTCTCTGGCCTTGACGGAAAGTTTGCTGATCTAGATATTTAAA GGCAGAGAAGATCAGAAAGTTGAA AATTTATATGGAAGGTTAGCAAACATATGGCCACAGGCCCATCTAGCCATGCTATTTTTGTG TGCCTGATGGCTGTTGGTGTGTCACGCAGTTGAGCCATTGTGACAGAGGCTGTTATJTGGOCTTC AAAGCCAAAAAATAATTTACTCTCTGGCCTTGACGGAAAGTTTGCTGATCTAGATATTTAAAAG GCAGAGAAGATCAGAAAGTTGAA
WI-9826	125	A T ...			---	TGACATTATAT AAACGTAAAA GAAAAATGT
WI-15986	60	T G	TTGTTTGTGT	TTGGGTTTTT	GAAAAATGT	CGGACACGTGATATACAAATACAGATCGTATGGGTTGTTGTGTGGGTTTTTTTTTTT/GJTTAC ATTTCTTTTACGTTTATATAATGTCAGCAITTCAA
WI-8655	29	A G AG	AACTGCAAAT	AGGAAACCAG	CCACCTGGGSC TCCC	TTCAAGTAACTGCAAATAGGAAACCAGAGAG/GGGAGCCCCAGGTGGGACAAATCATGGCTACCCC TCCCAACAGAACAGGGGGAGGAGGTGGCCCTACACCCCTTTAT
WI-8170b	259	G A ...			---	GCACCTCTCTCTGAGCAACAGGTACACTTTTTTCTCTAACATTGATCTATAACACACCAGAACCG TGTTTAATAGCTGCTGATAAATGAACCTATTTTAAGTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTGTGGAGAGATTACAAGGTTAAGATCATGTGCCATCAAGTGCAATCCTATCAATCAGAA ATAAAGGTAAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACACAAGA
WI-8170a	204	T A ...			---	GCACCTCTCTCTGAGCAACAGGTACACTTTTTTCTCTAACATTGATCTATAACACACCAGAACCG TGTTTAATAGCTGCTGATAAATGAACCTATTTTAAGTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTGTGGAGAGATTACAAGGTTAAGATCATGTGCCATCAAGTGCAATCCTATCAATCAGAA A/T/A/AAAGGTAAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACACAC
WI-8172	136	C G GACA	CCTTTATTAA	ATTGTTTCTT	GAAGAGAAAT GTAATACCTGT AAAGGTAC	CAGGATTCCTTAAGTCATCTTCCAATACTCCAGGTACATGGTGAAGAGTCACCTGTTAAACACGAA ATCTAACCATTAACAAGCTTTTAAATCCTTCGGTAACCTCCTTTATTAATAATGTTTCTTGACAT A/C/GIAGTACCTTTACAGGTATTACATTTCTCTCACCGTTTACA
WI-8183	56	G A TGC	TGAAATAAAA	ACAATTTCTGT	TGTGTTGAAAT CAACCTGC	AGCAGGTTTGAATGATCCCTTATTTACATGAAATAAAACAATTTCTGTTGC/GA/GCAGGTT TGATTTCAACACAGTTGAATCTGTAAACCAAGCTGTTTCTGATGCAGGACAAATATCCACAAT ATTTAAACTGCAAGCACCATGC
WI-14149	83	CT ...			---	GCCTTATGGGATTGCAAGGTTACAAGGTTAAAGACAAAACCAAGCATGGGATTTTGCCGGAAT ATTAGCGTTAAAGGAG/C/JTGAGTTGAGTCAAAACACGGG
WI-8712	44	G A G	CACAGGGAAG	AGGTAGTGGA	CAGGAAGCCTG ACCATCTC	TCACAATGACACTGTGTAAACAGCACAGGGAAGAGGTAGTGGAG/GA/GAGATGGTCAGGCTTCTCTG TTCCTTAACAGCAGAGCCCGACCAACCTAGAACGCCCTCACCTAGCCTCTTAAT

WI-8827	22	C	T	TCCTGGGAG ACTATGG	GCATTAGGAT TTTAGTGTCA C	GGTGTCCCTGGGAGACTATGG[C/T]AGTGAACACTAAATCCTAATCGCCATGCATTGGAATTATT CCGACTATTACTTTCTTAGTCTCTTATCCACCCAGTCTCT
WI-8833	51	A	T	TTTCATGOC ATTCTCTG	CCTCACACATT ATAGGGGCA	CTCCGGCCTCTTAAAGCTCTCTAGACTGCTCTTCCATGCCATTCTCTG[A/T]TGCCCCCTATAATGT GTGAGGGTATTACAATAGTCCCTATTCAAACCTGCCITGTGCTATAAAAGGTCAGCTATGT
WI-8377	63	A	G	---	---	ATTTTTAGCCATGTTGGTAAAGTTCATTTTCAGTACATGGGTAAACCCAGGCCCTTCC[C/A/G]T TATATCCAGGTATGCTACAAGTCTTTAACTCTTATCAGAAGTTATTACTGTTCTCTTAGAGAG GCTACAGGCTAAATTCACCTAGTTGGTTGTCTAATGTCTCATTTTATCTGAAAGCTCGTG
WI-8850	21	A	G	GGGACTTAAC CTTTGGCCT	CAACAGCCA GGCAGG	GAGGGACTTAACCTTTGGCCT[A/G]CTGCCCTGGCTGTTGGCTCTGCGCTGCTGTTTTGGTTCTT TCTCTTCTACTGGTCTTCTTTGTCTTTTGCAGCCACCTATGCTGCTGT
WI-8853	79	C	T	CCGGGCAATG AGGATA	AGTCTTCTGA GCCCTCCAT	ACTTTCTTGAAGTGAACCTCATCTCTTACTCTTGGTTGATAACGCTGGTTAATCCCCGGG CATTGAGGATA[C/T]ATGGAAGGCTCAGGAAGACTTCATTCTCAA
WI-8865b	52	A	G	---	---	AGGTGACTGGGAATCACAGGCACAGACTGAGGAAGACAGTCAATGTCGAACA[A/G]JACAACATGCT TCGGACTTACCAAAGGAGAGTCGAGCTTTCCATATAA
WI-8865a	42	T	C	CACAGCTGA GGAAGACAGT CA	GGTAAGTCCGA AGCATGTTG	AGGTGACTGGGAATCACAGGCACAGACTGAGGAAGACAGTCA[T/C]GGTCGAACAAACAACATGCT TCGGACTTACCAAAGGGAGAGTCGAGCTTTCCATATAA
WI-8895	32	A	C	---	---	GTGCCACAAACCTGGACACCAACCAAGAA[T/A/C]CTCCCCCTTTGAAATTTCCATTAAAGAGCA CAATGGGGTAATTATACCAGGATGCTCCAATCGCTTTTC
WI-8456	93	G	C	---	---	CCTTTAAAGTCACAGTCAACTCGACTGTGGACTGATATATTTTGAAATATAATAAACTCTTTTCC AAGCTCCCATGCTTGGATGTCACA[G/C]TTATGTCAAAGTTAATATAAACATTTCTAAGTGTCACTC TCAACTCTGTGTTATCTTGCCATGGTCCAGTAACAGTTCAACGGCAGACCAAGTTGTGTAGCAC TGGCATAGACGAGGGCTTCTCAAACCTCCGCTCGCTCAGTCAACCAC
WI-8496b	157	A	G	---	---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGATGGTAATGTTGTATCAGTGCATATTTCTATGGAAA ATTATATCTCAAGTAAGTACCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAGGTCA AAGACACAATGCTGCCAATGCA[A/G]TTAGTATATAGAAATAATACGCAGCTGTTAGAAAAAGTCT GTGGCCAAAGTGGGATAAAACAGTAGCAGTGCAC
WI-8496	41	G	A	---	---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGATGGTAAT[G/A]TTGTATCAGTGCATATTTCTATGG AAATTCATATCTCAAGTAAGTACCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAG GTCAAAGACACAATGCTGCCAATGCAATTAGTATATAGAAATAATACGCAGCTGTTAGAAAAAGTC TGTGGCCAAAGTGGGATAAAACAGTAGCAGTGCAC
WI-14153	28	A	G	GTGCAGGAAG GCCAGC	AACGGCAGGA GGGGA	CTGCAGGTCTATGTGCAGGAAGGCCAGC[A/G]TCCCCCTCTGCCGTTGTCAACCCACATCCACAGAGCA GCCCCAGTGGCAGGCCACTGCCACCCAGGCACACGGGAACAGGACCCATGCTGTC

WI-12108	40 C T A T A	TGAAAAGGG TAAACTCAA	TTGACCTGGTA TAATGAAAGT ATTTC	TCATGTATTACTTTCTGGAAAAGGGTTAAACTCAAATATC[C/T]GAAATACTTTCAATTATACCAGGT CAAGAAAATGCCACAGCCAGAAAATTTATTTAA
WI-5989	29 G A C A G G C A	CCACAAAGGT CACAGGCA	GGGTATAACAG AACCGTATGTA CG	CAGGCAAAACGTCCACAAAAGGTACAGGCA[G/A]CGTACATACGGTTCTGTTATACCCCATATATTAC CCCTTCATGTCTCTAAAGAGACATTTCTCTTAGAGATTTTCATTTTAGTGATCTTTAAAAAAAAT CTTGTTAACTTGCTCCCATCTTTTCTTGGTGAGGACACC
WI-12201	61 C T C O T G C A T G	CCACTGATCA COTGCATG	CCGACCACATA CCTGGC	ATAGTCTTTAGCCTTTTCTGGAGTGTATGTCCCAAGCCCACTGATCACCTGCATG[C/T]GCCA GGTATGGTGGGGGTGTGACGCTGGGTTGCAGCCCTCCACTGCTCGATAAAAGGC
WI-12018	31 A T T C T G A C T T	GGCAGCCAGC TCTGACTT	GGAGAGATGAC AGAAACAGAG AG	TTTTATCTGTGAGGAGCCAGCTCTGACTT[A/T]CTCTCTGTTTCTGTCTCTCTCCCCACATACCA ACTTCTTCAACATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGAAAATTAGAC AGTGAAGCATGTTGCAG
WI-14162	57 A G C C T C	TGGCTCGCTG CCTC	AGGGATCAAA GAGAAAAGGC	TTTTTCGTTTGTAAATGATCCGAATGCTTGAGAAGAAACCCCTGGCTCGCTC[A/G]GCCTTTT CTCTTTGATCCCTGAGTTGCTGAGATTAAAGATGAGGTCCCAAATGAGAGCTACCAAGATGTAGTCG AGCGG
WI-15407	92 A G T T	CATGCCCTTTA AGGATTAAGT GTT	TCTTTTCTCTTT TGGTAGTGTGG	AGCATGTAAGGAGCAGTTTTATTGATTGGTATATTCAGGTTCTAACCCAGCTGAAAAATTCAAATA CATGCCCTTTAAGGATTAAGTTTAA[G/C]CCACACTACCAAAAGAGAAAAGATTTATATGATCACAT ATAAGCAATGGAATCAGCA
WI-12319	109 T C A A T T	GTTGAGTATT GTTCTGCTCAT	GGGAAGTCTG GTACATATTGG	TCTGATGTCATTTATTGGCACAAAAATTATTCTGATACAACATGGTGTCTAGACATGGCTACACTTTA TACTTTGTGCATTTAGTTGAGTATTTGTTCTGCTCATAATTT[C/C]CCAATATGTACCAGACCTTCCC
WI-12326	25 G A C A	GACAGACTTC AAAAGCAAAT CA	AGGTTGAAAA TATGTATTAAAG TACTTTGT	CTGACAGACTTCAAAAAGCAATTCAC[G/A]CTTCCAGAATACAAAAGTACTTAATACATATTTTCAAAG CTGTTTGCAATTTCAAAACAAAGTTAGCGTTTTTGTAAATCAAATTTGATAACCCGACTAAAAAT
WI-12361	63 C T	TTAAATCCACACTGAAGATCTGGAGTATGGGGGGATATAGGAATTTTCAGCATATGTATTAT[C/T] TGAACATAATTTACAAAAGTGGAAACAGTTGGAAGGTACTTATAGGTAGACCTGAGGGTCTGTTACC
WI-11305	87 C T A T C A C A C C A	CAGACACAGC ATCACACCA	GACCTCCCGT GGC	ATACTGGTTTAAATCCATGTCAAATGTAGTTTACAAAGGGAAGGACAAAGTACCTTTGTATAGAATAT ACAGACACAGCATCACACCA[C/T]AGGGCCCCACGGGAGGGTCGGGAGACGACACTTTTCCCTGGG AAAGG
WI-11321	67 A G T T T T	GGGAGGAAAA TCCAATAAT TTTT	CATTGGGGAAT AGCTAAACCTT	ATTTTATATGAAGGTTTTCTGGTGAATCTTTTAAGCAGGGAGGAAAAATCCAATAAATTTTTTAA[A/G]AAGGTTTAGCTATCCCCAATGCTATTTAATACAATTTAGGTTAGGACGTTAAGTCTTATCAGA CTGTGTACTGGAGCCCCG
WI-11324	40 C G T G T G C C C C A	GGATAAATCA TGTCGCCA	ATCAAGCTTTG GGCTCT	AGCATACTGCATCTCCTTTATGGATAAATCATGTGCCCA[C/G]AGAGCCCCAAAGCTTGATGACAT TCTGTAAAGTTACACAAATGTATCTGAAGAAGTTATCTGTCTTGTCC

WI-11352a	69	T C G	AGCACAGCAC ATAGTGGAAA	GACCTCTCGTA GGACACTTAGC	TGACACATGGTTCTGTTTCCAGAAAGGAGAGAGAGTCATCTACATAAGCACAGCACATAGTGGAA AGT/C/GCTAAGTGTCCTACGAGAGGTGAGATCATATCCATAGAAAAACAGCTCTCTTTTACTTGCA CACTTA
WI-11371	84	C T G	CAGCTTGGAG ATTCTGATTCA	GCCCCGCTGA GCAC	TTAGCCCATGCTGTCATTGCAATCACCTGTGAACCTATGAAAACCTATACCTGCCAGGCTCAGCTT GGAGATTCTGATTACAG/C/TGTGCTCAGGCGGGCTGGACATCCATGTTTGGGAAGAGTTGGCGGGGT GATTCGATGCGTATAT
WI-11385	75	T C G	ACAGAAGACT TTCATATTCTT	GATTCTATTCT AGTCATGGTCA	CTTAAAGCATTATAGTTTGGCCTGATGGTGACACAGAGACTTTCATATTCTGTTTTTAAAAAGTC TCTTCAGT/CJAGGAAAAAGCTACAGATTAAAAAATATGACCATGACTAGATAGAAATCAGC
WI-11388	88	C A A G T T C	GGTTATGTGT CTTGAACITTA	TGCTTGTATC CAAGTTAAAT T	TCATGTGCCAGTTAGCTCAGTTGGTTAGAGTGTGGAGCTCATAAAAAATTAAGAAATGAATGTTTG AAATTACACGTAAGTTC/C/A/TATAATTTTAACTTGGATACAAAGGCAATTTGTTATGCTAAT
WI-11392	55	T G A T A A A T A C	TTTTGTTTTG AAATGGTGTTT	AGCTTATTTTC ATATTCACCCA TC	TTCTATCATTCATTAAAAATGGCAGGTTATGTGTTCTTGAACCTTAAATAATAC/T/G/C/T/T/T/TACA AAACACGTGAATGACTTTCTTGTGAGAAGGGGAACACTGAGTCTCCGCTCTAGATCCATTAACTGT CATACTCCTTCCCCAGA
WI-11396	52	A T T	TTTTGTTTTG AAATGGTGTTT	AGCTTATTTTC ATATTCACCCA TC	AAAGAAATAAGATGGCATTTGTTTCAGTTAAATTTTGTGTTTGAATGGTGT/T/AT/GATGGTGAATA TGAAATAAGCTTACCTCATCCACTCTAAAGGTAGTTGGTATTTTGAACCGTTGTCAAT
WI-11441	100	C A C A G C	TCCCACCAAC TGAGAAGCCA	TGCCAGGGCT TATTTG	CTGTAGCTTTTCCCAACTAAACGTGAGTCCAGTATGCTGGCAGCACGTCTGTCTTGTCTGGTG TATCCCATTAAGTGAATCCCACCAACCAGC/C/A/CAATAAGGCCCTGGCACAAAGTAAGCTCTCC ATTTTGTAGAATGAAT
WI-11466	26	C T T T A T T T G C A	TGAGAAGCCA TTTATTTTGA	GTTTATTGTTA TAAAAATGAC CTACAACCT	ACTTTGAGAAGCCATTTATTTTGCAG/C/T/CTTCAGTCCAAAAAAGTCAACATTTTCAGAAATTTTT TATATAAGTTGTAGGTCAATTTTATAACAATAAACTTTCTATTATCTATTATCTCTCACATACATTT CATGTATCCTG
WI-13364	35	A G	TTTTCTTTGTGCTCTTTTATTTAGTAGAAGC/A/G/GGAACAGTTGTCAATACTACCTTCTGTGG TCCCCTGTTAGACAACATACCTTTCTTTGAAATGTAAATGTCA
WI-11276	41	A G A G A C	GGCAGCAGG AGCAGAC	TGTACTGAGGA GCGGTG	AGGCAACACTGCTTTATTAGGCCGGCAGCCAGGAGCAGAC/A/G/CACCGGCTCCTCAGTACACATT OCCCCACCCCTGCTCGGTGCTCCCACTCAGGGCTGGCATGGAGGGGCGAGCTAGGCTCTGGAA
WI-12210	76	A G A	ACTGGGAAAA CAACTATTGC	TGCTAGTTTGC ATATGTTTTCC	ATTGGAACAACCTTAATAATTTGCATCTCTACATATAGAAAGCTGCTTTGAATAACTGGGAAAAACAA CTATTGCAT/A/GGGAAACATATGCAAACTAGCATCATTTGCTCTAGA
WI-14186b	88	A G	AATGGTCTGTTTTATTGAGAAGCTGTTGGTCAATTTGATGGAAAGACACATACGGGTACAAAAATTACA GGTGGTTAGTTCAATTACATG/A/G/TAACAATCAATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT

WI-14186a	52	C T A	GGTCATTGAT GGAAGACAC	AACTAAACCA CCTGTAAATTT GTAAC	AATGGTCTGGTTTTATTGAGAAAGCTGTGGTCAATTTGATGGAAGACACATA[C/T]GGTACAAAATT ACAGGTGGTTAGTTTCATTACATGATACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT
WI-12234	66	A G	GAGAACACTT GTGGGCTT	GGACCTATCAG TCCATGTTTGA	ATTTTTTTGGCTATAGGTCAAGTGTCTAAACCTTGAGCTTGCAGAGAACACACTTGTGGGCTT[A] GTTCAACATGGACTGATAGTCCACCCAGATTTCTAACTGGTAGGCTGGGGTG
WI-12345	37	C A	GTGGCAGGAA AAAGAGGAA	TTGCAGAGGGG TTCAGG	GGAACAGACCTGATCCACGTGGCAGGAAAGAGGAA[C/A]CCTGAACCCCTCTGCAAGTATTCCT TTCTGACCAGCTGGCTTGGCACTTTGTGAGATTGCAAAA
WI-13416	71	C A	AAATTTTGG AAGTTTTTCAG	AGTGTATTAG TTCATGAATA	GAAAGGCTGTAATTTTATTTCAAATTTTGGAAATTTTCAGAAAAAATAAAATGACAAGAACAA CATA[C/A]AAATATTGAAATTTATTCAATTGAACATAAACAACCTTAGCAGAGGAAGGACCTTTTGAT
WI-12310	46	G A	TTATCCCAAG TATAATTTTA	TGTTTAAATAT GTTTGGTCTT AAA	TTGAAAAGATGCTGAATTTATCCCAAGTATAATTTTAAAAAGCT[G/A]TTTAGACCCCAACATA TTTAAACATCTCTTACACATACAGAATTTCAAGTTTACAAATATCCAGAAGGCATTTTCTTAAGCAG T
WI-12086	72	C T	CCGGGAAAC TTGGATTT	GGAGTCTCGG GTCTGG	GAACCGAGCTTTATTGGAGCAAGAGTGTGGACACTGTTTACAAACAAACGTTTCCGGGAAACCTTG GATTT[C/T]CCAAAGACCCGAAGACTCCTCCAAGTCTCACTGTTAGTAAGTCAATTTGGGGCAGA ACAGGAACATGCCTAGCT
WI-11549	102	T G	GGCATAAAGT TCATAATATTC	GGAAAGTCTGT ACAAATCCCC	ATGTCTTACAGGTTGTATTTTGTAAAGATTTGTCTATCTAAATTTTCATATTTATTTGGCATAAAGT TCATAATATTTCTTTTATGATCTTTTAAATATCTG[T/G]GGGATTTTGTACAGACTTTCTCTC
WI-11585	79	T C	TGGTTTGCAA AAACAAAA	CCATGCTTCAC TGATCTTCC	TTAGAAGGAAAGAAATAAACAACCGTAAATGGGAAATCAGTTCAAGGTTAGGAAGGAGCTGGGTT TGCAAAACAAAAAT[C/G]GGAAGTATCAGTGAAGCATGGCCTAGAAAGTCCCAAGAGCAGGGGTAGAGT TT
WI-11604	68	G C	TTAGTTGGTTTCTGAAACTTTATGCTGTTTATTTTAAACCAATAGGATGTTCCAGTTACCAGCATTT G/CJAGAACTAGGGACTTTTCCATGAAATAATTAAGAGCTAAGGAATTTCTGACGCTCACCATTTTTC TTTGTTACTCTGCAGTT
WI-11614c	108	C A	CAAAATCAAAAAATTGAGGAGGCAAGAACAGAAAGTAAATCCAGAAAGACTCAGCTGCTTGAGGCAT GTCCCAACCTGGACTTGCCCAACTTTCACGTGAAACTGCA[C/A]ATATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11614a	60	A G	CCAGAAGACT CAGCTGCTTG	AGGTGGGAAC ATGCC	CAAAATCAAAAAATTGAGGAGGCAAGAACAGAAAGTAAATCCAGAAAGACTCAGCTGCTTG[A/G]GG CATGTTCCCAACCTGGACTTGCCAACTTTCACTGTGAAACTGCAACATATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11626b	83	T C	TTGATTTACTAAGGTCTTCCACTGGAACATGAAGGTAGGGATAAGTGTACAGGATAATATACTCAG ATATTTTAAAAATAAAT[C/T]ACTTAATAAAGAAATTAGCCATACCACATTTGTTCCATTTTGCTAC AAGAACAAATTGGCAATGA

WI-11626a	39	G A G	T C C A C T G G A A C A T G A A G G T A	G T G G T A T G G C T A A T T C T C T A T T A T T A A G T	T T G A T T T A C T A A G G T C T T C C A C T G G A A C A T G A A G G T A G [G/A] G A T A A G T G T A C A G G A T A A T A T A C T C A G A T A T T T T A A A A T A A A T A C T T A A T A A T A A G A A A T T A G C C A T A C C A C A T T G T T C C A T T T G C T A C A A G A A C A A A T T G G C A A T G A
WI-11627	23	T C	C C T T C C T T C C C A T T G T C C T C	C A T T T G C A A C C C A T C T C A A G	A C C C C T T T C C T T C C A T T G T C C T C T [C/G] C T T G A G A T G G G T T G C A A T G G G A A G T A A A A G C A A A A G G G A G A T G A G A A T A C T A G A T G C C T T T T T G T C T G G C T T A C T T C C A T T C G C A T G T C A A G T C C A T C C A T G
WI-11636	61	A G T C C T	G G A C T T A A A A A G A T C T G C T T A	A G A A C T T G C T A A A T A T T T T A T G T A A C A C T	T C A G A A A T G T T G C A A G C A A A T A C T A T T T G T A A A G G T G G A C T T A A A A A A G A T C T G C T T A T C C T [A/G] J A T A T C C A C A T A A C T C T A G T G T T A C A T A A A A T A T T T A G C A A G T T T C T G T G A C A G G T G C T C A G T A A A C A C T T T G A C T C C T T T T T T G G T A
WI-11537	119	C G T	A T T G C T C A T C T T A C T C T G A C C A	G A C C C A G C A A A A A G A A T G A T T	G T A C C A T T T C T T A T G T G G C A A A T A A G C A A A C T G T G A G T A A C A G A G G G C A G C T G A A T A A A T T T A C A G T A T A C A A T A T T A G A G A A T A T T A T G T T G C A A T T G C T A C T T A C T C T G A C C A T [C/G] J A T A A T C A T T C T T T T T G C T G G G T C C A G G A C C
WI-11654	37	G C C T G	G C C A A A A G A C T A T T C A G C A A	G G C T C T C C C A G G A C A G I T T	A G T A G A A C A T C A G T G C C A A A A G A C A T A T T C A G C A A C T G [G/C] J A A A C T G T C C T G G G A G A G C C A C T C C A G A G C T A T T T C T A A G A C T T T C T G T G T T T C A T A C T A C T A C T A C A G A G T T C A C A C T C A T A T T T C A T A T T T T A T T T T G G G T G T T G G G T
WI-11656	28	G A A A	A T T G A T T T T A G A A G G A A C T G C	C A A G G C T T T G T C C T C A A G T A A A	A C C T G A T T G A T T T A G A A G G A A C T G C A A [G/A] C T T T A C T T G A G G A C A A A G C C T T G C C T G C A G T T G T T T A A A T G T C C T G A A A C A A T C A G A T T C C A G C C T G G A T
WI-11680	55	T C	A C A G A T A C T T T C C A C G C A A C A T T T C T G A A A T G A A G C T T T G A T T C T C C C C T T T [C/G] J T T G C A T A A A G G C T G G A A G G T G T T T G C C A G A C C G T A C A T C T T T T
WI-11696	47	T C A G G G A C A G	T T A T C A C A G C A G G G G A C A G	G G C A T T A G A G A A G C C A A C C T T	G T C C A A G A C A A A G A T A C T T T G A C A T C T T T A T C A C A G C A G G G A C A G [C/G] J A A G G T T G G C T T C T C T A A T G C C C A C C A T C T T G I G T T T C A G A A T C T T C C A C T T G C C
WI-11702	69	C T C A G C A G	G A A T A A T A C T G A A A T A A C C A	A G A A C A A C T T A A G C A A A T T A T A C T G A A A	T T A C A T G T G G T C A A T G G T G A C A T A C T T T C A A T A A T A A A A A T C G A A T A A T A C T G A A A T A A C C A C A G C A G [C/G] J T T T C A G T A T A A T T T G C T T A A G T T G T T C T A G A A A A C A C T G C T A A T T T T T G T T C T G C A G A
WI-11706	60	T T C T C T C T T	T G G C T G G A A T T T T C T C T C T T	A T C A C C A A A G A A C A A A T C C A	T G C T G A T T C A T C G C T T C T A C C A T C T G G C T G G A A T T T T C T C T T C T T G T A C A A T T A T T T G C [C/G] J G G C T G G A A T T T G T C T T T G G T G A T T T G T C C C C T T G C T G C T
WI-11709	105	T A T T C A G T T T G C	A G A A G C T T G C T T C A G T T T G C	T C A T T T C T T C T A A T T T A C G G G A	A A T A T C A C T C A T A T C A G G C A T G T T A T A A A A A T G A G A G A T T A T G T C C T T T T T G G C A T A C T T C A T C T T C T T C A G G A C A C A G A G A G A G C T T G C T T C A G T T T G C T [A/G] T C C C G T A A A A T T A G A A G A A A T G A A T G G C C A G A T G G A T G G A A A A
WI-11710	103	C A C A G T C T T C A	G C A C C T A G C C T C A G T C T T C A	G T G T G G A G G A G G G A G G A G	T T A T T A C C A T C A A C C T G T C C C C A G C T T T C C A G C A C A A C A G C C A C C C A C A C T C T A G A C A C G C C T T C A G T C C A G T C C A T T C T G G C A C C T A G C C T A G T C T T C A C [C/A] C T C C T C C C T C C T C C A C A C A C T C C T T C

WI-11715b	123	C T	AGCTGGCTGC AGCTT	TOCCATCCTG TGGCT	AGAATGGAGCTGTTGGGAGGGACATGCACACAATGTAAACAGACAAAAATGCATTACAACCTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTT[C/T]AGCCAC AGGATGGGGACTGGGGAAGA
WI-11715a	49	A C A A A	GCACACAATG TAAACAGAC	CATTACACCAC AGTTGTAATGC A	AGAATGGAGCTGTTGGGAGGGACATGCACACAATGTAAACAGACAAAA[A/C]TGCATTACAACCTG TGGTGAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTTCAGCCAC AGGATGGGGACTGGGGAAGA
WI-11727	43	G C T C A A C A	AACAATCCTT AAAACAATA	CCTGTGGTTTG TGTTGCAG	CTGGATTTCTTATACCTAACAATCCTTAAAAAACAATATCAACA[G/C]CTGCAACACAAAAACCACAGGC AAATGAAAAACAGATGCCCCAGACAGACCCACCACATGGCACAC
WI-11728	16	C G ...	ATCTGTGGTTT TCGCTG	...	TTTTATTATCAAACT[C/G]CAATTCATTTCCAAATGTAAAGTTATCATCAGCTCCCATCCACTTT CTCCCATCTTCTATCTCTTCCACCCCTACACTTCTCTCCCTACAACCCGGTTCCAAA
WI-11758	61	A G	ATCTGTGGTTT TCGCTG	TGATTGGCCCT GTGGTCTA	TTTTCCCTCTTTTATTAAGTCGGCTATACTAAGAGGAGAATCTGTGGTTTTCGCCTG[A/G]TAG ACCACAGGGCCAAATCACACAGCTTCTGTAGAGAACATGGAGAGTGCCCAAGATCACCATCA
WI-11295	37	A G A T A T A A	GCCTCACAAA GTATTTCTAA	AAAGTGCTCA TCTGTGAATC T	CCGGCCTCACAAAAGTATTTTCTAAAATATAATTTGCT[A/G]TAGAGTTCCAGATGAGCACTTTTCA CATTAGGTGATATGCAAAACAATCACTATTGGCTCAGCAGGAAACAGACTTTT
WI-11773	93	T C ...	GGCTCAGAGA GCAAGGGA	...	AGCAGATGATATTCGCTGGAGTTTCTGTGAGCTCAGCAAAACAGCAGAGTCAGAGATTAAAGAAAT ATTTATTGCCTCTTTTTCCTCCCT[C/G]GTGATTGTTAATTAGGAGTCAAGGCCAAGTTATC
WI-11282	42	C G	GGCTCAGAGA GCAAGGGA	AAAACTCAGA CTGTAAATTTT GTGTG	CATGACAACCTCTTTTATTTAATGGGCTCAGAGAGCAAGGAA[C/G]CAGACAAAAATTTACAGTCTGA GTTTTCGCGCAGAGACCCCTCTCCACCTTTTTCATGCCTGTGTGTACACACACACTGTCCAAAGCCTC AGA
WI-11790	28	A G	CCCAACTTACC AAACCTCTG	OGGTAGGCGAG GCTAAGC	TAATTCACCCCAACTTACCAACCTCTGT[A/G]GCTTAGCCTCGCCTACCGTACACATGCTCAGAGCAC TTACATTAACTACAAATGGGCAAAATCATCTAACACAAAGC
WI-11879	61	C A A G T A T A C A	TCATCTAATCT GTGAGGTATTT	GATAGTTGAAC CTCTTCACTTT ATAAAA	TTTTAATCCCAAAGCTTACAACCATCTTTTCATCTAATCTGTGAGGTATTAGTATACAG[C/A]AGT GATTTCTCTCTTCTTTTATAAAGTGAAGAGGTTCAACTATCCAGACAGTCCCATCTA
WI-12489b	91	C T A A G T T A A A	GTGAGGTATTT AGTTTAAATG	CAATTTTCAGA TTGTCTATAGC AAAC	TTTACTAATTTTCCCAATTCCTCCCTTTTATAGTTTTTAATGTGGTATTAGAAAAGTTTAAATTACAT ATGTGGCTTATATCTATTCTA[C/T]TTGACAGCAGATCTTCTTCAAGTTTCTTCAAGTTTGTATAGACAATCTGA AAATTGGGTTCTGAACT
WI-11806	52	A G A T C T G A A	TGTATAACAT CAAAGAAAGA	TTAATTTCTGC AGTTCCCTCA	ACATTTGAGTAGGAATGACTTTGTGTTTATAACATCAAAAGAAAGAAATCTGAAT[A/G]TGAGGGAACCTG CAGAAATTAACCTTCAGTCTAATTTCTCAGAATGCCAGAGTAAGATGAACCCCTTTACAG

WI-11909	78 A G	TTTGTTGGG TGGTCAAG	CCTCTCTGAG ATTTCTGAAT AG	GCAGTTCTCTGAAAGACAATGGATTGTGGAGCATACTGAAGACTATTCTCTAAATGGCTATTTGTGTG GGTGGTCAAGAG/GCTATTAGAAAAATCTCAGAGGAGGACAAATGATAGTGCACCTGCAGCCAGCTCG GACTGGCTTGAAGAGTC
WI-11806	60 T G	CATGAAGAGT GGGCAGTTCA	TCCTGTAAGC CAATTTTATAT ACTAATAA	AAAAATACCATTTAGCATCAATGCCCCAAGTTTGGCAGGCATGAAGAGTGGGCAGTTCA[T/G]GTT TTATTAGTATATAAAATGGCTTTACAGGAAGCATTTATGG
WI-11846	31 C A	CCCTAGTGAATACAACCTTTGTCTCTGGAGAC[C/A]CCAGCTAGTCTAAGAAAACTTCTTAGGCTGAG CTCTCTTGGGAATCTAAGATAAAGAACTGAGATCTCTGGGAAGAGGGAA
WI-11965	65 T G	TGAAGATCAG ATCTCTGGTTT ATTT	CAGCTGTGGTG AATGTTGAT	ACAAAAATCACAAGTACAACACTGCTTATTTCTTGTCTTGAAGATCAGATCTCTGGTTTATTTAA[T/ GIATCAACATTCACCACAGCTGAAGGAAATTAACCTGAACCT
WI-11027	90 T A A	TGCCCTACTAC GCTTTTAAAA TTTATT	TGAGGAAATGT GTTACAGTATT TTTATT	ACCTATTTTGAACCTGCAGAAAGGGCAGGACAAAAACAATCAGTTTCTAGATTCTTCTGGGAAATAT TGCCCTACTACGCTTTTAAAAA[T/A]AATAAAAAATCTGTAAACACATTTCTCATTCTCTTACGA ATACCTTCTTTTGATATTGCAAAATCTATGGCATACACAGAGGCACCTCTCAATGCCCTG
WI-11049	95 C T	TTCTGCTGAAGATCACAAAAACAATTTCAACCTCTGTGGTTCAAAAAATTTAAGGATCTTGTACCTTT GTGTTATTTTCTGTTTCAACTAAGG[C/T]AGACTTCAGAAAGGCATAGCTTCCCTTGTAAACGTTTTT AAACATCTTTTCA[T/T]GTAGGAAGGAACATTTCAAAAGCCCAA
WI-15488	69 C T	AAAGGACAG CCAGATATCA AC	TTTCCATCTTA TTTCATTTCTG TAAC	CAACATTTATCAACATGGTAGGGAAAAAGTTCTCACTCTGCACCTATAAAAGGACAGCCAGATATCA AC[C/T]GTTACAGAAATGAATAAGATGGAAAAATTTTAAACAAATTG
WI-13654	49 A G	AACAGTTAAT GAAACACATC OGT	GGCTGGTGAAA TGATGTCAT	TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAACACATCCGTA[A/G]GTATGACATCATTT CACACGCCAGCTACTTTCATGTGGCAGAAAAAGGTAACCTTTTCCCATTTTACAGACAAAACCCAGT
WI-11070b	135 C T	ATGAGACCCCTGCTTTGAACGTTTAAACGTTTGGAAATAATGGAAAGGAGCTAGGACAATTTCTTGCTT TCAAGTAAATTTGTGACTGAGCAGAAAAATCAGCCAGCTATCTTGGTGCAGAGAGGTACTCCAAAGTA C[C/T]GTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAACAGAAAGGGAA
WI-11070a	110 G T	CAGAAAAATCA GCCAGCTATCT T	TGGAGTACCT CTCTGCACC	ATGAGACCCCTGCTTTGAACGTTTAAACGTTTGGAAATAATGGAAAGGAGCTAGGACAATTTCTTGCTT TCAAGTAAATTTGTGACTGAGCAGAAAAATCAGCCAGCTATCTT[G/T]GGTGCAGAGAGGTACTCCAA GTACCGTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAACAGAAAGGGAA
WI-12020	121 T C	AATCTTTATATTTCCAGCTTTGAGACAGTATTTTGAGGGCTGATGTTACCTCTAGCGGGGAAACC AGAGCCAGCTATTAAAGCAGCCAGAAAGCTACAGTAATTGAATACATGACCATT[T/C]CTCTTTTAGC ACGTTCTTTGTTCTCTC

WI-11076b	142 G A		CATGGTTCTGCCAGCTTACAGGAAGCATGGTGGCTGGCATCGGCTTATCTTCTGGAGGCCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGGAGCATGTGCATATCCAGAGGAGGAGAGAGAG AAAGAGAG[G/A]AAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCAT G
WI-11076a	106 T C AGGCA	AAGGGGAGC GTATGTGAC	TOCTGCTCTGG GGTTATTCAA AATTAGTATGG GACA	CATGGTTCTGCCAGCTTACAGGAAGCATGGTGGCTGGCATCGGCTTATCTTCTGGAGGCCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGGAGGAGCAT/GTGCATATCCAGAGGAGGAGAGAG GAGAAAGAGAGGAAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCAT G
WI-14263	48 T C GGCATATTCA	CGCAGAAAA GGCATATTCA	AATTAGTATGG GACA	ACCTTTAAAGTTTCTCCACCTACTCCCGCAGAAAAAGGCATATTCAA/TCTGTCCCATACTAATT TTTGAATAACCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTCTTTTGGCTACAAAGTAACA
WI-14267	28 T C	AATTATTGCTGAAATTAGGAAGGGAGCAT/GTGAATGGGAAGGGGAGGTTAGAGAAAGACAGAG ATTTAAAGAAAGCAAGTACCATTTTCCAAGTATAAAACCTCGTA
WI-13892	50 G A TAGAAC	CTTTTCATTT TGCTTTTAA TACTATAA ATCAAAG	TGATGATGCA TATACTAAA ATCAAAG	GATTTGTTTATTTCATCTCGCTTTTCTTTTAAATAGAACA[G/A]CTTTGATTTTAGTA TATGACATCATCATGAATTTTCTCTTACTTTGATTTAGGCTCCACCTCAGTAGTTTGACAA AGGTAGAATGAGTTCA
WI-15288	108 C G TCCCTCTCTC	CATGAGAGGA TCCCTCTCTC	AAAAGCTTCTT TCCCTTGA	ACCTCTTTCTGATGACACTGTACTGTAAAGGGTCTAGAGAGAAAGAGTAGTAGACTCCTACTTTGC TACAATTCAGGATGCGAGGCGATGAGAGGATTCCTCTCTC/GTCCAGGGAAGAGCTTTTGGC
WI-13951b	88 G C ...	GGAGTGAACA AAGTAATGAA CAAAA	...	AATAATGGAAGAGGAGTGAACAAAGTAATGAACAAA[G/C]TAGACCCCGATCAGAGGAAGAG ATGGCTTTCTTGTAACTCTGGAGCAGATTCAAGCAGCAATAATTTACTGAACACTTGCTATGTGCTG G
WI-13951a	39 C T CAAA	AAAAAGGCTC TTGCCAT	TTCTCTGATC TGGGGTCT	GAGACAAAAAAGGCTCTTGCCCAT/GA/TATCCCGTCTCTCCCTCCTGACTGACCCAGTGTCTT ACAAATGAACATCCCTCAGCCCCCATGGCATGGTGATCCCTTCTCTTGGGATCTGTGAATATAOCCA ACTGTCTTGTCATGGC
WI-13264	25 G A TTGCCAT	AGCAAAAGGA AGTTAAATAC CTGATAGA	CATGAAAGGA CAAAATTGAT C	TTATTTGTCTATTAGCAAAAGGAGTTAAATACTGATAGA/GATGCAAAATTTGTCTTTTCATGCA TTTGTGGAGCAAAAGTAACTAAGTTGTCATTTCCCTCACAAGGAGTTGAGCCCTAGATGAC
WI-15843	62 C T CAG	ATCTTATAACC AAGAAGCCTT CAG	CTCTGGCTCAG ACTTGCTCT	AACTCTTTATTGTTAGCTAGCCCCAGTGACTTTATGCATCTTATAACCAAGAACCTTCAG/C/TAG AGCAAGTCTGAGCCAGAGGTTTATCACACTTTGTCTCAGGGTCCACAGGAACCCAGGCTTTGGCT

WI-13983	52 G A	TCTCTCCACT CCTTAAACCT	CAATACTCTCT TAGCCCACTGG	TTGTGTATCTGATTTCCGAAACATAGAAATCTCTCTCCACTCCTTAAACCT[G/A]CCACTGGGCTAA GAGAGTATTGTACAGAATATGCACACTGACTGACTTAAACAGATTAGAACATCCAGGCACACTGAGAG
WI-13850	51 A G TT	AATCTCAGGG TCACAGCTTTA	TGTTCCCTGAC AATGTTTGTA	CATGAATCTCAGGGTCACAGCTTTATTTTATAGATTTTTTAAACACAGCCAT[G/G]TACAAACATTGT CAGGGAACATTTACAAGAATAAATAAGATGGACTTGCAGGTGTAAAAAGATTACACTTCA
WI-15295	27 G C A	TGTCAGTTTGA ATGTATTCTCTG	TGAATAGTTGG CAAGGAAAA	AGATGTCAGTTTGAATGTATTCTCTGAT[G/C]TTTTCCTTTGCCAACTATTCAATTATGACCATCTTTTC CTCGTCAAGTGACCTGCCATCATCACAAGAAAGGCCCGAAAAATATGAGTGAGACTCA
WI-14284	55 C T	ATTTCAACAAAAATCCAGAACAGGTTCTCACACTTTGAGCCTTTAGTGCAAAAAACA[C/T]TATGCCAT GCGGGAATAAAATGCTTATCCAGTGGAGCGCTCCCTGATGCATTGA
WI-14288	85 G C CCCAGAT	CCGCTGCTATT CCCAGAT	GGTCTCTCTCC ACCAATCTT	ATGACCAGACCAGAAAGCCCTGTTCTATATGAAGACAAACAGGTGGCCATACCTTGGGTGGAGGGATA CCGCTGCTATTCCCAGAT[G/C]AAGATTGGTGGAGGAGACCATGACAGATGACAAACGG
WI-13522	33 C T ACAAC	TGATGTAGTTA CCCCACTAAT	CATAATATTG AAGTCAGTGGT	TTTATTTGTAGTAGTTACCCCACTAATACAAC[C/T]GAGAACCACCTGACTTCAATATTATGAGAG AAATTAATCTCCAGGAAATTTTGCAGAGAGATAATA
WI-13529	42 T C TTACCA	CACAAACATT TATTGAACAG	TCTATACACTT CTCACTCTCTT	AAATATGATTCCTATCCACAACATTTATTGAACAGTTACCAIT/C]AAGCAAGAGAGTGAGAAGTGT ATAGAGGTGATTTAAGAGTGGTCCCTGCTCGAGGGGTTTATAGTCTAACAGGGGAACAACTCTC A
WI-13859	84 G A	TTATTTGTCAGAAATTCAGAAATCAGAGTCTCTACTGGGCAAGTAGAAAAATAGAAAAAGTTTACTAC TTTGAAAAAGGAAACTAT[G/A]ACAAACAAGTATATATTGAGGAAAGGACTCTCTAGAACTTGAGCA ACA
WI-13536	29 T C	TGAAAGGATACAGAAAAAATCAGCGAAGT[C/G]AAAAAGGTGGATAGCGTGGAGTAGAGGAGAAAT TAAGCACCACTCCAGTTGCTCTCTCCAGTGCCATGACATGGAGTACACTTAATTTTCTCAGCA
WI-13373	52 G A	TTTATTGTTTGGTAGAAAAACAGGCTCTTTAACACTGAATAAACATCTCAC[G/A]AAGTGTGCTC CTAGATTACAAAAAGTCAAAACCAATTTCTTTGACGCCGGCCCTTGAATCTGACATTCAAGTCAC CGTAATAGAAACCAGAGCT
WI-13477b	61 A G	TTGGTTTTTAATACCTCTGTTGGATAAAAGGACATTTTTCATTAGCTTGTCTTCAAA[G/G]GAC AGAGAAATAAGATAAATACCTTAAAGAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCTCAGTT
WI-13477a	32 A G AAG	TTAATACCTCT TGTTGGATAA	GAAGACAAGC TAATGAAAAA	TTGGTTTTTAATACCTCTGTTGGATAAAAGG[G/G]CATTGTTTTTTCATTAGCTTGTCTTCAAAAGAC AGAGAAATAAGATAAATACCTTAAAGAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCTCAGTT

WI-14297	86 A T G	AATGTTGGGT ACTTTTCCAA	TGTGCACATTC AGAAACATTT	CTGACTTTATTAGCATGCAATGCAATTTATTCTGGCAATAAATTAATATGTGCAGTTATAAAAAAT GTTGGGTACTTTTCCAAG(A/T)AAATGTTTCTGAAATGTGCACACTAGAATATATGCAGAATCCCTTT AAACAGTCGACT
WI-12229	89 T G AAA	CATGTGCACA AAAAGAGTAA	ACATGTGAATT GTCCCAAAA	TCCATGTAATATTCTCAACAGAGAACACTATCTTTAAATGAAGGATTTACCATTAAGAAATCAACA TGTGCACAAAAGAGTAAAAAT(T/G)ACCAAAAAATTAAGATTTTTTGGGACAATTCACATGTTT AAAAAT
WI-13582	43 C A AGACTGGGA	TGCAATCTAG	TCTGCGCAGTT AGATTCCA	AAGGTGCCCCCTTACTGGACCAATGCAATCTAGAGACTGGGGA(C/A)TGGAAATCTAACTGCGCAGAG AAATCAAGACCGATGGTGTGAAATCTGGGGCAGCTTCAAAATTTCTGCCTCTAAACATTTTCAC CCAAATTTTCATTATTGCC
WI-13857	28 A G	TCTGAGTTGATAAAATGCTTTTCTGAAC(A/G)TACATTTTAGGTATCTGGCACAAATTAACCAAAATGT CTGCCCATTTTGTAGCTTTTACAGTACAGATTCATTGATGTGCTGCCACATCTG
WI-15809	77 T G TGTAATGCC	TGGTTTCTGT TGTAATGCC	TAAGGTAGCTA ATTCAATGTTT GTAAA	GTTTTAAGTTGCAGAGATGTGAATGGTTTACAAATCTGAAGCTGAAGTTCAATCTTTGGTTTCTGTT GTAAATGCC(T/G)TTTACAACATTAATAGCTACCTTAAGTATTGAAGAGCTTCCATT
WI-15892	123 A T	TTAATCAGTCTGTGTCAGAAGAAACAGGACTTGATCAAGCTTCCAGCCCTCACCACCTCTATCAGCA TAGCAATTTTAAGGATCAGAGCTTTGTTTACATTTGTCTAAACCAAGAGAA(GAA/A)TGGAAATCA ACTCCACAGATCAACATGT
WI-15801b	81 T G AA	CATACTCCACT CTAGCTGCAGT	AGAAGAGTGG ATGGGATGC	TCTTTTATCCAAAGATGGGAAGCGCATTTTCATTGGCTTGAATGAGAAAGCTTCATCTCCACTCTA GCTGCAGTAATACT(G/G)CATCCCATCCACTCTCTCTCTTTTGTGACTGAAACTCTTCAAAGAACT GCTGAATGTCCTCTCTC
WI-15801a	24 G A AATGGGAAGC	TTTATTCCAAG AATGGGAAGC	TCATTCAAGCC AATGAAAATG	TCTTTTATCCAAAGATGGGAAGC(G/A)CATTTTTCATTGGCTTGAATGAGAAAGCTTCATCTCCACT CTAGCTGCAGTAATACTGCATCCCATCCACTCTCTCTCTTTTGTGACTGAAACTCTTCAAAGAACT GCTGAATGTCCTCTCTC
WI-13763	59 T C GCAGTGAT	GGCTGGACACT	CCCACACCTGC CCCT	GCTCGTAATGAGACAGAACGCTACAATCTGTTCAACACTGGGCTGGACACTGCAGTGATT(C/J)AGGG GCAGGTGTTGGGCGAGGTGGGGCTCTGAGCCGAGGACAAATGTCCATGGCAGAGCTTCCAGAA
WI-13578	48 T A ACC	TCAATAAAGA GCAGAAAGAA	CAGTGTGTAAG AACATCTTTT GTC	TTTTTTTTGGTGAGTGTGTTGCTTCAATAAAGAGCAGAAAGAAACC(T/A)AGACAAAAGATGTT CTTACACACTGAGCTTTACACAGTACCCCAACATTTGATATTTTCCCGAGGGCAAAAAGA GAGCTTCCCAGAAACCTC
WI-13789	62 G A AGGGAG	TTGGATGGCTG	CAGTGGCTTC CTCTGTTT	TCCAAGGAAAAAGAAAGAAACCAATCAGTGAGAAAACTCAAGAAATTGGATGGCTGAGGGAG(G/A) GAACAGAGGAAGCGCACTGGGGCTGGGACTGAATATGACAGATGGATGGTAGGGTCTCACTCTCTT GAGGTCCCT
WI-13594	66 G A AGC	TTTTTAACACA GATCACAAA	CCTTTGGGCA GTACTTTT	AATAACAAAGTTTAAGTTCGAGCTGCAATGTTGGCAATGCAGGTTTTTAAACACAGATCAAAAAAGC G/ATGCACAAAAAGTACTGGCGCAAGGACAAAAATATGCTAAGAAATTAGGCCAAACAGCTGC

WI-15625	40 C T ...	---	GTTCCTCCACCTACTCCGCGAGAAAAAGGCATATTCAA[C/T]TGTCCTACTATAATTTTGAATAA CCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTTCTTTTGGCTACAAGTAACA
WI-13367	84 C G A	TCCCACCCCCA CCCT	GTCTCATTCTTGCTAGGCTGTAAATTTTTCAGTTTAAACAAGTTCTTATGTGATTTGTGGCCACACT GAAGACTCACCAGAA[C/G]AGGGTGGGTGGGAATACTTAATCAATATTTGTGGAATTTACCCGAT GAAATCCAGTTATCCCT
WI-13600	26 G T	CATATTGAAAA TTGTTACTAGA TGATGG	CTCACITTTAATGAGCCAGCATCCATG/TJCCATCATCTAGTAACAATTTTCAATATGCACATTATAT TATACTGGAACAAGAAATACGGATTGTGAGGGAAGAGCATAGAGGACCACCATCAGCAACCCCTCT TGATCCCTTCTCTACCC
WI-13602	89 G T	GCATACCTCAT GACAATATTTA ATATTAAT	GATAGGAAAAAGAAATGAAGTCAATAGTCTTTAGCAAGCCCACTAGCTCAAGGAATAGACAGCCG CTTTCCATTCTGGAGACAACACA[G/T]AAATCTATTAAATATTAAATATTGTCTAGGATGACACCT GCCCCA
WI-13650	76 A T	CAGCTAGGAT ATGAAGAGTA GTTTT	GCATTAAACATTTAAAAATTTCTGAGGATATTGATGAGAACTATGATGAAAGATTTCACAATATTTTAC TTTTAAACIATTTAAAAAACTACTCTTCATATCCTAGCCTGATGACTTAAAGTTACCGG
WI-14319	83 C T A	CCAAATCATCT ATATTGTTGCA TG	TGTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAAGATAAAAAAGGAATAGCAATT CAAGGCACAAAGCTAAG[C/T]ACATGCAACAATATAGATGATTTGGGGTGGGACAGTACAGAAATT
WI-13528	80 A G AAAA	CATGATACCAC AGTTTCTCTG AA	ATTGGATACATGCTTTTAAAAATGGTAGCTTTTAAACTGTAATCAATACATTTTGCAATTTTCTAAAA AAAGAAGACATTT[A/G]TTACAGAGAAAACCTGGTATCATGCAGGAAAAGCAGAAAAAATTT
WI-13909c	93 A T ...	---	ACTTAACTGGCTTATCTTCACGGTAATCTATTCTGTATTTCCAGTGAAGTTTCTCTCACACT CTCTTCAAACTCGAATATCTTTT[C]ATGAGATGCTAGTAGTACCCACTGCAACATCTCTCAA
WI-13909b	80 G A C	GCAGTGGGTAC TAGCTAGACAT CTC	ACTTAACTGGCTTATCTTCACGGTAATCTATTCTGTATTTCCAGTGAAGTTTCTCTCACACT CTCTTCAAACTC[G/A]AATATCTTTTTCAGAGATGTCTAGTAGTACCCACTGCAACATCTCTCAA
WI-14323b	86 C A ...	---	TTTTATTGAATTCCAAATGTAGCAAAATCATTAAAACAAAATTTATAAAGGGACAGAAAAAATTAAG AATCAAAACATCATCTGGAC[C/A]ATGGGAACCTTGAAAAGGCATGGCAGTGGAGACCAGTAACATA
WI-14323a	78 T C ACATCA	GCCTTTTCAAG GTTCCCAT	TTTTATTGAATTCCAAATGTAGCAAAATCATTAAAACAAAATTTATAAAGGGACAGAAAAAATTAAG AATCAAAACATCAT[C/T]CTGGACCATTGGGAACCTTGAAAAGGCATGGCAGTGGAGACCAGTAACATA
WI-15389b	104 G A AAA	GATGAGGTGAT TCCCACACTT	AAAAATTGACAAATCAACTAGCTTGCTTTTGTGCTTTTGGAGACTACCATTATTCAAATTTATTATGT AATACACTCATCCAGATAATGAAACATCTCGGAAA[G/A]AAGTGGGAATCACCTCATCTGTGC

WI-15389a	33 G A TC	AATCAACTAG CTTGCTTTTG	TTTGAATAATG GTAGTCTTCCA AA	AAAAATTGACAAATCAACTAGCTTGCTTTTGTG[C/GA]TTTGAAGACTACCATTTATTTCAAAATTTAT ATGTAATACACTCATCCAGATAATGAACATCTGCGAAAGAGTGTGGGAATCACCTCATCTGTCG
WI-15747	88 T C AGTGTT	TGCTTCATTT AAACTAATTT	CATAATTACCC AAAAGTTTCATA TAATTT	TGTAATCTGCTTACAGTCCCTTTGCAAGACAGACATATGTTTTGCATAAAGATATAAATTTGCTTCAT TTTAAACTAATTTAGTGTTC[C/TTTAAATATATGAACCTTTTGGTGAATATGAACCTGTACCAAAAC C
WI-13752b	117 C T	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCTTCTCGTTAAGTCTGGATATACTTGGCTTGCA[C/TTGGACACCTTTTACG GAGGGATTCGGGACAACT
WI-13752a	106 T C AGTGCTGA	CCTTCTGTTA AGTGCTGA	CCCTCCGTAAA AGGTGTCC	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCTTCTCGTTAAGTCTGGATATAC[C/TTGGCTTGACCGGACACCTTTTACG GAGGGATTCGGGACAACT
WI-14339	102 T G TTAC	CCCAATCAAA CAGTACATGA	TCCAGATTTCT GGAAACCG	AATCATTTAATGAATGTTCCAAACACACCCCTTCACTGGGCTACAGGTAAATTTCACTGGGATGGAAG CAGATGAACCCACCCCAATCAACACAGTACATGATTACT[G/CGGTTCCAGAAATCTGGATAC
WI-13744	115 C T AAACTGAA GC	TGGTGTGAAC AAACTGAA	AATCAGGAAA GATAAGCACA GC	TGGATGGATGGATGAGGCCACCTGTGTTCAACAAAACACGTAAATGGAACCTTCATGCAGCTTTAGAT TTCTTTGCCAGCTAGGAGCTTGATGTTGGTCTGAACAAAACCTGA[C/TTGCTGTGCTTATCTTTC CTGATTCT
WI-14061	68 C T	CCTTGACTATATTGTTTTTCCAAAATAGGACTATGTGTAGAGAGAGCCCCCGTACATACCTTAT [C/TTAACCATTTTCATCCACCATTTGTAAAATCTCATCTTCTGGGTCTGGATACTCAAAAACAGAT
WI-15719	69 A C CATTGAGC	ACCTTTTCATC CATTGAGC	TGATACTGGC AAGAGTTTTAA ATT	TTACAGTTGGATTAACTACCTACCTGAATATAGTGAATTAACCTATTCAACCTTTTCATCCATTGAG C[A/C]AATTTAAAACCTCTTGCCAAGTATCATGAATTTACGAAGAGGAGATAAGAGATCTGATC
WI-13810	106 T C AACTT	CTCTAAATCG ATACATCCAA	GAACTGATGCT TGCTGCTAACT	TAATCCATCAATCTAAAATCACACATAGATCAAAACAGAAGTACCACAGTATGCTTTATTTTGCA GGTATTAAATGGTCTCTAAATCGATACATCCAAAACCTT[C/AGTTAGCAGCAAGCATCAGTTCTTC
WI-15736a	27 G T CACA	ATTTTATTGAG ATTAACCTTG	GTCTTTTGATA TGTCGCTTAGT TTT	GGATTTTATTCACATTAACTTGACAG[C/TTAGCAAAAAAAATCAAAACATAAAAACTAAGCCACA TATCAAAAGAACAAATATACAAATAGAGATTTCATATTTCTCAATAGCATTGGAAGGTATTTCCATAAATA
WI-13785d	72 G A	TCAAACTGCACACTATAAAGTGCTTTAAATGCAGCAGCAGGAGATGTGAAGACACAAAATGAAC AAGTG[C/ATAGTGACACATAGCTGTCAACACACAGTG
WI-13785c	56 A C	TCAAACTGCACACTATAAAGTGCTTTAAATGCAGCAGCAGGAGATGTGAAGAC[A/C]CAAAATG AACAAAGTGCAGTAGTGACACATAGCTGTCAACACACAGTG

WI-13785b	40 C G	TCAAACTGCACACTATAAAAGTGCTTTAAATGCAGCAG[C/G]AGGAGATGTGAAGACACAAATG AACAAAGTCGTAGTGACACATAGCTGTCAACACACAGTG
WI-13785a	27 T C TGCTT	AAACTGCAC ACTATAAAAG	TGTTGTGACAG CTATGTGTAC T	TCAAAACTGCACACTATAAAAGTGCTTT[C/J]AAATGCAGCAGCAGGAGATGTGAAGACACAAATG AACAAAGTCGTAGTGACACATAGCTGTCAACACACAGTG
WI-13793	88 C G ATAGG	GGATTTTACAT TCAGCCTAGAT	GGCAGGAGGA TTTGTACT	AGAAACCAAGTATATCATAGGCAATAAAATAGTTTTTACCCCATTTGATACAACATAAAGGGATTT TACATTCAGCCTAGATATAGG[C/G]AGTAACAAATCCTCTGCCCATAAATCTATGACTTG
WI-13794	52 A G TTTCTTCTC	TTCTCACCCCT	AGAATGGGCTC TTAACCTTGA	TAGTCTCTACAAATCCTTCAATCCATTTCTCTCTCAACCTTTCTTTCTC[C/J]TACAAGGTTAAGA GCCCCATTTCTCAACAAACAAACAAACATAGAGCAAT
WI-15729	35 A G GTGTAGACTGC	CTTTGAACCAT GTGTAGACTGC	CTCAGCTTCTT TCTAAAGTGCC	TCATTTAAGTGCACCTTTGAACCATGTGTAGACTGC[C/J]GGCACTTTAGAAAGAAAGCTGAGACTGAA AAGTCTGTCTTGACTTCCAAAGGAAGGTAAAGTCCCTGTTTGAGCCCGGGGCTGTCTCATTTGTA
WI-13424	66 G A C	TGAGGTTTTTC ACCTATTCTT	TTTTTCTCCCC AGGGTCTA	GTCTTTGCACAAAGTCTCCCAACTGGTTTGGAGTTTTCCCTCTGAGGTTTTTCAACCTATTCTTC[C/J]A JTAGACCTGGGAGAAACACACATGTGTAAAGTGCTCAGGACATGAGGCAGGCCGTTTCAACAAGAT GCTGGCTAAGCGGCTTC
WI-14065	29 T C AATT	TCTTATAAAA GGTCAGAGGC	CAAGCTGAATC TGGGATCTC	AACTGTCTTATAAAAGGTGAGAGGCAATTT[C/J]GAGATCCAGATTGAGCTGTCTCATAAAGAT TCAACTTCAAGTAGCACAATTTCTGTCTGCTTTTAACTCTGAACATCTTGAAGCACGAA
WI-13446	22 G C TCACTCATCA	GCCATGTTCTT	AAGGGAATCA AAATCAGAAG G	TGCCATGTTCTTTCACTCATCA[C/J]CCTCTCTGATTTTGAATCCCTTTCTGCTCTGTAATTTTTTCTTC TTCCCTTTTAGGGCCTAGTCTGTTTAGAAATCTGTTTTTGAGAGTAGTGAGCCCTTTTACTTTTTT CTGACTGCCTAATT
WI-13725	56 A C TGGGTGOC	TGAGCACATA	CCTGCTGTCTC GGGC	TCACACAAAGGCATTTGGAAATGTCACCTTACACATGGTGAGCACATATGGGTGCC[C/J]GCCCGAG ACAGCAGGATAAGTTTACAAAACCTTGACCAGGAGGTTAGAAGCAAGGCATGGTTTCAAGGATG
WI-15702d	107 T C	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACCTGTAAACAATACTAA[C/J]GGGTCTTTGAACAAATAGTTT TGA
WI-15702c	101 T C	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACCTGTAAACAATACTAA[C/J]GGGTCTTTGAACAAATAGTTT TGA
WI-15702b	90 C T	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAAC[C/J]CTGTAAACAATACTAAATGGGTCTTTGAACAAATAGTTT TGA

50

WI-15702a	48	G C A A A G	A A C A A A A T A A A G G C T T T C A A	C C T C A C C C C T T T A C C C C	C A A A T G T T T A T G A A G A G A C T C C G A A C A A A A T A A A G G C T T C A A A A G [G/C] G G G T A A A G G G T G A G G A A A G C A T G T G A G A G A A A C T G T A A C C C T G T A A C A A T A C T A A T G G G T C T T T G A A C A A A T A G T T T T G A
WI-13831b	113	T C	T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A G C G A A G G T G A C T T G G A A A G G A G A T T C A C A T A C T T C C A C T G T A T C C T C C G G T A A G T T T C C T C T C T G T A G A T [G/C] G T C C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
WI-13831a	56	G C	T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A G C G A A G G T G A C T T G G A A A A [G/C] G A G A T T C A C A T A C T T C C A C T G T A T C C T C C G G T A A G T T T C C T C T C T G T A G A T G T C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
WI-13806	62	G A	T G A T T G A G C T T A G A A G G A A G T C A T G T T G A A A T C A G A G A G G C C A A A A C T A G G C C T C A G G T [G/A] C C C A T T A A G C A T G C T G T G A A T G C A A A G G A A A G C T T A A A A A A T T T T T A A G G G T G A C T C C A G T A A A C A T
WI-14372	86	A G	C A C A T T T C A G C A A C A A A T C G A G G T G C A A C A G G G T T A T T C A C A T T A A T A T A A C T G G A T T T T T G T C A A A T A A A T A G G G A [A/G] T T C T C T T A A A T A C C A T C T C T C A C T T C A T G G C C A G T
WI-14373	95	A G	A G G C T G T T T T G A G G C C T G A G A C C C C A A C A C A T G A C A C G T A A G A C T G T A C C A T G T C A T G T G A G T T A T G A G C T A G G A A C C C T G G A C G A A A C C A [A/G] C A C A T A T A C A A T C A T C T C C A C C T C C A A C G C C T T A C T T T C A C A G C C T G C A
WI-14078	61	C T	G C A A G	T G T G T C A T G T C T C T T A C T G C	A G A A C C G A G A A C T C A A A G A A C C A C A C A T G G T G T A T C A A A G A G T A A A T T A G G A A G A C A A G [C/T] G C A G T A A G A G A C A T G C A C A C A A A T C G A A A C A A G G G C A T G G A G A A G G A C T T A G A T G G T C A C G
WI-14083	47	C T	A C A C T	G C C T A C T G G A C C T C T A A A C T A C T G A	T T G C T A C A T A A C A C A T T A C T C C A G A C T T G A G A G C T T A A A A C A C A C T [C/T] A T T T G T T A T T T C A C A G C T C A G T A G T T T A G A G G T C C A G T A G G C T T G G C T G A G T T G T T G C T T A A G G T C T T A C A A G G C C A A
WI-14085	31	A G	A G A A A A A	C A G T C A T G T T C A C G T G C T A G T T	T G C A T T T A T T T C A T G T G T A A G A A G A A A A C [A/G] T A A C T A G C A C G T G A A C A C A T G A C T G C A T G G A T A C A C G G C T C A G C A C G A G G C T A A A G T C A G A A G T G A G T G A A A A C A A A A T A G C A T G T T G A T T A A G T G A A A T A A C A G A A C A G G A G G C C T T T
WI-12169	121	G C	T T G C T T	G G G T T C T G A G G T G A A A G A A A A A	G T C A A A G G T T G G C A A A T T T A T T T C C A C T T A T C A A G A A C T T A C A A A A T A T T T T G T T T C A T T C T A A A T T T T C A C C T T A T T G C T A A G T T A T A A A A T A A A A C T C C T A T T T C T T T G C T T [G/C] T T T T T C T T T C A C C T C A G A A C C C C T T A
WI-15705	50	A G A T C	G G A G G G A G A T T T T A G A C T G A	A G C T G T A G T C G T C A A A T A C T C T A G A A	T T G T T T T A T T T G G G A G A A T G A A G G A G A G G G A G A T T T A G A C T G A A T C [A/G] T T C T A G A G T A T T T G A C G A C T A C A G C T C C T C T C T T T G T A C T A C G A G A C C C T G C T T A T A G C C C C A A C A G G A A A T C C T C A T C T G C G G T T G C A G A C A G

WI-14379	102 C T	TCTATTAACA GGGTATGTCA CACC	ATCATCTGTT TGAGGTTGACA	TTATGCTGTTGTTTCTACTGGTGGTCTCGCTCACTAAATATCCAATCCTAGTATGATTTCTTT TACITGCTGCTATTAAACAGGGTTATGTCACACCIC/TGTCAACCTCAAAACAGATGATACT TAAATAAAACAAAAGCAGAAA/C/ACCCACCATTAAACAGAGGACACTGCAGAGGCTTATGTACA ACACGTCGCCGCGAGGCTGGCGCAGGACTGCCACTCACTCCAAAATTTCTTTGGAGCAGAG
WI-14102	22 C A	ACCGCAGAGCTGCTGTATTTAAAA/G/JACAAGCGTCTGATCTCTGAGGGCTGGACCCAGCTGC AGTGGGGCTCGGCACTGCTCTGCTCTOCAGGACTCTTCCACCCACCC
WI-15937	24 A G A	CGCAGAGCTG CTGTATTTAA A	GCAGAGATCCA GACGCTTGT	TGAAACTGAAACGTAATTTCTCCAC/JACACCCGTAGAACTTAAAGGCCGCAAAAGACTCACACCC ACCACCTAGCGCGGCAAAAAGGAAGTTTCAGGTGATACAAGATGCTCTGCCATCACACCTGAAGGAT GGTT
WI-15944	24 A C A	AAACTGAAAC GTATTTCCCTCC A	GGCCTTTAAGT TTCTACGGTG	ATGTTTATGATCAATTCCAAACATACAGTACAGGGAGGTGAAATGAGTAAGAAAAAATCAT ATTTAAGTCCCGTTAACACTAAGCC/A/GJTATTTTCAAAATGTGTTTCAAAATACTCAGCCAGAT CACCAAAGCTCAGTCACTAC
WI-14124	92 A G	GACAAAGAGGCAGTTTCTGTAGTTCCAGCAGGGCCAGAGCAGTTATCAGAACGGGTTGGTTTGACCT GCATAGATTTTGGACGACTA/C/JGTGGCCATGCCATTCCTGTAAGTGAAATTAATGAACA GTTATTTCTCAGAGTTCTGGAGTTAGAAAGTCTGAGATGAGGATATCACCAGCATGGTTAGGTTCT GGTGAGGACTCTCTGGCTTACAGCTGGCTGCTTCTCACCATGCTCTTCCATG/A/GCCCCAAAGAGAC AGAACAAAGCTCTCTGGT
WI-14138	23 C T	TGTTGGCACC GTGACATAACA TAGAACA	CAGTATGTACA GTGACATAACA TAGAACA	TTGTTGTTGGCACCAGAAAAGCTC/JATGTTCTATGTTATGCTACTGTACATCTGTAAACAAGACT GCATTAATATTGTTTCTTATGATTTGTTTCAATG
WI-13551	74 G A	TCCTTCAGTAG TAGTATATTCA GACAATC	GCTCATTCTT TTAGTGCTAAG TAATATT	GGCAGGTTTATTCATAATTTTCAAAACTTGGAAAGCAACCAAGATGTCCTTCAGTAGTATATTCA GACAATC/G/AJAATATTACTTAGCACTAAAGAAATGAGCTATCAAGTCATGAAAAGACATGCAGG AACCTTAAATGGATATTACT
WI-15953b	59 C T	TTTTTAAGAGTGCTTCCATCATTATATTGATTGACACAAAACCTTTTAACTC/C/TGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCCCAGTGTCTTTTGAGATAGAAGCCTTCTTCAGAAATCA CCTCC
WI-15953a	26 T G A T	TTTAAGAGTG TCCTTCACATC A	TCATCTGTCT TGTTGTTTTG A	TTTTTAAGAGTGCTTCCATCATT/JJTATATTGATTGACACAAAACCTTTTAACTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCCCAGTGTCTTTTGAGATAGAAGCCTTCTTCAGAAATCA CCTCC

WI-14631	82 G A	TGAATTCAATGGACAGTTTGGCTCTGTTTGTAGTGAACCCCTCACAAGCACTCTGCATAGTCGGCTTTCTGTCTCTTTAAACG/AJTGCTGGTCCCTCTGCTGCCAACTTTAGGATTGGGCTCCTCAGGGCCTTGTCTGTA
WI-8053	24 A G	ATCACACCCTGTCTAAGAACAC/AJTGCTTCATGTCCAATCATATCCCCGGGACTTTGTCAACTGCAGTACACTTCTGCTGCAATGAACCTGGCTTCTGTGAGGGAAGCTCCTAGAGCCAGGTAAGGGGGTGCAGCAGTGAGGGGTATATCTGGGCTGGCCAGTTGGAAACCACGGAG
WI-15984	99 T A CTGGAGTA	GACTTCTCCAC CCTCTTGC	GCTCTCTGTCC CTGGAGTA	CAGAAACCTCTTCTGTGTAATAAGCTGATGCTAAAGTCAGAGCAGTCCAAAGCGAGGCTGCCTTGGGAGGTAGTAAGCTCTCTGCTCCCTGGAGGTAT/AJGCAAGAGGGTGGAGAAGCTTTGGCAAG
WI-12075	103 G A GGCAC	CCCTTCTTTC TCTTCCCTC	AGCAGCTGGG GGCAC	CAGCTAAGGATCACTGCAGCTAAATACAGATAGAGAAGCAACAAAGCCAGGCAAAATACCCATCAGAGACAGTGACAAGAGCAGCTGGGGGCACGGGGGAGGC/G/AJGAAGGAAGAGAAAGAGGGGGAGGAGCCT
WI-12179	96 G A TGGAGTCA	TCGAATGACCC TGATAGTGC	GGAGGTACGG TGGAGTCA	TAATTTAAACACGCCCTTCCACATAGTGGGTGAGGCATCTGCACATTTTCTAGAGGACATGAATAGTGATGTGGAGGTACGGTGGAGGTCA/G/AJGCACTCTACAGGTCATTCGAGGAGGAACAG
WI-14651	49 C G ATTGT	GGAGATATTGA TCTCTTTCTGA CTTATTT	CAAGAATCAT TCTCATTTAAA	CACAAATAGTGAATTAATCTGAGCAAGAATCATTTCTCATTTAAATTTG/C/GJAAATAAGTCAGAAAGATCAATATCTCCCTGCTTCAAAAATGACACTCCCAATTTTACAGGTAACCACTGTTA
WI-14666	105 T A	AATGTGGACTTCAACAAGGGTTTAAACTAATCTAATACAATCTTACAACACATTCACAGAGCATATAACAAGAATTAATTTACAGGCGACTAATGTATTTAAAT/AJAAACCATGAAAAAAGAAAACTTG
WI-13473	31 C T	ATCTAGATGTCAGCAATGGGCTGAGACTG/C/JTGCTGTGTAGTGCAGTGTGTGTATTTCTTCTACCTATTACAAAAATTAACAGAAATATGGCTTCGCTTTGTGCAAAATGTTTATATCACAGTC
WI-13987	103 A C AAATAAAAA	AAAAGACTAC AGATACAAGG TG	TTGTGTTTTCA TCTCTAAAAG TG	AATTTAATAGCAGCTCTGTGTTGTGATTTTAAAGAAACAAGATAAAATATGTCAATTCAGCAGTCATTTAAAAATAAAAGACTACAGATACAAGGAAATAAAAA/A/CJCACTTTTAGGAGATGAAAAACACAAAA
WI-14408	60 T A G	GCAGACAC TATTACAGGCT	TTAATTGTGA AAACTCATTG TTACTTT	TTAATAATTCAGCAAGTTATTGCAACAGGTTGAAAATGCAGACACACTATTACAGGCTGT/AJAAATAACAATGAGTTTTACACAATTAATAATTAACACATACTATTGGGATTTGTTGAATGA
WI-13683	47 C G	TTTTGTGTTAAGAACAAGCATTTTGAATAAAACCTATCTGCCCCATG/C/GJTTTACAGCCTTTTAAATTTGTAATTTATATAGTCGTGTTTATGGTACATATTGATTGTC
WI-13910b	63 C T CGTCT	CATTGAGATAA AGCACACTTAT CAC	CACCATTGGA CGTCT	TTAGAAAACCTGATAAAAGCAACACAACTTTTGGGGAAGCACCATTGGCACGTCCTTTGTGCTA/C/TGTGATAAGTGCTTTTATCTCAATGAAGCAACCCCA
WI-14635	22 G A	ACATGGCAGATACAGAGCTGTC/G/AJCTTTGAAGACCACCACTGACCAGGAAATGCCACTTTTACAAATCATCCCCCTTTTCTGATTGGAACAGTTTCTGACCGTCTGGGAGCGTTGAAGGGGTGACCAGCACATTGACATGCAAAA

WI-16002	59 T C	GATAACATAA AATGATCATG CAGAAATTC	GCATCTCCTC TTTGACTTTT	CCAACATTTTAAACCTATGACTGGTCAATTGATAACATAAAATGATCATGAGAAATTTCA[T/C]GTTA AAAGTCAAAGAGGAGATGGCTAATGCATGCTGGGCT
WI-15361b	101 A G A	CCACATTGAAC TCAAGTCATC A A A	AAACTAAAC CTTTGTGCCTA AAA	GTGGAATTTTATTAAAGCCATCAAAATTTCTTCACACTCAATACTGTTGAACAACAAGATAACACAT CTTCTGTCTCATCCCACTTGAACCTCAAGTCATCA[G/T]TTTAGGCACAAGGTTTTAGTTTTCTCGG GAAATCAAGTTTAAACCA
WI-14759	73 T C	GGGTTTGACTT GTGCGG	TCCACACTGC O O C C	TGAGTTACAACAATGAGCAACAAGTTAGAAAAATGGTTTTATTCAAACCTCCTAGCGTTTGACTT GTGCGG[T/C]GTACTCAATGGGGGCAGTGGGACGGGAGGGATTGCAACCCAGAGTTTCATACTG CAA
WI-12535	50 A T T A T	CTAGGAGGGTT GAGGTGTAGA T A T	GCTCCACGAGA AGAGAGGAA	TCCCTAACATTTATTTCAGGTGGTGACTAGGAGGGTTGAGGTGTAGATATAT[T/C]TCTCCTCTCTCTC GTGGAGCCTTACTGAAGACAGGATGCGGTTCTTGTTTATCAGCTGAGAAGGGCAGTCTCGCCATC TTAAAGACCTGCCCTCC
WI-13805a	112 G A GGGAA	AAAGGCACAC A A A	CTCAGCCTGOC TTGACC	TTCCATTCAATTGCTGGCTTTACCAATTTTATAGCTATTGGGAGGCAGGAAAGGGAATTTTGGC CCCAGAAACCATGAGATTTGGTGCAGAAAAAGGCACACGGGGA[G/A]GGGTCAAGGCAGGCTGAG AGTCACATTTCCAGACCTC
WI-12340	18 T C	ACACAATAAATTCCTATT[T/C]CGAGTGATTAACACCTATTGTTGTTTGAACCAACAAACAACTAG AAGAAAAACATTTTCAAAACCTTTTTTTTTCAGGCTGA
WI-14808	52 T A C TACCCTGT	ACCACCACA CTACCCTGT	GAGGCATCACA ATGTTAAGATT T T	CTTTGAAACACTTTAAGCAACAGTTAAAAAGTACCCACCACACTACCCTGT[T/A]AAAACTTTAAAC ATTGTGATGCCTCTGCATCAATTTTAGAAAAACAAGAAACACAACACTGAAGGCCCATGTA
WI-14816	29 A T	AGTTAAAAAAATCGAGTCAGCATTTATT[T/A]TAAAACTGGACACGCTTCTATATTGCAAGCTCAT TCAAATGCATTTATTTTGATCCCAAGCCCTGAAACATGAAAAAATATTACTAAAGGAATGTTG ATTACCAGCTACGACTTTC
WI-12542c	71 G T	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG[T]TAGGTGATTGATACAAATACGATCCATAA
WI-12542b	70 G T	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG[T]TAGGTGATTGATACAAATACGATCCATAA
WI-12542a	45 C T	GCTATTAGGC AAACTGAACA TTTAAA	TCTAGAGCCCT CACATGGAT	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTT[C/T]ATCCATGTGAGGGCTCTAG ATCATGGTAGGTGATTGATACAAATACGATCCATAA
WI-12173	57 C T CAAAAA	GGATACAGCA GTAAGAATA TAAAAA	CCACCTCTAGA ATGTATGCTCT ATAA	CACCTAAATCATCTAGAAAACTGGGGATACAGCAGTAAAGAAATACAAAAATCCTGC[C/T]CTTATA GAGCATACATCTAGAGGTGGGAAAGAGGCAATAAATA

WI-14836	28	T C ---			---	TC TT TG AG GG GA TAG AG GAC AG AG T G T T / C / G T T G A T T T T C G T T C G G T T T C A G T T T G G T T G T C A T T G G T T T T G T T T T T G T C T A T T T T G C C C C A C C C T A T A A A A G C A G T G C C A C C C A G A G G C A G
			TGGTGACAG GAAATAC TT	TTTGTTGCTA CTTTTACAAA CTTT		ACATTTCC TTATGATAGCAACAAC TAAATATGATGGATGGTGACACGGAAATAC TTAAT[AT]TAA AGTTTGTA AAAAGTAGCAACAAAATTTGAGTATATACTATAAGTGATAGAGGATGTATATGAAAAA GGCTATAAAAAGCTCCAAA
WI-14856	60	A T A A				ATGGCAATTTACTTTATAGCAATGAACAAATATTTGTCAAAGGGCAAAATATTTTGTCTG[A]AG TTAATAAAGTTAATATCTTTTACCACAAAGCTAGAGGTCAACAGTACCAC TATATTGATTGCCACT ACCTGGC
WI-14863	61	G A ---			---	
			GACATTCCAA GGCTCTTAAC	TGGGGCTGCAG ACACTC		TTTTAATTAACGTAAAAAGGAGGACATTC CAAAGGCTCTCTAACA T / C / G A G T G T C T G C A G C C C C A TTCGCTTTGAGATGTGAATGTGTTAACCCAGGGTGGA
WI-14867	46	T C A				ACGGAGTCGTCTCTGATGTA TTTCTGTCAAAAAATGTTTGCCTGATTCTTAATCATGAAGAACAAT AGAAAAATCCAAATTGACAGATATTCTGCA[G/A]AATAAATGGCCTGACCTCATCAAAAAACATCA ATGTCATGA AAAACACAAA
WI-14733	98	G A A				TTTTGTACCTATCCCTGTTTCAAGTGCATGTACAGGAAGAGTTGTCTCATAAGGTGCCACTAAGGAAA ACTTCTCCAT / A / C / A A G C T G C T G C T G C A C G T T G C C T G G G C T T T G C T A A C C C C T G T G C A T C T GCCTGTGTTCTGTCT
WI-14898b	79	A C ---			---	TTTTGTACCTATCCCTGTTTCAAGTGCATGTACAGGAAGAGTTGTCTCAT / A / C / A G G T G C C A C T A A G G AAAACTTTCTCCATAAAGCTGCCTGTGTCACGTTGCTGGGCTTTGCTAAACCCCTGGTGTGCTGCATC TGCTGTGTTCTGTCT
WI-14898a	50	A C C A				TGGTATTTATTTCCGACATTA CTGTAGAGGACACATTTGGACTCTGAC[G/A]ATTCCCTTGCAGCAG ACATTTGTGAAGCTGCTGGTGGCACACCCCATCAATCAGTGACTCTCTGCACTGCAGAGGGGGCCACATG CAGCATGCTCAGGTG
WI-14907	48	G A				CTAGAATCTGGGAAGTCCAAGCTCAGTGCACCAATACATTCAGTTCTGGT[C/G]AAGGTCCTTTTC CTGGTTGCAGACAGATACTTGTCTGTATCTCTACATGGCAGAGAAAGAGGAAGTAATCT
WI-14911	52	G A C				CTGATGCTTTGACATCTGGGCAATTTGCTGTCTCTAGAGAGACTACTTCTCCTGGGACCGCAATTC TAGTGATAGTAGAGGACTCA / C / A / C C T G C A C G T G C A C C T T T C A T A T A C A G A T C A A C C A A T C C A A A C CTACACCTCCAACCACT
WI-14913	88	C A ---			---	
			CTGGACACAG TTTTCTTAGC	CAAGCCCAGGA CAATAAATTC		ATTTCCCTTGATTGGCTGTGTAAGCCTGTGAAGTCATGCACATCTGGACACAGTTTCTCTAGCA[G/ C]GAATTTATTGTCCTGGGCTTGATGGCTTTACAGC
WI-14914	66	G C A				GTTATTTTCAAAAATGACACATCCAGATTTGAAATGGGCACCTAGCGAAT / C / A C T T G T G G A C C A C A AGACTTGCTGTGAGAACATGTTCAAAGACAGTTTTCAAAATAAAAAATTTTCCCTTAATCAGGTCCA
WI-14926	49	T C ---			---	

WI-16083	89 C T	ATGTTTAAACA CAAACATATC AAGGAT	TGAAAAAGATT OCAGCC	GCATCTTTATTACCACAGAAACTCATTTATGTCCTTAATCATTTGTTTAAATATAATATAAGCATGTT TAACACAAACATATCAAGGATC/TGGGCTGGAATCTTTCCATTCTATAGAAAAAGCACTAACCATC CATTAAAGCAG
WI-14930	55 C T	GGAGGAGTCC CTCATGGAT	CACAACCAACC AATACCGC	CAGTCTGTGTTCTGGAACAGCTCTCCTTTTCCACAGGAGGAGTCCCTCATGGATC/TGGCGGTATTG GTTGGTTGGTGATTGGGGAGCAAGAGGAGAGCAA
WI-14946	47 T C	TCAATCTGAAGGTGTCAAAGTGGTCTATTTGCCCCACAGACATAACA/TCTCTCTAAATCATCTCTCTA GATCAGGGAGTCATAAGGACCAATTAAGGCTCATACACACAGTACTTTATGGAAAGGATT
WI-15987b	80 A G	ACATTAAACACGACACAATTAAGGGGTCCCAACGAGGTTGGTAGTGCCTTCCACTATGTGAGGACAC TAAGAAGATGGTC/A/GTCTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
WI-15987a	32 C T	CACAAATAAA GGGTCCCAA	GGAAGGCACTA CCAACCTC	ACATTAAACACGACACAATTAAGGGGTCCCA/C/TGAGGTTGGTAGTGCTTCCACTATGTGAGGA CACTAAGAAGATGGTCATCTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
WI-14948	56 T C	AGGGAACCTG CTAAGTTGTCA G	GATGATCTTAC ATCAGTTGTTG GA	GAATAAGTTCTTATGCGGTTCTTCCAGGGAACAGGGAACCTGCTAACCTTGTCAGT/C/TCCAAACA ACTGATGTAAGATCATCTTCTGACCATAGCGAACCTGTGAAGGCTTGCTGTTCCCTCCAGCTGA
WI-16100	52 A G	CAAAAAGCTA TTTCTCTACAG TTGA	ACAGGAATGTC AGAAAACAGT ATATTAC	TTGTGTTAAATTCATCAAGGAATTGACAAAAAGCTATTTTCTACACTTGAC/A/GJGTAATATACTG TTTTCTGACATTCCTGTTATCAACTCCTCTGAAAATC
WI-14958	83 A G	AATAATTTAT CTCTTCTTTT CAAGG	AATGCATTAT TTGGGTTTT	GTGATTGATCTGTAATTAATGGGATTATTTTCAACTCTAAATTTCCAAGATGAAAATAATTTATCT CTTCTTTTCAAGGG/A/GJAAAAACCCCAATGAATGCATTTTCAGTTTCTCCAGGCTTTTGAACCTGC AGCAGAAAAATCAAGGA
WI-14976	35 C T	GTTGATTGCT TCGTTCAAAG	TCAAACATAAT CTTCCATTCTA AGC	TATTTTAAATGGTTGATTGCTTCGTTCAAAG/C/TGCTTAGAATGGAAGATTTAGTTTGAGGAG GGCAGGTTTGGGGTAGGCTCAGCGGGCATAGTGGCCACAGAAGATGCCATCTCACACCTGGAG ACGTCCATGAGCACCTCG
WI-14981	31 G T	TCAGTGGTGT TATTGGATTT T	CACCTCTGACA TAATACCTTAGC ATAAA	TAATTGATTCAGTGGTGTATTGGATTTT/G/TJTTTATGCTAAGTATTATGTCAGAGGTGGAGAAT AAAGAGGAAAAAGAAACAAGTGTGGCTCTCGCATCAACGACCTGATCTTGTACAGGAAGTTTTTGA GAGCTCACAAA
WI-14992	80 C T	TGCATTAAT GAAGCTGCAG	GCTATGTGCTC AGCTTTCT	TGATTACATTTTAAATCATGCCTACCAGCCCATCTAAGCCAAATTCAAACACCCTCTGCATTA AATGAAGCTGCAG/C/TJAGGAAAGCTGAGCACATAGCACCCAACTGATCGGAAAGAAACGTA
WI-15002	72 T A	AAATCTCTTCTTTCACACACAGATGAACCTTTAATAAATTACAAATGCACCTGAAAATGCCTTCTTGA TTTCC/T/ATTCAGTTTAGGCCTCAAATGGGCTCTCCCTCAAGGCTGGACCTCAAAGGCCAGTT
WI-15000	90 G A	GACAGAAAAA GACTCAGACT GTCTAA	GTTTCTAGTTC TGCACAAACTT CA	TCAAGCCAAATATCTGCAACAATAACATGTATTGAAAGGTATAGAAATAAACAGATGGATAGACAG AAAAAGACTCAGACTGTCTAAGTA/G/ATGAAGTTTGTGCAGAACTAGAAACAAAAATCCACCT

WI-12323	68	G A	C A C A A T A C T T C A T G T A C C T A T	C A C T G G A C A T A T T C C C T A C C T G	A T T T T G T T G A T G T T G G T T A A A T C T T A T C T C T T T T T T T A T A C A C A A T A C T T C A T G T A C C T A T G A A A T A A [G/A] J A C A G G T A G G A A T A T G T C C A G T G C A A C A G A G G A C T C A C A C C T G T G C A T A G A C A G C A C C
WI-14883	91	A T	A A G G G A C G A T T T A G T A T C T A A	G G C A T G T C C C A G T G T T T T	C A T A A G T T G C A T T A T T C A C G T C C A C G C C A T C T A A A G C T A C T G T G T A C A G T A A T C A G G A C T G G A G A A G G A C G A T T T A G T A T C T A A A A C A [A/T] C A A A A A A A C A C T G G G A C A T G C C C C C T G A A T T G C A A G T T G G A G T C G T A A G A A T C T A C
WI-13470	100	C A T	C C T G C C T T T A T A T T G G A A T T T C	G G G A G A C C A T G G G T C T C T	A T T T T G T T G T T A T T T A G C A C C T G A A T T T A G G C A A G A G A A A C A T T T C A C C T G A A G A C T O C A T G C A G T C A A A T T T C C T G C C T T A T A T T T G G A A T T C T A [C/A] A G A G A C C C A T G G T C T C C C A A G T G A G G A A G C A G G C A C T C A G C C C T T C
WI-14712	38	T A C A	T G A A T G C T T C C A A G T A C A A A T	T G A A A G T A T G T T G T A T A T G G T A	T T T G G T G C T A C T T T T G T G A A T G C T T C C A A G T A C A A A T C A [T/A] C T C A C A A T A C C A T A T A C A A C A T A C T T T C A A T C A C A A C T C A A A T A T A A A T A A C C T A C A A A A T C A C A T T G C
WI-13712	40	A C T A T T G	T T T A C T T T G T T G T C A T T T T A T	C C A T A A G G T C T C A C A C T T T T C T	T G G A T A C C C T T T A C T T T G T T G T C A T T T T A T T C T A T T G [A/C] A T T A T A A G A A A A G T G T G A G A C C T T A T G G C T T C T G T T A T T G G C A A T A T G C A A T A T A T T G T G T T G T T A A A T T T A T G C A T
WI-16163	35	C T A	T C T G G T G A T G C A A T T G A A A T A	G C T G C C A A T T A C A T T A A C T T T A C	T C T A A G A T T T A C T C T G G T G A T G C A A T T G A A A T A A [C/T] A T T G T A A G T T A A T G T A A T T G G C A G C A T T G C C A A A G T T A A G A G A C T A T T C T T T T A A C A A A G A C A G T G T C G A C A T T A T T T C A G G T
WI-13453	88	T A T C	A A T G C A C A A A A T C T T G T C T C T	T C A G A T T T T T A C A T C T C T T T C T	T T T T T T A T T T G C A T T T G A T G C T T A T T A T A T T A T T G G A A T T G C A G I G A T A T T A A C A T T T G T A C A A A T G C A C A A A A T C T T G T C T C T [T/A] J T G C T A G A A A G A G A T G T A A A A A T C T G A C C T A G T T G A A C A G T C T T A A T G A A C T C A T T G T C C A T
WI-16167	58	T C G A T T T T	C G C A C T C T A A A T T A G A G A T A	T G C T C G T G G T G A A T A A G A T G	C G G A T A T A A T T A T G T A C C G C A C T C T A A A T T A G A G A T A G A T T T T T T C T G A T A T A C A T T T [C] C A T C T T A T C A C C A G A C A C C A C A C G C A G T A G A C A G T T C C A C A C C T G A T A A A T T G C A C A A G A T G
WI-14482	17	G A	G C A G A C C A A T T A A T A A [G/A] A A T C T G C A A G T T T T C C C C A A G A A A C T C T G G A A C C A T A G T G C C T A A T G C C C T T T A A A A T C G A T A C T A A A G G A G A G A G A T A A A A G G A C T G C T T G A T G T G A C A G T C A C T G G T
WI-15069	81	T C	T G T A G T T C T T C A A A A G A C A T G T T G G C A G A T A G C C A G G C C A T A C T A T G T G T A T C C C A G T A T C A T G T A C G C A T A A A A A A A A [T/C] G T G T G C T T G C T G C T G T G A G T G A C C A T T G C T T A A G A T A A A
WI-16156	97	A C C C A G A G T C G C	T G A A G A T T A A C C C A G A G T C G C	A A T T G T G T G C A T T T T G A A G A G A	A T C T G G T A T T T G T G T A T C C C A C A A G T A T A C A G A A T A C T C T A T A A A C C A A A C C C A C C C T T C A A T A T T A C A C T A A T G A A G A T T A C C C A G A G T C G C [A/C] T C T C T T C A A A A T G C A C A C A A T T A A G A C G
WI-15012	59	G T A T G T	G C A G C A A G A T T A C A T C A G T A	C T C C A A A T A G C C T A G A G T A T A G	C A T G G C A G C A A G A T T A C A T C A G T A A T G T A A T A T A T A C A G C T T T T T C A T T G A A G C T T T [G/T] A C C T T A C T A C T A G G C T A T T T G G A G T T C C C C C A C

WI-15100	74 G A GTCACCATGTT ATATTTCTTT TAAGAC	TCTTATTCACAGCCAAATAACCAATATTTCCAAATAAGCAAAAAATTGGAACAGACTGGA GTGAGAAC[G/A]GGTCCACCACCAAGCCCTCAAGACAAGATGGACACGGCAGCTGGTTCTGGGGT GCATTTCTAGTGGACTTTAT
WI-14492	92 A T AATTACT		CCTTTATTTTC CCAAATATAA AATTACT	ATATTTCTTT TAAGAC	TGGTACAGAAATGTTTAAATTACAGCAGGGCAGTGATCCAGTTAAATAAATAAACCCTTTATTTT CCCAATATAAATAATTACTAAATTAA[A/T]GTCTTAAAGAAATAATAACATGGTGACAGCTTT
WI-12002c	89 T C	TCTTTAATTTTATCGGAATCCAGGACACAAACAAGAAAAACACCCAAAAACCACATGGAGACAGAAG ACGAGACACAACCTCTCCCCAC[T/C]GCCTCCCTGCTCTAGAGTGGGACAAAAGTGGGGGTGAGAC AG
WI-12002b	68 G A	TCTTTAATTTTATCGGAATCCAGGACACAAACAAGAAAAACCCAAAAACCACATGGAGACAGAAG AC[G/A]AGACACAACCTCTCCCCACTGCCTCCCTGCTCTAGAGTGGGACAAAAGTGGGGGTGAGAC AG
WI-12002a	30 C G GGACACAA		TCGGAATOCA GGGAGCCCTA GTTGCAGTAA	TGGTTTTGGG TGTTTTCTT	TCTTTAATTTTATCGGAATCCAGGACACAA[C/G]AAGAAAAACACCCAAAAACCACATGGAGACAG AAGACGAGACACAACCTCTCCCCACTGCCTCCCTGCTCTAGAGTGGGACAAAAGTGGGGGTGAGAC AG
WI-15116	96 C T GTTGCAGTAA		GGGAGCCCTA GTTGCAGTAA	ATGACA	TTTTCAATTTTATTCAGAAAAAGAAATCACATTTTCAGTAACAACCTTACATATAGAATTAACCTTTG TTCTGGAATGGAGCCCTAGTTGCAGTAA[C/T]GTGTCAATAAATAATTCATATTCAGGATTTTG TGAATAGGTGATTGGGA
WI-12578	37 C T AATGGGAA		GGCCTAAAGG AATGGGAA	TCAAGCGACCA CCAAAC	GCAAAAGCAAAGCTATGGAGGCCCTAAGGAATGGGA[C/T]GTGTGGTGGTGGCTTGTACTTGGT GCTTGTGTGCATGGAGCAGAAAGTCTCTGCTGCTCATGCAGGGGGTGCATATTTTAACTGCACATAAT TTGGCAAACTGTCATTG
WI-15153	40 A G GCATTGCA		CCCTTATGTTG GCATTGCA	AACCTCAGATA AGTGCAGTGT T	ATTCACGTTGGCCAAGATCTCCCTTATGTTGGCATTGCA[G/A]GACACTGCACCTTATCTGAGGTTA GAAAAAATGTAGTCTTAATAGCCCTCTTAATGTGTAGCAAGGCAAAATTACCATTTTCCTAA
WI-15215	84 G C TCAAATGGG		TGGCTTTAGAA TCAAATGGG	CCAAAGGGGA AAAAGTCA	CCTTGTCTCTGAACTGGGACCAGGATGTGAATAATTTTGAATCTGTGACAGGTGAGGTATGGC TTTGAATCAAATGGG[G/C]TGACTTTTCCCTGTTGGTGGAAAACTCTGTGAGGGTTTGGCA
WI-15225	80 C T C		CTTGAGGACCT AGAAAGCAAA	TTTGATTGGCA TAATCACTCC	AGGAAAGAGTGGTAAAGCAAAGGCGATCATTTGGATGGAATGATTATGTGTACAGGACCTTGGAGAC CTAGAAAGCAAAC[C/T]GGAGTGATTATGCCAATCAAATGCAAGGTTGGAGATATGCTAAAA
WI-15152	51 G A	AATTTGCTAGTGCAAATGGACCCAGAAATTTGGAAGGGCTATGTAACTACACA[G/A]TATGCACACCAC AGCCATGTCAGTGTACAGATCCTCTTGTGCACTTCTTCTTAAAAACACATCAAAGGCTGCA
WI-15123	55 C T TAGGATG		TGTTAGTGACA GACAGATAAA	TGCTTAAGGG CAACAGAC	TGACTGTATACCAAATGCTGTGCTTAATGTTAGTGACAGACAGATAAATAGGATG[C/T]GTCTGTTT GCCCTTAAGCAATTTACAACTCACTGGGGAAGAAACAGACATGCAACACGAGATAAACAACAAAT

WI-15182	49 C A	GCACAACAG GGCAAAATA	GCATGGGTTAA TCCAGCA	GAGACTGCCCTGTGACACA ATGCTAATGGGTTA	GAGACTGCCCTGTGACACA ATGCTAATGGGTTA
WI-15198	38 T C	GGGCGCTGGC ACTATCCGC	AGGCAGAGTAG AGGCAGAGTAG	GTGGACCTCTACAAGT ATATGGTTTCAGATT	GTGGACCTCTACAAGT ATATGGTTTCAGATT
WI-12801	42 T C	TATCTTGCTT TAGAT	ACATGCTTACG TAGAC	TCAAGTGGTAAATAGCC ACAACATTACGACCC	TCAAGTGGTAAATAGCC ACAACATTACGACCC
WI-14510	104 A T	TGCAAAATA TGCATAACAA	TTGAAAATGGT TAACTGGCA	ATGTTGAGAGTAAATAT TTGTTTGGCTTTT	ATGTTGAGAGTAAATAT TTGTTTGGCTTTT
WI-15239	57 T C	CATTGCAAT AAACACCATC	GGACCTTATCT GTGGACTCAGG	CAGTGTGATGACATTT TCCACAGATAAGGT	CAGTGTGATGACATTT TCCACAGATAAGGT
WI-12634	52 T C	GCATCATATG AACTGTCTAGC	GGACAAATTGT AAACATAGCT	ATGAGTTTATAAATG TGTTTACAATT	ATGAGTTTATAAATG TGTTTACAATT
WI-15249	34 T C	GGGCTTGACAC GAAAGTTCTAA	AGATTTTAAAC AA	TTTGC TTGAAGGGCTT TGAGGAGGCACAGG	TTTGC TTGAAGGGCTT TGAGGAGGCACAGG
WI-12159	28 C T	AAGACACCGT GCAATGTC	CCCTCTCCTCA GTGCACCTT	CTGTCCGGGGAAGACAC CCAAACCCCTCGA	CTGTCCGGGGAAGACAC CCAAACCCCTCGA
WI-12648	41 A G	CCTAGTGGCAT TAAGGATGC	AGTGGACATCC T	TCCCCAGATTGTGGA AACCGATGTTA	TCCCCAGATTGTGGA AACCGATGTTA
WI-12684	64 G T	CATGCTGTAA ACAGCTGTGC	GGAACAACAA AGCCTAAATGG	ATGAGAGGTAAGTGT TCCATTAGGCTTT	ATGAGAGGTAAGTGT TCCATTAGGCTTT
WI-15260	75 G A	AAAGGATGAA GCTAATCATG	TCTCTCCAGGG AGCTTGC	TTTATAAGCTGAATG AATCATGGA[G/A]	TTTATAAGCTGAATG AATCATGGA[G/A]
WI-15325	39 T C	CATGTGGCTGG GAGGC	CCTTCCACCAT GATTGTGA	AAGGTTAATGGACTC GGCACATCTTACAT	AAGGTTAATGGACTC GGCACATCTTACAT
WI-13936	123 C T	AGTTGGCATT AATAGCCAT	TGAAACTCCCA CATGGAGTT	TATTTGAGTATTCATC CCATAGGTTTCAGAA	TATTTGAGTATTCATC CCATAGGTTTCAGAA

WI-14528	62	T G T A A A T	TTTAACTTTT TCTGGATGGTA	CTCGATTAGCA CTTATTATAAA AATTA AAA	TATGCTTTATTGAAGAGAAATAGGCTATTAAATATATATTTTAACTTTTCTGGATGGTATAAATTT/GJTT GAAATTATAAATTTTAAATTTTATAATAAGTCTAATCGAGACATCACTGGGTATAATTGA TATTCTTTTCGGTTTCGGATGCAAAACAAAAATTTTAAAGAAAAATGTGACTTCAAAAGGAAAAAGA ACAAATTTTC/AAAGACTTGGGGAGTGAAGGAGAGAGCTGGTGCAGATGGACGAGGTCTGCAGA CG
WI-15347	74	C T A A T T	GACTTCAAAG GAAAAGAACAA	TCACTCCCCCA AGTCTTTG	GTATTTCTGATGCTTTGACATCTGGGGCATTGCTGTCTCTAGAGAGACTACTTCTCCTGGGACCAGC CAATTTCTAGTGATAGTAGGACTCA/C/CTGCGACGTGCACCTTTTATATACAGATCA TTTATTGGCTGTCTCTGTAAATACAATGTGGTGAACAC/G/ATCTTAATTCAGGACATCTTCCACCTTG TTTTGGCTTCCAGTTGTACTGCAAGACCAGTGTGAGGCACATAGGCTGATTAAATCAGTGG
WI-14546	95	C A G G A C T C A	CGAATTTCTAG TGATAGTAGA	AAGGTGCACGT GCAGG	AGAAATTTTCCCTTTTAAACAGGACAAGTAACAGATTACATCAAACTTCAGAACTTCTCAATAC CTAGTTATTATACACATTCCTCATCTGCTTGA/G/AGAGGGATCTTGGTGGCTTAACA CCAGCTGGAGGTGGAATAATGCGGCAACCACAGAAAAACACACAGCTACACACAGGCCTGCATT TGGCTTAT/C/CTGCTGAAAAAGAGGGCGGACCTCTTGATAAAGAAATGTCT
WI-15353	37	G A ...	CATCCCATCT GTCITGCA	CCGACCAAGAT CCCTOC	AAGTAGAACACAATAGAAATGGCTCAAAAATATCAGAAATGCACTACGCACATCACGAGTAAATACTG TTTGGTAAAACTTTGTTTCAGTTTAAATATGTA/T/C/CTGTCCTGTCATGTGATTAATATCCTTCT TACCAGTCACTCCCTAAAGAACCAAGCTTAGGACTAGGACACAACTGAGAAAAAGAGCAGGGA GACCAGACACTCTGGGTGAGATGATGATTTTAAATGCCGACGCGACACCCACA
WI-14580	100	G A G T C T T G C A	GGCCTGCATT T C G G C T T A	GCCCTCTTTT TCAGGAC	AAGTAGAACACAATAGAAATGGCTCAAAAATATCAGAAATGCACTACGCACATCACGAGTAAATACTG TTTGGTAAAACTTTGTTTCAGTTTAAATATGTA/T/C/CTGTCCTGTCATGTGATTAATATCCTTCT TACCAGTCACTCCCTAAAGAACCAAGCTTAGGACTAGGACACAACTGAGAAAAAGAGCAGGGA GACCAGACACTCTGGGTGAGATGATGATTTTAAATGCCGACGCGACACCCACA
WI-8039b	97	T C ...		---	AAGTAGAACACAATAGAAATGGCTCAAAAATATCAGAAATGCACTACGCACATCACGAGTAAATACTG TTTGGTAAAACTTTGTTTCAGTTTAAATATGTA/T/C/CTGTCCTGTCATGTGATTAATATCCTTCT TACCAGTCACTCCCTAAAGAACCAAGCTTAGGACTAGGACACAACTGAGAAAAAGAGCAGGGA GACCAGACACTCTGGGTGAGATGATGATTTTAAATGCCGACGCGACACCCACA
WI-8039a	87	T C ...		---	CACAACATTCAGAAGTTTTTCTGCATTGTCTTCTCTGATGCTCTAAAGATTTGAGCTTTGACTAT ACGATTTCCACACTGAACGCAATTCATAAGGTTTCTCCCTC/A/JAGTATGGATTCTCTGATGATTAATA AGCCCCGAATTCCTGGCTAAAGGCTTTCCACATTCAGACATTTGTAAGTTTTTCTCCAGTGTGGAC TCTCTGGTGTTCACAAGAATGGAACCTCGGCTGAATGCTTTCCACACT
WI-8044	107	C A ...		---	CTTACTACATGGGAACATCAATGCAACAAGTA/G/AJAATTTGTAACTCAAGCCACAACCTTAGTTA ATAATCATGGTTAAGGGACATTCGCAAGAGCAACTGATGCCTCAGTGAA
WI-8550	32	G A A T G C A A C A A G	GGGAACATCA ATGCAACAAG T	AGTTTACAAT T	TATTAGATAAAACCTTTGTTCCCGATTTCAGGATGTTTAAATTTGCTTCTCTTTAAACTCTGTGACTTTT CCTGGTTCAAAAGGACAGTT/A/JATGGACAGCAGCAGAGGAGTGGGGTCTGAAAAATGTAATCTTT GTGCAAGGCACTCTGTGGCTCACAACCTGCCCTCTGTCAGAGGATGCTGCCCTCCAGCCCTAAAG ACACTAGGGCTTTTCAATGGACGGGTGTTGAAGCAGCAGATGGTAAGG
WI-8057	87	T A ...		---	

WI-6192	91 A G	GACTGCTAAG GATTTAATTTG GAT	TGAAGTGTAG ATGGCTAAGTA TTAAAA	AAGAGGAACAAATTAGCTCAGTCCAACATGATTGGCAGTTGGCATATTCTAGTGAAGCAAGTGTCT GACTGCTAAGGATTTAATTTGGATG/G/ATTTTAACTTAGCCATCTAACACTTCAAGCATAAAC
WI-6194	105 T A GAAA	CACATGGCAA TGATAATAAA	TCTATCCTCAG AGTGTAGTCTG CA	AAGTGATGTGTCCTCACAAATACATTTCTCAAACCTCAAACATCATGCTTGAAATATCACTGAACTT GTCACCAAGAAGTCACATGGCAATGATAATAAGAAAT/ATATGCAGACTACACTCTGAGGATAG AGCTCTAAAGAGTAAACAAATGGAATTTTGGAAAAATAGGAGTAA
WI-6213	164 C T ...		---	CATATGCTGCTTTATTTCTGTGAAGATACACTGAAACGTTAGATGATAATAGCTAATGACAGAAATGT AGAAATGAGGCATCAGCTTCTCTAACCACTCTACAAGAAATGTTAGTATGTATTGTCTATTACATGTTT ACTTTTGATATTGTCTCATTA TACTATGTCT/ATATAATAATGTAGAATACAGTAAGTAGGTGATCC TGCATTTCAAGTAAGCGGTAGGTGGAATCCAGATTTCTCTTGAGGAAAA
WI-6217	131 C T ...		---	CGGGTTAAGAAATACCTTTAAATTTAGGTAAATAAAGCTCAAGGAGGTGGGCTGTCTGTGGTGTG TCAGTCTTCTGGCCCTGGCTGTGAGTGTGCTCCAGGGCTTGACAAGCAGCTCATTCAAAG[C/T] GGCCACCATGGCCCTAGGGTGTCTCAAGTCCAGCAGCAATCATGGCGTTCTCGTATATCTGATCC AC
WI-6238	175 G A ...		---	ATAGTCTTTATTTGTCAACGAAGGCTACACGGGATCACTTCTGGTTTGTGTTTATGCTTTTTTTTTTTC TAGAAGGTATCTACATCTGCATTTATTTACAGCCTTGTGGTATTTACAGAGTCAAGTACAGATGTTA GAAACACAAAAAGTGTGAGAAAAAACTTCTCAAAAT/G/ATTCAGAGCTTCAGGAAAAATGATT TCCACATGGTAAGGCCAGAGTCTCCAGTGTGGTATCCAGAAAGCAGCTTG
WI-6272	86 C T TAA	GCATTTATTCA GGGAAACTT	CTGTTTTTGA GAAGACAAAG AA	CTTGATTTAATCAGGGCTTTGGGTCATAGGGGATTAGTCACTGTACAGTCATAATAATGCATTTA TTCAAGGAAAACTTTAAT/C/TTCTTTGTCTCTCCAAAAACAGCTGTCTGGAACACCTCAAAATTA GGGATGTTCACTCTAAACACCTTTACTGAACTTGATTCCTTGGCCAGAGGAGGCTTTACTGTAG CAGAGGACTTAATGCAATGCCTATTCGGGCAATAAATGAATACCTTGATGCATTCACAGGCAAGAA TCCCAGCATCCAGAGAAGCTCTGTCTGC/G/ATGCAAGCCATGGCTGCAGACATCAGGGAAGCT GGTGCAGTTCTAGTCTCGCCTCCTCGATTTCCCTGCCAGCAGTCTTCTCTCTCATCTCTCTGGCCC TCTG
WI-6303	96 G A CTCTGTCTGC	CCCAGAGAAG CTCTGTCTGC	CAGCCATGGCT TTGCAG	ATGCTTTTGCATGATTCTAATTATTGCCTTTTTCAGAGCTGTGCTGGTAAAAAGTGGGGTGCCATACA AACAGTCCCTTTTCAAGCCAGCGTGTGCATGCTGCTGCCAATCAATCACTGTAATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAAACTGGATAAAGAGTTGCTGATAGTGT/C/CTCTGTT CTCCCTTTACATCTTTTGGGGA
WI-6315b	193 C T ...		---	ATGCTTTTGCATGATTCTAATTATTGCCTTTTTCAGAGCTGTGCTGGTAAAAAGTGGGGTGCCATACA AACAGTCCCTTTTCAAGCCAGCGTGTGCATGCTGCTGCCAATCAATCACTGTAATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAAACTGGATAAAGAGTTGCTGATAGT/C/AGTGTCTCTGTT CTCCCTTTACATCTTTTGGGGA
WI-6315	187 T C ...		---	ATGCTTTTGCATGATTCTAATTATTGCCTTTTTCAGAGCTGTGCTGGTAAAAAGTGGGGTGCCATACA AACAGTCCCTTTTCAAGCCAGCGTGTGCATGCTGCTGCCAATCAATCACTGTAATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAAACTGGATAAAGAGTTGCTGATAGT/C/AGTGTCTCTGTT CTCCCTTTACATCTTTTGGGGA

WI-6375	28 A G A A	GGTTATTGCA TATGGAAATC	AATGTGAGATC TTTATTCTAAC CTTTTT	AAGGTTTATTGCATATGGAAATCAATAG[A/G]TATCTTTTACAAAAAAGGTTAGAAATAAAGATCTC ACATTTGTAAAGGCACATATGAACATTTTATAGCAAGCACAAAGGCAGTGAGACATCAACAA TTGTCTCAACAGATGAAATTCATAACCTTGTTTCTGATAAGACAAATTCAAACATACAAATCAAT TACAACAATGTGCTTATCAGTCCCTCCACCCCTATATTTAA[T/A]GCAACTGACAGTTTTGAAG GACACCAAGACAATAGGGCT
WI-6409b	112 T A	TTGTGCTCAACAGATGAAATTCATAACCTTGTTTCTGATAAGACAAATTCAAACATACAAATCAAT TACAAC[A/T]ATGTGCTTATCAGTCCCTCCACCCCTATATTTAATGCAACTGACAGTTTTGAAG GACACCAAGACAATAGGGCT
WI-6409a	73 A T	CTAATATAATCTGGGCACATGGATTCCAAGAGAGATTTTGCAGCAGATTTTCATTATAGTTACTTAA CAGCTAAATAATAAGGGTGATTTAACTTACTTACAGAGTCACTAAATAATGGAGGGGAAAGGAAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCT[G/T]ATCAACCTTCCCTAAGCATCTGTCTGGTCCG CAGC
WI-6523	165 G T C T G	GCTAATCCAGT AGAGACTGAA	AGATGCTTAGG GAAGGTGATA	TCTCTAGCCCTATTAGGCTACACTGTAGTCACCTTCTATGAGAGCAAGGAAACAGGAAGATGGGC TCCTGGAGTCCAAACAGGATGGACGTCCCTGGTAGTCTCTCTTTTACACAACTTTTCCCTGAGA ACTGTCCAGTCAGGTGGACCTTCAACAACACAGCAAGCTAAACCTCTGAGAGAAAAAC[C/G]CTG ACTTTCAGAAAGCATAAAGCTGAGAAAAA
WI-6554	195 C G	ATTGTAATTAATAATTTACATGGGCTATTATTAAGGACATTGTGTAATGTTTCCACTTGTGTTTAAA [C/T]AATTACAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAGTTTGAAAAATGGGCG
WI-6558b	68 C T	ATTGTAATTAATAATTTACATGGGCTATTATTAAGGACATT[G/C]TGTAAATGTTTCCACTTGTGTTT AAACAATTACAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAGTTTGAAAAATGGGCG
WI-6558a	42 G C	AACCAACAAAACTAAGAAATGGGAAAAAGAAATGGCAGGTGAAGAACTCTTTTCAGAGAAATAAA AGTTGTCATA[T/C]AGCAATGGATGCTGTGTCAGAACATACTGCCAATAAACTTTAAGAAAAAAGGA ACTCAATGAAGTTACTGTTATATAAACACAGGAGCTCACAGCAGGGATGAAGAGTTAATGGAAGAT ATCGTGAGCCAAAAAC
WI-6629	75 T C G T C A T A	TCITTTTCAGAG AATAAAAAGTT	TGACACAGCAT CCATTGCT	CTGCCCTGAACCAATCAGATTTAGTTTAAATCAATCAATCAAACTCCAGCTGTTTCTCTTGTCTTT TTACTTAGCAAGGAAAACTTTAGTGAATGCTACTTGACAAGAAAGAAAGTCATTCTCAAGCACAC T/C]ACCCAAACTTGAAGGTGATTGAACCCAAAAATAATGGGTGGGAAACACCAATGAGGTGGAGGA ATGAGAAAGATGTGTGGGCCAAAGCTATCTGTTTATATTTTATGTTTGCCAAT
WI-6644	134 T C	TGCTAAACACCACCATTAATTAAGGAGAGTACTAGGAAAAAACTACCAAAACACAGCATGTGAAAAACAGT TGGGCACGGTGTAAAGGGCACAGACTCTGGAGCCACAGC[C/T]GGCTAATACACTGCAATATTTTA TGTTAGCAAATTATAGCTGGTCTGTGTATTAACCAAGAGCGGTATCTGG
WI-6690b	108 C T A G C C A G C	CAGACTCTGG	ACATAAAATA TTGCAGTGTAT TAGCC	

WI-6690a	28 T C	AAACACCACC ATTATTAAAGG AGAG	GCTGTGTTGG TAGTTTTTCT	TGCTAAACACCACCAATTATTAAAGGAGAGTC/JACTAGGAAAACTACCAACACAGCATGTGAAAC AGTTGGGCACGGTGTAAAGGGCACAGACTCTGGAGCCACAGCGGCTAATACACTGCAATATTTTA TGTTAGCAAATTATAGCTGGTCTGTGTATACCAAGAGAGCGGTATCTGG
WI-6770	53 A G	CAACCCCAA AACATCACA	GCCTTTGGAGT GTATAATAGTA TGAATAA	GATGTTTATGACACAGATCTTCCCAAAGTAATCCAAACCCCAACATCACA/JGJAATTATTGAT ACTATTATACACTCCAAAGCAAAATACTTCAACTGCAATCC
WI-6686	151 A G A	GCATCTTCCA AAACAAAGA	CCTTGTAAAGT ACTATTCCAAT GTT	ATTCTGTAGGCAAGGTTTCAGCAAAATCAGCTAGCACTAATCTTGACCAATGGTGAGTCAGCCTCA TCACAGAGATTTTTTTTTTAATTAGATGAAATTTTACATTTAAACACATGGTAACCTCCAAGCATTTCT TCCAAAACAAAGAAT/JG/JACATTGGAAATAGTCACCTTACAAGGAC
WI-6761	32 C A G	GATCTAACAG CTGCAGAATG	AAAGCTGGG AAGGAAGAAG	CCTGAGAGGCAGATCTAACAGCTGCAGAATGGC/JACTCTTCTCCCTCCAGCTTTTGTGAACAAAAC AATTCCTTAAGGCATCAGAAAGCACTGAGTGCAAAATGGTTGTTCAAGGTACAAGGTCTC
WI-6844	225 T C		---	TAAATACTGCCAACTAGCATTACGTCCACTCTTGATCATCAATTAACAAAGGGTATTTCCCTCTTG GTATTTTCAAATGATGCATTATACAATAAACGAAGTTAGAACTTAAATGCACCCCTGATTAAATTATG TAAACTGGTAATTTGTTTTAAAGGCATAATAATTTGGTCCCTTCTCATAAATGGAAATTTAAA TATTTCTCTGATAGTCTTGAGGTT/C/JATCATATGAGTAGTGCAAGTGTG
WI-6824	112 A G		---	CGGTTTGTCTACACTTAATGGTTTTTTTTTAAAGGGATTTTTTTCAGGCTTGTGTCAGCAACATCAA ACAAAGGTACTGAGTACTCCACAGGGTACAGAGTGTGCCAA/JG/CACCTTAGAAAAATTACAT GACACGGAGAAATGCGCCTCTTGTCTTGAAGAGCTTACAGTCTAGGGATTGACAACCTCACAGT CTTAGGAACTGGGCAAGTAAGGCAAAATTCATCCCTAGAGCTATTGTG
WI-6889	139 T C AATC	GAAAAATGAG ATGCAGTTAA	TCACTTTGTGG CTTTTAATTAT TCT	GTACAAAAAGCTGAGAGAGGCCAACATGGAAGTGTCAAGAAACATTTCTGATAGGTACGGACAA AAGAGCTCCTTCAATCAAGGAGTTACATATTAGTTCTCACCATGCTAGAAAAATGAGATGCAGTTA AAATTC/JC/JAGAATAATTAAAGGCCACAAAGTGAAACTGTTCTGGGGCCCTATGTTGTAGATT CTCT
WI-6911	216 T C		---	TCCCAGCTCATATTTATTTGGGCACAGAGTGGGCACCTCAAAATATCTGATGAACCTGTGAACTGAA AAGAGGTCTCCTTAAACAAAGATATCATCTCCGAAGAGAGAGTCCCAACCATATAAAATGTATGAT CAAGTCCCAGAAAACTTGGCTTCCCAAGGAATGTGTTCTAATTTGGTTCAAAGCACACTGGTTCC CACTTTTACCACCTT/JC/JCATGACATGGACAATAGTACTACTCTTTCTAC
WI-9413	112 G C		---	GCCAGTCTCTAGTAAGTCTCTAGGGACATGACCAGACCAGAGCCCTGTTCTATATGAAGACAAAC AGGTGGCCATACCTGGGTGGAGGATACCGCTGCTATTTCCAGATG/JC/JAAGATTTGGTGAAGGAG ACCATGACAGATGACAAACGGAACAGTTTCTCAAAACAGAGGTATGA
WI-9557	74 C T		---	AAAGCTTTAAAAAAAAGTGGTGTCTATCTTTAGAAAACTTTTCAGCAAGATCAAGTAGCCACGCT ACAGCCTCTCTGGTGCATCTTAACCCCTCTCCTTTT

WI-9617	37	G T	---	---	TGCTCTTTTATTACAGTTTCACAAACACACGCCCGTG[G/T]GGCACAGTCTACCAAAGTGCCCCGAG CGCCACGCTGGGCCGGAAGGTCTCATTCTGTCCTCTATGGACTGATTGAATTTGGGATGGCCAG CTCCAGAAATGTTCCACGTGGGGCACTCTGTGGCAGAGAGGCTGAGCCCTTGCCACACTGGCACCA AAGAGGTGCACGATGCAGTGCAGTGGTCCAAAGCCGGTGTGCTGTG
WI-9657	121	T G	---	---	AATGCTGGAGAAACATCAACATTGAGTTGACATTTGTTTGTCTGAAGTATAGTACCATCCACTAT CATGAATTTTGTTCATTACAAATGATAGAAAAGCCAGATTCTCAAAATAAAGT/GJATAATTCCT TGTTAAATAAATGTTTATAAATGTTTATGAAGTCAATTACATTATCTTTTAAAAAAGTAAAAA TTTGAACATATGACGCTTTTCATAATTAATGCTTTTGATAGATTGAGG
WI-13119b	114	G C	GCTGGGA	AAAAATTAAAC CAGGTGTGGTG T	CAGGGTCTGCTCTCTCCAGGCTAGAGTGAGGTGACACAATCAAGACTCACAGTAGCCTCAACCT CCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGT[G/C]JACACCCACACCTGGTTAA TTTTTTTAAITTTTGTAAAGATAGGTCTCACTATGTTGCCCGCTCTCAAAAACAAACCAACTAAC CAGGGTCTGCTCTGCTCTCCAGGCTAGAGTGAGGTGACACAATCAAGACT[G/C]JACAGTAGCCTCA ACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACACACACCTGGTTA ATTTTTTTAAITTTTGTAAAGATAGGTCTCACTATGTTGCCCGCTCTCAAAAACAAACCAACTAA C
WI-13119a	51	C G	---	---	ACAGGAATCTGAAAGTTACCAAGGCAATTTCCCTTTTAGGATCATAAAGACTACAGACTTAAGCTT TTTT[C/T]CTTTTCCATATAATACACAAAATTTCTAAATATCCTTAAAAAAGAAAATATAAAATAGT TTCAGTATGTTATGTAGAGTCACATACTATGGCAAAAATATTTTATTAATTGAGGGAATAGGCCAAT TT
WI-13112	71	C T	AGCTTTT	GGAAAAAG	TGTTAACATTTTATTGGTACGTGCTCTCAGTACAA[C/A]AAACAGCATCAGTAGTGACACTTTGAT AAAAAGGAATTTTAGCTTAGTAAAAAGAAAGCCCAAGGTGAGAAGTATAATGAATATGTACAT CTTTATGGAAACTGTTTGTGTGACCCTTTATCTTCCCTGTGGATGAGATGTATGCACACACAAAGT AAA
WI-12988	36	C A	CTCAGTACAA	GTTT	TGCTATTCTATGACAGACACGTGAGACAAAATATCTTATTTACAGATGGAATAGACCCAGACATTA TTCAGTACTTTAACCACTAATAGTGAACCCCTGAGACTTTA[G/A]ATCTGCAAAGGGTTTAAATAT GCAAAATATCAGATATATTTCCATTTTAAACCCATATTTAAGTTTCCATTTTCTTAATAGAAAATGA TAAAAATGTTTCCCAATAT
WI-13020a	108	G A	CTTT	CATTATTAAAC CCCTTTCAGA	TGTATAAAAAATCCAACTTGTTCACAAGTACATATGTCCTATGATTTTATGCATACATCCATATAC ATATATCAAGGTAAAGTCCA[G/T]ACAAAAAACAAGCAATTTCTATGGCCAGTGTCTACAGAAGT AAGACTGTGCAAACTTTATCGTATAGTCAAAATGAGATTGCACACTAAGGCAGGATGAGGCAGAAAGCA AGTGTGTCCA
WI-12837	87	A G	AAAGTCCA	ATGCTGTTTTT	

L42611b	50	G C ...			GTCTCAGGCCCTTCTCTGGCTGCAGAGCGTCTTCTCAGGTTGCCTGTGCTGCTCTCCTGGCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCTCACTTCTCTCTGTCTATACCT GCCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTACATCATATGTTATTCACCA CTGGAGCTTCACTTTGTTAC
L42611	34	T C ...			GTCTCAGGCCCTTCTCTGGCTGCAGAGCGTCTTCTCAGGTTGCCTGTGCTGCTCTCCTGGCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCTCACTTCTCTCTGTCTATACCT GCCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTACATCATATGTTATTCACCA CTGGAGCTTCACTTTGTTAC
WI-1172b	179	C T A	TGAAGAAATG GCTGATACCA	ATGTGCATTTT TCACTGCAG	TGAACGTGTGGTTAAACTAGGCAATTGTTAAATCAATTTAAAAACAGGCCTAGAAACAGTG ACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAATACCATTTTCTGCTTC AAAAGAAAGACATGAGGCTTCTTGAAGAAATGGCTGATACCAAGCTGCAGTGAATAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1172a	17	C A ...			TGAACGTGTGGTTAAAC[C/A]TAGGCAATTGGTTAAAAATCAATTTAAAAACAGGCCTAGAAACA GTGACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAATACCATTTTCTGCT TTCAAAAGAAAGACATGAGGCTTCTTGAAGAAATGGCTGATACCAAGCTGCAGTGAATAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1177	35	G C A	GCAGATTGGA AGTGTGAAAA	CACTTACATTT CTGAATATTTA GACTCTTT	AGAGGCAGATTGGAAGTGTGAAAAAATGAAAGAA[G/C]AAGAAAAAAGAGTCTAAATATTGAG AAATGTAAAGTGTGCGCTCAACTGTTCTTTACCCACTTAATCTGCAATTTTGAAAACTAGATTGAAT TCCTTTGCAAAACCCCTTGCATCATGGATACCCGAGTTAAACCGTTAATTTAAAGACATTAACATGG OCTGGTG
WI-1231b	141	G A ...			TCCATGGTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCACTATGCATTGGAACATTCCTCATATTC CAACTAAGCAGGAGTGTTCACAATAAACACATAGGCTCTTTATCTCCTTCTTTCATTAATTTCTT TCAC[G/A]TTATTCCTCACCCTGAACGCCCTTCTTCTCGTAGTGACATTTTAAATCCACCTTTAC ACATTGGAGCC
WI-1231a	126	T C A	GGTCTTTATT CTCCTTCTTC	CGTTCAGGGTG AGGGAATAA	TCCATGGTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCACTATGCATTGGAACATTCCTCATATTC CAACTAAGCAGGAGTGTTCACAATAAACACATAGGCTCTTTATCTCCTTCTTTCATTAATTTCTT CTTTCACGTTATCCCTCACCCTGAACGCCCTTCTTCTCGTAGTGACATTTTAAATCCACCTTTACA CATTCGGAGCC
WI-472	114	G C ACAGAAAAG	ACATACATAT CCATTATACA	GACCTTTCTTT TCCAGCC	GAAGGCAGGACTGTGTTTGGAGGACAAAAGTAAATCTTTTATATCTTTTAAATTTTATT TTTTTTCAGGCATATAGACATACATATCCATTATACAACAGAAAAG[G/C]GGGCTGGAAGAAAAG GTCAAGTGAGATTTCAGATATCTTAAATGAAGGCTGACAAATTTGGGCTTGATT

WI-478	46 C T	GCATGCTGTG T TACTCTATTT TGTTT	AAATGCCACAG GTGGCT	AAACCACTGCAACCTTCAAGCATGCTGTGTTACTCTATTTTGTTC/TAAGCCACCTGTGGCATTTT CAAAATATGATAATCTCTGCCACCATACTGCTTTAAACACAAAATAGAATCTGGCAGCAAAATATAGC ATAAGCTTACTTCTTAATCAAGGCTACCATCAGTACCTTAGCACATTTAAAAAATAAAAAACCAAC ACTGCCCA
WI-533	29 T C	ATCACAGCAG AGTACCTTTCT AACT	CTTCCAACT CTACACAATCT T	AGCCATCACAGCAGTACCTTTCTAACTT/CJATAAGATTGTGTAGAGTTGGAAAGGAGGACACAGGA CTGTTCTGTGGTATAATGACCTGTGTCCAGTTAATCCA
WI-601b	112 T A	TCACCTATCTCTTTTTTGTGGTGAGAACACTTAAATCTAAGAATGATCAATTTCAAAATAAAGATGG TAGTGAGCGAACAGAGAGGTTTCATTGACTCTAACTGAGTACTTAACTGAGTACTCAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-601a	74 C T	TCACCTATCTCTTTTTTGTGGTGAGAACACTTAAATCTAAGAATGATCAATTTCAAAATAAAGATGG TAGTGAGC/TJGAACAGAGAGGTTTCATTGACTCTAACTGAGTACTCAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-863	107 A G	CTCCTTCACAA CCTCACCA	CTTCCCGTAA GCCAAGT	AACAAAACAGACACCCCTGGCTTCTCTCACCAGTCCACATGGGTGCCAAACAATCCACATTCCT ACATCTCCCACTGGGCTGCTCTTCAACACTCACCA/AGACTTGGCTTACCGGGAAGCATAAA GCCAAGCATTTAGTCTTTTATTGCAACATGGTCTGGCTGCAATAC
WI-919	36 G A C	ACTGCTTGCTT GTTGATTTAAT C	TTATTTCTAATC CCACATGACAG C	ACTCACTGCTTGCTTGATTATTAATCAACCTAGCCG/AJGCTGTCATGTGGGATTAGAATAAAATA AACACAAAATGAAACACACAGATTGCTAACAAAGCAGATTCTTTTTTCAAGGCACACGCTAAAGAT AATAACTTCAA
WI-991	37 A T	TGCATTATTATGACCAATAATAACTCTGTACAT/ATJCATTTATTGTTTTCATTATCACAAAAT TATGAGTGAGGATGATTGTATCCCTATTTACAGATGAGAACACTGAGACTTAGAAGAAGTATCT TTCCCAAAGTCACAAAAGTTAGTGACAGAGCCGGATTGGAATCCATCAACTTGAATCCAGAGAAAAT GTTCTGCATCACTGTACACACTGACTCCTTTTCTCCTTTGAAAACAAGGC
WI-1011	70 G C	CAGTATCTGA AGTTTTTGCT CCA	AGGAACACCTA CAAAATGACTT CT	CTTCCTGACCTGTTGTCAGTGGATGTTTGAAGGCTCTGTCTCAGTATCTGAAGTTTTTGTCTCC A/GC/JAGAAGTCAATTTGTAGGTGTTCTGGGGTTTTTGTCTAGCTTCCATTTCTCTAATACACTGC CGTCTTAAGGGAGGGCTTGCAGAGCATTTATCAGATGGCTTTTGTCTGCTGTCACCTGAAG
WI-5381	178 A T	TTTATGCAAGAGGTCCATGAGTTTACAGAACTCAAGGAAGAAAGGCCCTAGAGATGACACCCAGAA ATGAGAGTGGCTTGTCTCATGAAATTTGACAGCATGTTCCAGAGAGAGGGAACAGCATGGAGAAGA AAAATCATCTCTATCCACGTGCAGAAACTGGCAATTTAGTTTGTIA/TTTACTAAAAACACAAATGT TTAACTTGGGGTCCACAAAAGGATATGTTGGCAAAATGGTATTTCTGTGATG
WI-5791b	76 G A	CTATGTTATCCATCTAGCAAAAGCAAGACTATTTGGATAAGTTTCAAAAGATGAGAACAGGTCTCTA GAACCTCAG/G/ATCGAAAGGAAGTTTCATCTAGTCCATAGACCTTATCTCACTGACCCCAAGGTA AAAAATAAAATAAAGTAAAGAACTTACATCAGATTGTGCATTTCTTATTTTGCCACCCCTGTTTGT TAGGAA

WI-5791a	44 C G ---			---	CTATGTATCCATCTAGCAAAAAGCAAGACTATTTGGATAAGTTTC/G/ACAAAAGATGAGAACAGGTC CTAGAACCTCAGGATCGAAAGGAAGTTTCATCTAGTCCATAGACCCCTATCTCACTGACCCAAAAGGTA AAAAATAAAATAAAAGTAAAGAACTTACATCAGATTGTGCATTTCTTATTTGCCACCCCTGTTTGT TAGGAA
WI-5406c	120 C T ---			---	CACCTGCTGTTGTCCATGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTGAAGGAGCCCGAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC/C/TTTATGAGCCAC ACTTCTCATTTCTTCTAGAAATTTCTTGGACTCTGTGAAGAGGAAAGGAAAGAAAGAGAGGCAA GG
WI-5406b	118 C A A	CCAGGATGTC AAGGTGAGAA	AATGAGAAGT GTGGGCTCAT		CACCTGCTGTTGTCCATGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTGAAGGAGCCCGAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC/C/CTTATGAGCCAC ACTTCTCATTTCTTCTAGAAATTTCTTGGACTCTGTGAAGAGGAAAGGAAAGAAAGAGAGGCAA GG
WI-5406a	42 A G ---			---	CACCTGCTGTTGTCCATGGTGCCACAGACTCTTCCAGAAGAGGAGGAGGAGGAGGAGGAGGCAA GCCTTTTGAAGGAGCCCGAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCTTATGAGCCAC ACTTCTCATTTCTTCTAGAAATTTCTTGGACTCTGTGAAGAGGAGGAGGAGGAGGAGGAGGCAA GG
WI-5798	48 G C TG	TTTATCTCCC TTGTTTCTTT	ACTGTTAGAAA ACCAGTATTTT TCAAT		CCATTCTCTTCTCCCTCCCTTTATTCCTCCCTGTTTTTGG/G/C/JATTGAAAAATACTGGTT TTCTAACAGTGTGCTGGTATGGATACTATGTTATAACATGCATAGTTCTATATGGGTATCA
WI-5415	54 T A TTT	TCATCTTTTCAG	GGACTAATTC TGATCCGATCT		CCTGCTAATAATAATTTAAGCACGATTTGTCTTCATGAATTCATCTTTCAGTTTT/A/JTAGATCGGAT CATGAATTAGTCCAGGCTTTAGTTGTAATCGAAATTGGA
WI-5437	41 C T G	TCCCAGAGAA AAATCCAAGA	AGTTTCTAAAC ACAAAATATG GTTAAG		TGTTTTAACCCAGGACAGCTCCAGAGAAAAATCCAAGAG/C/TJCTTAAACCATATTTTGTGTTTA GAACTCTCTGTGCCAACCACTCTTGATGTGAGTGAC
WI-5481b	131 A G CTGCAGTCG	TGTCATTTATG	TTACTCCAGG CTCCAAGTAT		AAGCCAAATTCACATTAGTTGATGAATTTG/A/JAATTTTACAGTATCTAATGCATGGCATCTGTTTCAAC TCTGTGTTTTTCAAGAGGTAGTATATGTCTGAAAAATCTATTTTGTCAATTTATGCTGCAGTCG/A/GJA ATACTGGAGCCTGGAAGTAAAGACTTGGCTATTTTTCACAATTA
WI-5481a	29 G A AATTT	ATTAGTTGATG	CCCATGCAATTA GATACTGTAAA ATT		AAGCCAAATTCACATTAGTTGATGAATTTG/A/JAATTTTACAGTATCTAATGCATGGCATCTGTTTTC AACTCTGTGTTTTTCAAGAGGTAGTATATGTCTGAAAAATCTATTTTGTCAATTTATGCTGCAGTCGAA ATACTGGAGCCTGGAAGTAAAGACTTGGCTATTTTTCACAATTA
WI-5492	38 T C ---			---	TCATGAGTCTTTCTTCAAGATGCTTGTAAAGTCCCAT/C/JCAAAAGAAAGGATCCCATGGCCTAAT GAAGATGTACCTCCACCTTAGGATATTTTGCAGACCAA

WI-5826	134	T C ...	CCCAATACITTT TTCAGGTGAA	...	TATTTTTTTTCTCAATTCCTGGAGCACACCATGCTCTTTCTATTTTCATGCTTCACATTTATTTTTT TTTCACCTTAGTTAAATGCTTTTCCCTTGATCTAGCAATGGCCAGTTTATACATATCTTTAGTC[C] TTTCAAAATTAATGCCACCATAGAAATAATTTCTAACCAACAGCCAAACAGCCTCAGCTCTTCCTT CCTTGGTGCATTTACTCTTTACAC
WI-5546	40	C T A	GGCACCAGCCT TTTTAGAGT	CCTGTATTTTA GCAACATGGG	CCTTATAACCCCAATACITTTTCAGGTGAAAAAGGGAAAA[C]/JACCCCATGTTTGCTAAAAATACAGG AGTATAACAGCATGACATGTTAAGGGAATTACAAATGCTTGAGTGTAATCTGATGTGGGAAATAT TAGAAAATTAAAGCGAGAGAGGCA
WI-5552	97	C T	GGCACCAGCCT TTTTAGAGT	TGCACAAATTG CCCAGG	TGTTTGTTCTGCACCTCCCCAACAGTGGTCAATGAGCCTCAAGGGTTTTGATTGAGCGGGTATGGGT GGGGCTATCGGCACCGCCTTTTAGAGTC/JCCTGGGCAATTTGTGCACTAGTGTGAGA
WI-5836b	161	C T	TAA GTT GATTTAAACACTCTGTGCTCAATTTTCTCACCTATAAAATAAGATAATAGTATCTAAAA AAAAAGAGAGAGAAATTAAGTGGATAGACATGAATACTCTGATGATACTGGTGTATCCCTGAA TCCTGCAATATACACATGATTCAATGAT[C]/JCCATTTTGAAATTAAGCTTTTGAATTTGTTTCCA ATG
WI-5573	58	C T	GTTCATAAGG AGGTGGGA	TGAACAGTTGG AGAGTAATGTG TC	TCGGGTATTAGGATGGTTCAACCTCGATGATGATGGGGTTCATAAGGAGGTGGGA[C]/JGACAC ATTACTCTCAACTGTTTCATCAGAACACTTCAACAGCG
WI-5850b	134	G A	CAGGACCTTGGAGCCTTTGCTGTTTGCTCTCCACCTCACTCTTCTCTGCCCTGCCCATGGGTGGAGC CTCTCTCAGGCTTCCTCTATGCACGCTCTATCTCTATATGGGGCAATATCCAATGTCCCATTC[G/A] JTTTTGCCATTTCCCTGTATATCAACAGAGAGAGAGGGTGG
WI-5850a	92	C T	CAGGACCTTGGAGCCTTTGCTGTTTGCTCTCCACCTCACTCTTCTCTGCCCTGCCCATGGGTGGAGC CTCTCTCAGGCTTCCTCTATGCA[C]/JGCGTCTATCTCTATATGGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCCCTGTATATCAACAGAGAGAGAGGGTGG
WI-5612b	125	A T TTC	CTATTAATGA GCATCGTGCA	TTCTCTTGAGA AACCTAAAC ACTG	TGCCCTGATTGACACATAGTTATCTGACAGTAAATCATCTAACAT/ACACAAATATCTTATTCTGCCCTG TCACACTAATTTGCAAGCAATCAATGATTGACTATTAAATGAGCATCGTGTCAATTC[A]/JACAGTGT TTAGGTTTCTCAAGAGAAATTATGCTGTTCTCTCTCTGTAACCTCAAGTA
WI-5612a	44	T A	TGCCTGATTGACACATAGTTATCTGACAGTAAATCATCTAACAT/ACACAAATATCTTATTCTGCG CTGTACACTAATTTGCAAGCAATCAATGATTGACTATTAAATGAGCATCGTGTCAATTCACAGTGT TTAGGTTTCTCAAGAGAAATTATGCTGTTCTCTCTGTAACCTCAAGTA
WI-5636	26	A C CCGCAATAA	GCCAAATTTAT CCGCAATAA	CATCGAGGACT TTGGGA	TGAGAGCCCAATTTTATCCGCAATAAA[A/C]/JTTCCCAAGTCCCTCGATGGAGGCAATTCAGAAATCGGG GCAGGGAGGCAGAGGTGAGACAGATGTGAAGAAC

WI-5865c	103 C G ---			TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTTAAGAATCTTTTTTTCATTTATGCAATTC ACTGACTCACTCACTTGTCTATCAAAAATTAAC[G]AAATATAATTTTTATTACAGAGGAA CTCAGAAGCCAGAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGCACAGTCCCTTCA GAGAAGACAGACAACTAAATAATTCAGG
WI-5865b	99 T A ---			TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTTAAGAATCTTTTTTTCATTTATGCAATTC ACTGACTCACTCACTTGTCTATCAAAAATTAACAAATAATTAATTTTTATTACAGAGGAA CTCAGAAGCCAGAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGCACAGTCCCTTCA GAGAAGACAGACAACTAAATAATTCAGG
WI-5865	165 T A ---			TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTTAAGAATCTTTTTTTCATTTATGCAATTC ACTGACTCACTCACTTGTCTATCAAAAATTAACAAATAATTAATTTTTATTACAGAGGAACTC AGAAGCCAGAAAAATGACCAAGACACAGT[A]CCAGTCTCCATCTTCAAAAGGCACAGTCCCTTC AGAGAAGACAGACAACTAAATAATTCAGG
WI-5874	76 T G ACAGAAAA	CATAGCATGG ATAATATTAT	CCTAGTAAGTT TCAGTCATTTG ATATGT	CTCAGACATTCATTTTATTAGTTGTTAAATTTTGTGTTATTCATAGCATGGATAATATTATACAGAA AAAAAATTT/GTACATATCAATGACTGAACTACTAGGTAGCAATTTGTTTGCAATTTGCT CATGGAGCGAGCTTCAGCCTCTCAGTTTTTCCATC[A]TTTTTTCATAATTTACTCTCTTTCTGTC ACAATGTTCTGCTTCGTATTTCAACTCTCATTCATTCGTTGATGGTAGTCATAAAATATGGGTGATTC AGAAAAAAGTAAATG
WI-5752	36 A T TTTTCCATC	CAGCCTCTCAG AGAGTAAATT	GACAGAAAAAG AGAGTAAATT ATGAAAAA	TTAGCAGAAACAACAAAAATGTCACAACACTGCAGTAAAGAAAGTGTTCCTCCGATAAAT[A]C/GJC CATTAGGTATTAGATAAGCATCCCATAAACATTGTTGAAAACGAAGCCGAGTTTTCGATTACACACA GTTGCTGTTTTAACCTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCGTCCCACGAAA CATTGTTGAAAAACGAAGCCAGTTTTCCGATTACACAGTTAGTTGCTGTT
WI-5760b	61 C G ---			TTAGCAGAAACAACAAAAATGTCACAACACTGCAGTAAAGAAAGTGTTCCTCCGATAAATACCCAT TAGGTATTAGATAAGCATCCCATAAACATTGTTGAAAACGAAGCCGAGTTTTCGATTACACAGTT GTCTGTTTTAACCTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGC[G/A]TCCCACGAA ACATTGTTGAAAAACGAAGCCAGTTTTCCGATTACACAGTTAGTTGCTGTT
WI-5760	187 G A ---			AATATCTGGCCTTTTCTCTTAGGAGGAGATTTCACCATGGGAATCTTG[A/G]TGCAAGTTAGAT CCACCTCCTCACTATTGAGAAGCTAAAGTGTAAGACTACTCATTTCTCAGTCTCCTTGCTG
WI-5944	52 A G GGAATCTTG	TTCTCACCATG TTCTCACCATG	GGGTGGGATCT AACTTGCA	GAGTTTAATGAATCCTGTTCCCTCCTAAACCTCCTGTTCCCTCCCACTTCACATTCAGCAGATATT CTTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGATGTAATTTGATCATTTCAAGAGTGTGAG TAATGCTTGGT[A/C]TTTGCTCTGTGCCGTATCTGCTCCAATCACCCATCCACTTTATTTCCTATTAT GCTGAATGAAACGGTTATATTACAG
WI-5967b	148 C T ---			

WI-5967	165 C T ...				GAGTTAATGAATCCTGTTCCCTCCTAAACCTCCTGTTCCCCCACTTCACATTCCAGCAGATATT CTTTCATGGGTATTTGCCCAAGTCATGAGGAGATGCATGATTAATTGTGATCATTTCAAGAGGTGAG TAATGCTTGGTACTTGTCTGTGCGGTATC/TJTGCTCCAATCACCCATCCACTTTATTTCTTATTAT GCTGAATGAACGGTTATATTACAG
WI-6093	53 G C ...				GGGTAAAGATCCAGAGCCACAGGTGAACCTGCCGGTATTGAAGTCTTTGGGCCA/GC/GTCTGTAATG ATCTGACTTCTCCAGAACCCCTCTTCTCTGGAAGTCCAACTGTGCACTGAGCCCATTTGTAGGGA GCATTGAACCAAAACCCAGCGACACTGCTGACATTTGACTTTCAGCAAACTTGTATTGACGGTGAC ACACCATGCTTCGAGAAGGAATGAGG
WI-6141	80 T C AGGTACTT	CTTCTTAATTA AGCATCTACA	TGAAAACCCCA GAACAGTG		GACTCTGTCTCAAGAAAAAATAAATTGAAATTAATAATTAAAGCACTTCTTAATTAAGCAT CTACAAGGTACTTAT/CJCACTGTTCTGGGTTTCAATCCTCTTCACTTTTAGACTTCAGGAAAT CAGAAAAATGCATGAAACACAGGATTGTTACATGCAGAGAAATAGGGGAGATAAAATTTGTCTTTT CTC
WI-6450	45 T G TGTCACA	CCAATGACTT ATTCTATATCT	TTGTTTGAAT GTGTGGTACTT CT		ATAGGACAGTTTTTCTTCCAATGACTTATTCTATATCTTGTACAT/GJAGAAGTACCACACATTTCA AACAGAGCCAGGCTATGCCAGGTGGGATTATTTCAAGTCACTGATTAATGCATGTAAAGACTA TTTTACTGGCCTTCTTTATGCATAAAACAAGGTATTGGTCTATTCAACAAACATGTGCAATACAG CAGTTGTCATGTCCCTCTGGTACTAGAAATAGTCTTTATAGAAATATGTTTGAATAAAGCCACA AATTATCTATAAAACAACA/CJJAAGGAACGAGGCTCAAAAGTGAACAAACGGCCTTAGTTTC TAAGTGAAGACTAAGACGATATAGGAAATATAATCCGTGACCTCTTA
WI-7466c	141 G A TTTGTCTGG	TTTTCACAGTC	AGTGGCATGCC AATTTATAAT		GAACTATCCTTTAGTGGTCCACATTTTCTATTCTGATTTTGTGTCACACAGGACTTTCTGGGCT ATGAAATAGTCT/CJATTCACTGAACTAGTTATCATAAAGACATGCAAAAACCTTTTACAGTCTT CCTGG/GJA/ATAATCTCACAAAATTAATTATAAATTGGCATGCGACTTTCTGATTTAGCCTGACAGG ATTGTTCCCTT
WI-7466b	80 T C GTC	GACTTCTGGG CTATGAAATA	ACTGAA		GAACTATCCTTTAGTGGTCCACATTTTCTATTCTGATTTTGTGTCACACAGGACTTTCTGGGCT ATGAAATAGTCT/CJATTCACTGAACTAGTTATCATAAAGACATGCAAAAACCTTTTACAGTCTT TGCTCTGGGAATATCTCACAAAATTAATTATAAATTGGCATGCGACTTTCTGATTTAGCCTGACAGGA TTGTTCCCTT
WI-9814	104 C A ...				TGCTTTTAAAAATAACAATGACCACCACTGACACCATAGTCTGTCTCCATTTGCCACGTCTTCCCTC AGTAGAATAAGACAGGGACTTTGCTGGCTGCTATCT/CJATTCTCCTTCAGAAGAGCACTTTGGCCCT CATAGGCATTCCATAGATATTGTTGAATGAATGTGCTTTTGCATATTGATTCCTACATTTGATACA TTCTCAGGAGGGACATTTGGCCTAT
WI-9720b	55 A G ...				CCTCTAACAAAGAAACCTTGACTTCTCACTCAAAATACCCCTTCTCTAATAATTTJAGIAGTAACCA AAATATCCTTCAAATAAATTAATCTTTAATTAGAAGAGCAACAGTGTAGAGGTAGTACATTCA CCAAC

WI-9720a	47 A G	---	---	CCTCTAACAAAGAAACCTTGACTTCCTCAACTCAAAATACCCCTCTCTA/GJATAATTTAAGTAACCA AAATATTCCTTCAAATAAATTAATCTTTAATTAGAAGAAAGCAACAGTGTAGAGGTAGTACATTCA CCACC
WI-9825	123 A T	---	---	CACGCTCTAAGGCAGGATGTGGCTTATGAGATACCTTTGCACTTGTCTGTCACACACCTTGAATCTGCC TGCTGGCTCCCTTACTTACCTCTCTGTCATGTGCAGATGAAGGCTCAGGGTGCTA/TJGAGGATTAG TAAGATCTCTTTCTAAGACAGGAGGAGATTATTACAAGAAGAACTCACCAGGGTTTAGTTGCATT TAAGAAATGCCAGCTTTTGCTGTCATCATCTTGAACATTAAATCCACATG
WI-9748	74 C G	---	---	CCACTCAGTAAATCAATTTGTAGCACCTTATTCTAAAGATTCTTAATTTTTATATGTTTACCCTTT GTCATT/C/GJTCAGACCAAGTACATGTTTTACACAGCCATCTTTCTTCTGGAATCTTTCAGAAT TACAGTTATGATGTCCTTTTATATCCCA
WI-9943	91 T C	---	---	TGAGGCTATGTCAGATTGTAGTGACTAATACTATTAAAGCAATTTCAATGTTGTGGCACTGTT CGTTGTGTTTATATCCATCTTC/TJATTTTAAATTTCTACTGAGCAGAAAAAATGTATACATT AACCTTGTCTCCCTATTGTACCTTTTAAATATTGCAATTCACACCTTCTCTTTTGTCAATTTAGGGA
WI-9891	39 T C	---	---	AGGGCCTTCACAGATCCGTGAGCTCAACACTGCCTCCT/CJAGTGAGCCTGTGAACCCACCCAAAGAC GGCTGGTCATCAGTGTCATCTCTCTTTCCGGACAACATCTTTAAAGAAAAAAGAGTGT CTTTGAATGTATCCATTTATCCCCAAATAATCTTGTTTAAATAAATCCTTATTAGGCCAAATCCAAT GTGCTGAATATCTGCCAAGCATGTCTTCTACACAAAAGGATTGCAAA
WI-9897b	84 C T	---	---	CTCAGAAATTATCAGATCTCCCCAAATGTCATGATCTTGTTCTCAACATCCTATTTTCTCAAAC ATTTATCAGCCTGT/CJ/JAAGTCATCCAGTGAGGCTGTTTATTCAATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTGTACCCACATTA
WI-9897a	83 A T	---	---	CTCAGAAATTATCAGATCTCCCCAAATGTCATGATCTTGTTCTCAACATCCTATTTTCTCAAAC ATTTATCAGCCTGT/CJ/JAAGTCATCCAGTGAGGCTGTTTATTCAATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTGTACCCACATTA
WI-9935b	115 C A	---	---	AGATAACCCCTGGAAAACCTAGAAGAAATTAATAACGTGTTGCACACCTCACCAGAACTGGAAGGAGT CTGACTGTGTTCTTATGGGTGCTTGGAAGTGGCAGGGGGAGTTGAGACA/C/JAGCCAAGAAAAAGCC TGATATTAAGAGGCACCTTGCAATTA
WI-9935a	42 C T	---	---	AGATAACCCCTGGAAAACCTAGAAGAAATTAATAACGTGTTGC/CJ/JACCTCACCAGAACTGGAAGG AGTCTGACTGTGTTCTTATGGGTGCTTGGAAGTGGCAGGGGGAGTTGAGACA/C/JAGCCAAGAAAAAGCC TGATATTAAGAGGCACCTTGCAATTA
WI-9983	146 C T	---	---	CCTGTTAGGTGCCAGAGTCCATGCTCTTGGCCACAATGTTAGGCTGCCCTCCCATTTCTTGTCTTGA TTCCCCAAACCCCAAGGTTCTACCCCAATCTGATCAATGTGACTAGGTATGGCTGGTCAGGGTAA AGCATTATGA/C/JAGACACAAAAGACAAAAGAGGTTAAAGTTGCTGCTCTCAAGAGAGAGACATAA AAACAAATGGATCTGGAACCTAAGTAAGGCTTCGAGGAGGAGGTGAGCAAGG

WI-10019	139	A T	TGATGTAATGC TATGTAGCAA ATCT	TGATTACTGT GCTTAGGGA	ATATCAGTGGGTTGAGTATACAGCAATCTATTTGTTTATTTATGTGTGCTATAAATCAATGGTCTA ACATTCAAATAAGATCTTTTGCTTCTGCTCAGATGCTTTCAATGATGATGCTATGTAGCAAAAT CTA/ATTCCTTAAGCACAGTAATCAAGGCTTCTACCCCA
WI-10020b	122	T A	GGGAGAAAAG AAATCATGAC TTT	GACTGTTAATT TATTTAATCAT TAGTCTGG	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATTATGTTAACTGGCTCTGAAAAGAAATTTAGGC ATGCATAGAGAAATAGCAGTGTATTTATGGCGAGAAAAGAAATCATGACTTTT/AJAAAAATACC AGACTAATGATTAATAATAAATTAACAGTCTAGGGTTCCGGAAGTGGCCTAAAGCACGTAGTAGCCCT CCTTAGA
WI-10020a	39	T C	TGTCATCTTGA CTCGTATTAA ATAAATT	AAATTCTTTTC AGAGCCAGTTA AC	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATTAT/CJGTTAACTGGCTCTGAAAAGAAATTTA GGCATGCATAGAGAAATAGCAGTGTATTTATGGCGAGAAAAGAAATCATGACTTTTAAAAATACC AGACTAATGATTAATAATAAATTAACAGTCTAGGGTTCCGGAAGTGGCCTAAAGCACGTAGTAGCCCT CCTTAGA
WI-10064b	170	C T	CCTTTAGATAT ATTGTGATTGT TTTACATG	ACCTTTCTGAA GCCAGATTTC	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGGCATTATAATAAT ATAATTTGCAGAGCATCTCTCTCTATGCACCAGATATTGGTGACACTCTGTTTATCCAGTATCC CTACTCCTTTAGATATATTGTGATTGTTTACATG/CJGAAATCTGGCTTCAGAAAGGTTAGGTGTT T
WI-10064a	54	C A	GTAGCAGGAT CAGGGAAGG	GAGATGCTCTG CAAATTATATT TATTAT	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGG/CJATTATAATA AATATAATTTGCAGAGCATCTCTCTCTATGCACCAGATATTGGTGACACTCTGTTTAAATCCAGTA TCCCTACTCCTTTAGATATATTGTGATTGTTTACATGCGAAATCTGGCTTCAGAAAGGTTAGGTGTT T
WI-10289	29	T C	TCTCCTGTCCC CAAACCTCTT	ATCTTGTTGT ATTGAATGGAA TTAA	CCAGGGATTCTCCTGTCCCAAACTCTTAT/CJTAAATTCATTCAATACAACAAGAAATTTATAGAA TATGCACCACATGCCACAAGACACCCCTTATATTAGT
WI-1319	40	A T	TGGCACTTAG AACATAGTTT ATTCTTT	GCCACACACCC CTATGGT	AAGAAAATCCTTGTCACCTTAGAACATAGTTTATCTTTTATACCATAGGGGTGTGGCTTATCT TTTACCCTGGCATGGCTTAGGTCTGTTTATAAATTTGGTATCTTTTGGCACAAAGAGTGTGTTCTGAC AGTCTTATGATCTCTATTTTAACTTAACACTGGTCAGATGTGTTTAAACTTGTGAACCTGCAGC
WI-10316	104	T C	CTGTTGATTTT CTACCTCTATT CTCTT	GCTTTGGAATG TATCCAAAAGT TT	AGCAACGTGTACAACCTTAGTGAGGTGTAATCAGAAGCATCTATATTATCCAGTCAACCCCTG GACTATAGTCTGTGATTTTCTACCTCTATCTCTTAT/CJTAACCTTTTGGATACATTCCAAAGCAT CATGGTCACTTCCAGTTATGAAAGGATGTTTAAAGCCAGCC
WI-2572	61	C T	AGTGAGTTGTGCACAAATTTGGAGACATTTGTGACCCCAACTTAAACACTTCTCCACAC/CJAC AAAGTTAACTTCAGTTACCAGGTGATGAGCAGA

WI-10368	31 C T	TGAAGCAACC AGGCTTGTT	CAAGATAATTAT ATTTATTCTCT AAGAGGGG	GAGGAAGTGCCTGAAGCAACAGGCTTGTTTC/TCTACCCCTCTTAGAGAAATAATAATATCTT GAGATAGGAGGAGCAGCCTGAGCAGCTGGGTTTGTCTACCCACTGGAAGCAGAAATATCC TTCAAAGCTTTTCCAGTGAGTCATGTTGCTGCTAAACTATATGACCCTGATGGATTGOCCTTCAGGG T
WI-10391	32 A G	CTGTCTCAGGT ATGACTCCCA	GGGAGTTAGGA GTCAAGAAGTT GA	CTCCCGTTCTCTGTCTCAGGTATGACTCCCA/AGTCAACTCTTGACTCCTAACTCCCATCTCGGTG TCTGCTTCCAGGGGACGTCATCTGACACAGCCTTTTGCTTGCTGTGACAAACAGAACTTGCAGAAG TGATGCTGCGTGACCTCCAGGATA
WI-10567c	148 A C	GTTACCCAGA GTCCTCTAATA	TGCCGCTTCCA GTAGCT	AGCGATGAAATTTATATGTTATGCCTGACTTAGCGGGTGCTCAATAAATAATTATCTTTTTCATATT TTCCAAATTAATACTAGAAATTTACCAACAGAAATTTTAAACATTTTAAGTTACCCAGAGCTTT CTAATAGCAA/CJAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-10567b	82 A C	AGCGATGAAATTTATATGTTATGCCTGACTTAGCGGGTGCTCAATAAATAATTATCTTTTTCATATT TTCCAAATTAATA/CJTAGAAATTTTACCAACAGAAATTTTAAACATTTTAAAGTTACCCAGAG TCTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-10567a	60 T C	GGGTGCTCAAT AAATATTATT CTTT	AAAATTCGTGT GGTGAAATTC TAG	AGCGATGAAATTTATATGTTATGCCTGACTTAGCGGGTGCTCAATAAATAATTATCTTTTTCATATT ATTTCCAAATTAATACTAGAAATTTTACCAACAGAAATTTTAAACATTTTAAAGTTACCCAGAGT CTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-11153b	84 C G	TACTTTA C	...	CGTTGGGAATTTCTATCTCACCTAAATATG/C/AGTGATTAAATATACATTTTAAACAACTTC AAATGCTTTAAGTACTTTACGAAGACCTTGACTGTTGGATTTTGGATTTTCTTTTCTTAAATA AAAACATGCATATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATTATCTGATATCAGCATCCCTT TATGTATT
WI-11153a	33 C A	AATTATG C	GCAATTTGAAG TTTGTTAAAT GTAT	GTTGGGAATTTCTATCTCACCTAAATATG/C/AGTGATTAAATATACATTTTAAACAACTTC AAATGCTTTAAGTACTTTACGAAGACCTTGACTGTTGGATTTTGGATTTTCTTTTCTTAAATA AAAACATGCATATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATTATCTGATATCAGCATCCCTT TATGTATT
WI-2616	125 T C	CACAAATGTA ACAAGAAATTG ATCC	CCATGGCTGTA GTCCAGT	GTTGTAAACTCCAGTATCATTTCCCTCAAACCCAGCTTAAATCACAATCACTTTTCTTCTGTA GAGCTCAAACCTCAGTCTGAATGAAATTTGCTGCACAAATGTACAAGAAATGATCCTAT/C/ACTGGG ACTACAGCCATGGAGAAAAGCAATGTAGTCAGCAAAATGTTAACAG
WI-11163	58 C T	CAAGTGAATT ATGACCAAAA TGAGA	TGCTCTTTCA TTTGAGGTTTT T	TGACTCAAAGGAAACACACACAAAAAGTTTCCACCAAGTGAATTTATGACCAAAATGAGA/C/TAAAT TTGTTAAAAAAACCTCAAATGAAAGAGACAAATATAGTTCAAAGATTGAGTTCAATATTGT ACCTACAAATAGGGATAGTCAATGTTGTTGGCAGACTTTTCTTTCTTTTCTTTTGT/G/CTCTTA GAATCCATTTTGTCTTTTGGCCAGCATTCCTCTCCCATATTTTAAAGGAGAAATTCACCTTTTCT CTGTTGGATGATCACAGGTTCTGCTCTTCCCAATCCAGAGGAGTACTATTCACCCCATGGGGTCAAT AGAGAGGATTAAACAGGGTGATGCCTGCAATGGGAATATTTGAAAACC
WI-10656	59 T G

WI-1169b	154	T G	TTAACCAAGA GTTTTTCATTG TTTTT	CTAACTTAAAA ATCCTCATTCA AAATATAA	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTTCTATCGAGAAAGCAATAAGTGAAGTAA CTGACTTGAAAGAAAAAATTAAGCCTAAGAGTAGTGCTTTTAACCAAGAGTTTTTCATTCTTTT TTTAAAAAAGAGCAGACACA[T/G]TTTATCATGTGTCTGATAAATTTTTTATATTTTGAATGAGGATT TTTAAGTTAGCAT
WI-1169a	95	A G	AATAAGTGAA AGTAACTGAC TTGAAAAA	AACTCTTGGT TAAAAAGCAC TACTT	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTTCTATCGAGAAAGCAATAAGTGAAGTAA CTGACTTGAAAGAAAAAATTAAGCCTA/GAAGTAGTGCTTTTAAACCAAGAGTTTTTCATTCTT TTTTTTTAAAAAAGAGCAGACATTTTATCATGTGTCTGATAAATTTTTTATATTTTGAATGAGGAT TTTTAAGTTAGCAT
WI-10685	25	A G	---	---	CAAGTGCTTGGACCTTGGATAGGTC[A/G]JACCGGCTGAAGGTTGGACAGTTGTTGGTTAGGTTGGAG ACCAAAATTCAGTCATCCTGTAATATAGATCTTGTCTTTGGGTTTACCACTAGGGGTCACTAAAG AGAGATGGGAGACAGTCTCAATCTTGTCTAAATAATCCAAATAGCCATGGGTTTGGACAAAATAC AAGGTTAGTGCTCTCTAACTTTAATGGGCATA
WI-10686	133	C T	TGCCCTGTCC T AAGG	CAATCTCTAAA TTCATGTGTAG ACACA	AATAACCTGTGGCACATAAGGCAATACTGAGCCCCATACAGAGTGTTTTATGTTAATATTATGAAA AAAGTCAAGAGAACAAAGATATAGTTCTGCTAGAAATCTTGAAATCTGATGCCCTGTCCAAAGG[C/T]TGTGCTACACATGAATTTAGAGATTGAATGAAATGGCAAAATTCAGAAAAGGG
WI-11175	77	T A	AAATGATTCTT TCTGCTCAAAG	CTGTTCTCACA TCTTTTTTGAA AA	GGTAGGATGATTCTAGAATGCCACTTTACAGCCACTGAAATATATTGCCCTCCCAATGATTTCTTG CTCAAAAGAG[T/A]TTTTTTTTTAAAGTTATCTACTTATTATATTCTGCTTTTCAAAAAGAAATGTGAGA ACAGTACAAAATGTGTTTCAGTATAGCAAATTAATAATTAATAAAGTAAGAAAAAGAGCCCAATT TGGGC
WI-10694	144	A G	TGCAAAATGCTT TATGAGTTTTC TGAATTCATCC AGAAAACAG	GGCATTITGTA AAGGAGGAAA TCTCTTTCTC TCTTGTGTCA TTC	TAGAGAGGCTTTTCAGTTTCAGGGTTGGAGGGTGGTGAGGTGAGATTCACCTCTTAGAAGCACTGGC TATGTACAGAAAAGATAAACTCTGAGAAAGAACTCAGTTCTAAAGTGTTCAGTCTTTGCAAAATGCTTTA TGAGTTTTC[A/G]TTTCTCTCCTTTACAAAATGCCATCAATTCCTCAAGGAAAAAAGAGCTTTCT T
WI-2716	23	T C	TGAATTCATCC AGAAAACAG	TCTCTTTCTC TCTTGTGTCA TTC	GTGAATTCATCCAGAAAAACAGCT[T/C]GAATGACAACAAGAGAGAAAAAGAGAAATAAGGTTTTTGT ATACGACAAGTGGCTCAAGCAATTTTCTCTGTCCAGTGCATGGAGCAGTG
WI-10719	115	T C	TGACTCTCAAG TGCATTCTAG	GCACTGCCAGC AGCC	CAGGCCCAACTCTGTCTAATTAAGTGTTTTAGAACAGACACCTCAGTCACACAAAGTTTCTCTTGTATGT GCCCAACATAAACAGTTACTGGAGGATGACTCTCAAGGCCATCTAG[T/C]GGCTGCTGGCAGTGCTT TCCAGCCTGCTGCCATAACTAA
WI-10721	40	A G	TGGCTCTGCTA CTTGCCA	GAACTCCAC ATAAATAAAT CTCA	CAACCAATTCAGATTAAATTTTGGCTCTGCTACTTGCCA[A/G]ATGAGATTTATTTATGTGGGAGTT TCTGAAGATTCCCATGGTAAATAGTATTCTCTCTCCCTGCTTAGGTTTTGAAGAGTTGAA

WI-11204b	88 T C	GCACAGAAATTGATTAATATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAAAGGGTG AAAAAGAAAACTTTACCTTTT/CJATTTAAAGTAACATAAAGGTATTATGTACATTTTAAGTGAT CAAAAAATTTTAATTGGGAAGAGATTAGTGAATCAGAAAAAATAGTCTGAGGAAAAATTATTCAGAAAG GCAACATC
WI-11204a	80 T A AACTT	GTAAAAGGG TGAAAAGAAA	TGATCACTTAA AATGTACATAA TACCTTT	GCACACGAAATTGATTAATATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAAAGGGTG AAAAAGAAAACTTT/AJACACCTTTTATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAGTGAT CAAAAAATTTTAATTGGGAAGAGATTAGTGAATCAGAAAAAATAGTCTGAGGAAAAATTATTCAGAAAG GCAACATC
WI-10732	80 C A ATTGGTCACT	GCTGTGCTTC CTGTATGTACA	AAGAACAATG CATAACAGAA CTTTAA	ACATGTATTTCTTTAGTGGTCAAGCTTCCCTACCCCAAGAAATATCCCTGGTTTATTGCTGTGCTTC ATTGGTTCACCT/CJATTTAAAGTTCTGTATGCATTGTTCTTGAGTCCACATAGGTGTTAATCATTTCCA CACCACTCTGTTTAAACTGTC
WI-11206	127 A T ACTC	GGTTGTGTTTT CTGTATGTACA	GAGTGACAATC CTAATGGTTGG	TAGCTTTTCTTTGTACGAGTGTATAAAGAAATACCACCTCTGTACATTTTGTAAAAAGATAGCACAG AGAGAAAGCATTACAGGGCACAGCACAAACATGAGGTGTGTTTTCTGTATGTACAACTC/A/TJCCAA CCATTAGGATTGTCACCTCTCATATATAGACAGAAATTCAGTGGTGGTGAATTTGAATCCACACATGGA ATAAGTCTA
WI-11215	68 C T	GAAAAAAGTTTTAATTGGATTGCTTAGTTTGTCTTAAATTTGACCTACTTTTCCAGATTTATTTTAGT [C/T]ATTTTCTCTATAATATTTCTTGAAGTATGATTTCTATAAAATTAAGGAAACAGATATTT ACACAGAGAAGACAGGATTGCTTGAATTAGTATAACATTTCTTTATCCAAAGCCCCATCCACCATGT TTT
WI-11219b	89 G A AGAGAA	GAGAGAATAT TCCAAAAAGT	GGTCTCTAAT TTTTCTACACT TTCT	ATGAAAAATGCATTAGAAGAAATTGGAGGATAAAATTTGAGAGAATATTCAAAAAGTAGAGAAAA GAGACAAAGAGATGAAAAATAGGA[G/A]AGAAAGTGTAGAAAAATAGAGGACCATTTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC AAAACATCTC
WI-11219a	18 G A	ATGAAAAATGCATTAGAAG[G/A]AATTGGAGGATAAAATTTGAGAGAATATTCAAAAAGTAGAGAA AAAGAGACAAAGAGATGAAAAATAGGAGAGAAAGTGTAGAAAAATTAGAGGACCATTTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC AAAACATCTC
WI-11222b	136 G A GCCTGG	CATACCACCTGC AGTTGTGA	CCTGGTAGCCA AGTTGTGA	AGCCACAGTGGAAATCATTTACACTACCGAAATCAGCAAAATGCTAAAAATGGGGCTTTGGATTTTGT TTTTGTTTTTCCATAGACCCCGTTGAACATTTGTTAAACATTTACCAGCATACCACCTGCGGCTG G[G/A]TCACAACTTGGCTACCAGGAGAACCTGACACAGACTTCGTAATTGCTTTCACAGGCTACTGG AAAGCC

WI-11222a	25 C T A	GCCACAGTGG AATCATTTAC	TTTTAGCATTT GCTGATTCG	AGCCACAGTGAATCATTACACTA/C/TGAAATCAGCAATGCTAAATTTGGGCTTTGGATTT TGTTTTTTTCCATAGACCCACCGTTGAACATTTGTTAAACATTTACCAGCATACCACCTGCGG CTGGTCACAACTGGCTACCAGGAGAACTGACACAGACTTCGTAATGCTTTACAGGCTACTGGA AAGCC
WI-10775	39 C T CACTC	TTTATGCCATA TTAATTCATTA	CTAGATGTATT TGCTAAGAAA ATATGATG	TTGCAAGTTTGTATGCCATATTAAATTCATTACACTC/TJACATCATATTTTCTTAGCAAAATACA TCTAGACACCTGGCACTCAGTAAGGATATTCCTGGCAGGATAATCATTTGTTATCATTAGACATTGCA GGAACCACTATGGATGATAAATGTGTGTTTAAATGAAGGCAAGCAATTA
WI-11226	165 A C ---		---	TTGCATGCATTTATACGAAAGGAAATAAATATCTTCCTTATAGTTGAATTTAAGTAAAAATAAA GTTATACATATAATACAAAAAGTTGTAAGTATAGTAACAAATGAATAGAAAAATTGTCAGTGGTTGC TAGTACAGGAATCAAAATTTGGACTATGAACA/A/C/GACATAGTTGCTAAGGATATTCACAAAAATTAT TTCATGA
WI-10778	62 A G G	GCAAGGGAGG AACATTTACA	CTGGTGACATC AGAGATGGAC	CAGTGGCTGGCTACTGACAAAAACGTAAACATCGTGGCAGGTGGCAAGGGAGGAACATTTACAG/A/G/G TCCATCTCTGATGTACACAGCAGGGCCAGGAAGGTTGATCTGGAG
WI-10789	21 C T GCTCTAGACC	GGGACACACT GCTCTAGACC	TTGAGGGACCC TGGA	TGGGACACACTGCTCTAGACC/C/TJCCCAGGTCCTCAAGGTGGGTAGAGGCCCTACTGCCCT GCCCTGGGACGACAGGCATCAGGGCCTAGTCTCTCTGGGACAGTGAAGGGCCACCAAC
WI-10810	58 C T GCAGGAATT	CATCTTCATGG GCAGGAATT	CAACCCCTAAG AAACACAGAA ATG	ACAGAAAAATGCCTAGGCTTTGTAGCAAGAGAGGAAAGCATCTTCATGGCAGGAATTC/TJCATTT CTGTGTTCTTAGGGTTGTGGCTGGCCATCAGTTCACTCAGCCCTGTCCCTGATCCAGCAACATT TCCGTAACCTACCCTCTAGAAGTCATGCAAAAGAGAAATGATGA
WI-10828	23 T C ---		---	GGACCAACACAGAAATTACTTGGCA/TJAGGGTTTCTTAAACATATTTCTGCAGAACATTAGTAAAGT TTAAATAAGGATCAGGCTACCAGGAATACAGTTAGGAACATGTGGATGAATTTCTTTAGTAGAG GACTTCTAAAGGCTATAATATTTGGATACATTAGGCTCATTATGAATCTCAAAAGGAGCATGTAGT AGGGCATATCTAA
WI-10832	91 G C AGGCTCTCC	CATTAAATCTGC AGGCTCTCC	CCTAACTGCAG GTGACTTAGAA A	TATGCCCTCCCAACGAGCCATCCACGCTGCTTAGCACAAAAAATAGAAATACATCATCTGAATG GGCACATTAATCTGCAGGCTCTCC/G/C/JTCTAAGTCACCTGCAGTTAGGTCTGCAGACACTGTGTA TACCATATAAATCTGATTTCTGAGCAGGAGGAGGCGCAGATGAGAGAAGGGCTGCTCCGTGAAATAC TAGITCGG
WI-10834	96 C T GTGTTAAT	AGAAATTAAGT GTTCAAAAGT	TGGCCCTATAA AATTGGTATTA AG	GATTTGAGTATTATCAAAATTTGCCAAAGACCATTAACAAGATTTAATAGTTAAAGCCAAACTATA AAGAAATTAAGTGTTCAAAAGTGTGTTAA/TJCTTAATACCAATTTATAGGCCACCAATTAACCT CTGAAGAAGGTCAGCATATGCAACTAAATTTCTAAAGTCCAGT
WI-2287	24 T C ---		---	GGATGATGTTCTGTGGTCCCTTTAT/CJAAAGCCTCTTGATCCCAATGTGTAATATTTTATTCT TGGTATTTCTCGCTTACCCATAGTCACCTGTCAAGTGTCCACCCCT

WI-2296	81 A G	TGTTACTTTGA TTCCTTGCTCT	GCAATCAGAC AGCTAACTGG	TGGAGGGTTAGAAATGCAGGTGCATCCTAGAAAGGTCTCAGGCTTTAGAAATAGTTGTTACTTTGA TTCCTTGCTCTGACIAGICAGITTAGCTGTGTGATTTGCAGAGGTTACATTTGTTTGTG
WI-2300	77 G T	GGCAGAGAAG CCAGTCATAC	GGTTGGGTCAA TTTTAAAGCA	TTTCATCATGCTGCTTCCCTGGAAATTTCCCTTTATTTGAGCGGGCAGGTGGTAGGCACAGAAGC CAGTCATACIGTJTGCTTTAAATTGACCCCAACCATTAAGAAATAGCATTCA
WI-2371	55 G T	GTCTTGTTCTT CCAGCTTCT	CAAAGATTGAC AGCCACCAC	CAATGATCCCCCAACATTTCCAGGGAAAGGTCTGGTCTTGTCTCCAGCTCTTGTTGGTGGCT GTCAATCTTTGACATTTCCCTTGCTTGACGCTGTATAATCCCAATCCTTGCTCCAGCTTTACATGATGT TCTCTCGGTGTGCTGTG
WI-2395	122 A C	GAACATATTT GTAGAAAAT	TCACCTTTCTA TTTATTCTGAA TTCA	GGGGCACAATTTAGCTACAGTGCATATTTAAAGATAACATAGAATATCATATAACTTGGTTTAC TGAAATCTGAAAACCTTAGGATGAGTGAACATATTTGTAGAAAAATTAATCTCAAIA/CJCTGAATTC AGAATAAATAGAAAAGGTGAATCATCTTATATCATTTAAAGAAAGCTAAATTTAGTAACAATCTTTA CATTTACACAAACCCA
WI-2437c	192 G A	CACCAGCCACCACCCCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACCTTCTAAATAATAGACACCAAAAAATCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGACGAACATCACAGTGIG/AJGCTGTG GTGCCAAGGACGCAATTATG
WI-2437b	179 G A	CACCAGCCACCACCCCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACCTTCTAAATAATAGACACCAAAAAATCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGACIG/AJACATCACAGTGGGCTGTG GTGCCAAGGACGCAATTATG
WI-2437a	128 G A	CACCAGCCACCACCCCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACCTTCTAAATAATAGACACCAAAAAATCCCAATG/AJCTC TAAATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGACGAACATCACAGTGGGCTGTG GTGCCAAGGACGCAATTATG
WI-2440	71 G A	GCAACCTACT GACAAATTTAA TTTTAGTT	AACAACCTCTGC TATTGGTCTCA C	CAGTAGGAAACGGGTTCTTCTTAGACCCCTCCAGAAAAATAATGCAACCTACTGACAAATTTAATTTTA GTTGIG/AJGTGAGACCAATAGCAGAGTTGTACCTGCAGAACT
WI-1358	123 T C	TGTTTAGGAA ATAATGACAA GAAAAA	TGGTTACAACT GTACCAAAACAT G	CTGTAACCTACACACATCCTCCTGTACCTCTAGGTTACTTGTATAACAAACACAAATGTAATGCT ACATAAATAATTTGTCATATAATTTGTTAGGAAATAATGACAAGAAAAAGCCIT/CJGTACAT GTTTGGTACAGTTGTACCCAGCCATTTTCCCCCAATATTTCAATCCACAGTTGGTTTATCCACAG AAACCACGAATG
WI-2886	46 C A	CAGAGTCTGG GGGAGAAGA	TTGCCATGCTT TATCTCGTT	ACAGTTAAGAAAAAGGCTGCAGCCGTTGCAGAGTCTGGGGAGAAAGI/C/AJACGAGATAAAGCATG GCAAAGACCACGCTGAAAGTATCCAGGGTGTGTATGTGCACATAGGAAGATCACTTACCTCAGCA TAGGAGGAGGGCTAGGCAAGGAAAGGTGTGAGAAAGAAACAGAGGAGCGTT

WI-2906b	77 T A	---	---	CCTGAACACCTGGAGCACTCCCTCCCTGGACACCTTCATCTTCTGCTGGAACCTTGCCTGGAATGCTC TTCCCTCT/AJGAGCTTTGCTGGCTTACTTTCTTTCTTTAGGTTTCAGCTTCAAAGTGACCT CCTTAGAGTTGGTTTCTGACCAACAAA
WI-2906a	50 A C	GACACCTTCAT TCTTGCTGG	AGAGCATTCCA GGCAAAGT	CCTGAACACCTGGAGCACTCCCTCCCTGGACACCTTCATCTTCTGCTGG/A/CJACTTTGCCTGGAAT GCTCTTTCCCTCTGAGCTTTGCTTGGCTTACTTTCTTTCTTTAGGTTTCAGCTTCAAAGTGACCT CCTTAGAGTTGGTTTCTGACCAACAAA TACTCCTCATTCTCATGTCCTTAGACGTACTCAGATTTCCATGCCCTGAAACATTTATTTCTAAAT TAGATTTCCACCCCCAGCACTATTACACAGAAACAGCATGGAGCAGTTGGAGCTGGCTCTTAGA GAACTTACTTAAGGACAGTGTTTTCCATCTGCTTCCA/C/TJAGAGATCTAGGGTGTCTTTGGAACC ACCTTGG
WI-1736	175 C T	---	---	AATACCCACGTCCTAACACCATCACACTGATCATCAATCAGGTTTAAACATATTAACTCTGGGAGG ACACAAACATTTAGACCATAGCATTTGAATTAACATATAGATGTGTTAAGTAATTTATTAACATGGTA CA/G/A/JACAACCTCAGTTTAAACATTGCTAGTGATTCCATGTGGATACCATGTACCTTCTTACATCATG TGA
WI-1851	136 G A	GCATTGAATT AACTATAGAT GTGTTAAGTA	CACTAGCAATG TTAAACTGAAG TTG	CTGATGTTTGGGAAGCACTGCTTACATCTCTAAATGTAGCACCCCAACACAGAGACCCG/G/A/JT GAGCTTAGTCAATCCTATAGTGGCAGTACCTGAATCAGTGGCTGGTCATAGTAGACACT ATGGATCTGCTCAATTATAGTCCAGATAAACAGCCCTTCTCCCCCCCCCGGATTATTTTACT TAAGGGTTTAGCAAAATTCACCTGACAAAGAGTTAGGTTTCAACATGACCCCTCATAAAGTGATTTT TTCTCTTCTGTTTTGTTTTCTCCCTTCTTAAAGAGATAGTC/G/A/JCCAGAGGCAATTCGACTTTCTGT AGCCACAAGATT
WI-3000	62 G A	CCCAAAACAC AGAGACCCC	ATTGACTAAGA CTCA	ACAACACAGCAAAATTCACACAGATCTATTAGATTCT/AJACCCCATCTCAAAACTATCACATCAA AGAAGCAAGGAGACATATTACTGGTGAGGAAGCCAAATTCAA
WI-1754	177 G A	AAATTCAACC ACAGATCTAT TAGATTC	TGTGATAGTTT TGAGATGGGTG	CAAGCACACATTCAGGCAGTGGGCAGGTAGGAAGGTGGCAACTTGGCAGCAGAGAGAGGAAG AAGTTGAGACCGTTGGGTAGGATAAGTGATCCAAACCCCTTTGTAGGGCAGGTGGTGAGTGGGCAG ATAAAGA/G/A/JCCAAGCCCTAGTTTGAAGTACACTGTGGGGATTCAAAG
WI-3208	140 G A	GTGGAGTGGC AGATAAAGA	TCACTCAAACT AGGCTTGG	ACTCCACCAACAGTTTGTGAGCCCAACCCCTGCATGGTCTTCTCTCTG/TJTTTACATCATTTGCATA AATCTCAACTGACACATCAGTGTCTCTGCCACCCCA
WI-1775	47 C T	CCTGCATGGTC TTTTCTCTG	ATGACAATGAT GTAAA	CTGCCCTTTACATCCAAAGCCAGTTACTCGAGCATATTCAATTGATTTCCTTACAT/G/AJCAAATGCTC CTTTTAAGTCTCAACTTTAAAGCGGAAGTTGAGACATGCACAAAATAGATTTCCTTAGGA
WI-3402	55 G A	AGCATATTCA TTGATTTCTT ACAT	GAGGACTTAA AAGGAGCATTT G	



WI-3416	33	C T	CCAAGTTGTA GCATTGAGAA	ACGAGCACAA CTACCTCTAAG AG	TCTGGTTCTCCAAGTTGTAGCATTGAGAAGTC/C/TCTCTTAGAGGTAGTTGCTCGTCTGTTAAAA TATGTTTTCAAGATAGTATCTCCCTGTTGTCACCTCTCCCAACAAAGTGACCAACAGCATTGTTAAG GAAATGTGCAATGCTTGCTACCTCTGACGCAACATAATTAATCCATTGCCTAAAAAGACCAGG
WI-3453	70	C T	TTCTTAGGCC ATCAGAGAA	TCAATTTTCCC CATGACTTC	TCCTATTCCTACAACAACAGAAATTAACAAATTGAACAAATCAGTACTCTTCTTAGGCCCATCAGAG AATC/TJGAAGTCATGGGGAATTTGATGCCATGTGAATTTGGAGAAACAGACAGGCATATATGGAG AATTACAGTTTACCAGGGACACAATCCCACTCCAGAGCCATCATCTGTAAAGAC
WI-3474b	109	G A	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAAACCTTAATCATCAAGTGTGCAACTGGTTTGA GTCAGTTTCCCTAATTTTAGCACAC/GJGTATTTAATGAGGTGGTGGGAGAAAAATGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3474a	90	A G	AC	CAACCATCAAT TTTCTCCCA	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAAACCTTAATCATCAAGTGTGCAACTGGTTTGA TAGTTGAGTTTCTGTCCACC
WI-3502	79	C T	GGTGGTTTCT GGATGCT	GGGTGACCCCTG TCCTCA	TTTGACCCCATACATGAGAATAAACCAATAAGAAATGGTGGAAAAATAAACGGGAGAGACCTGGG TTTCTGGATGCTC/TJTGAGGACAGGGTCACCCAC
WI-3600b	146	G C	CATCT	GGTTCTAAC TGGATATAAA	TCACGGCAAGTTCTGCAGCAGTGTCTTGACTCTGCTGCTGTTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGT/GJGAGCCACCTAACTCGTTTCTGCTTAAGTTATCCAGAGGTGGTTTCTAACCTGG TAAACATCT/GCJATGGAAGGCTGCACTGGATGAGGTACAAA
WI-3600a	78	T G	ATAGTTCTG	CCATGCCCTG TAGGTGGCTC	TCACGGCAAGTTCTGCAGCAGTGTCTTGACTCTGCTGCTGTTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGT/GJGAGCCACCTAACTCGTTTCTGCTTAAGTTATCCAGAGGTGGTTTCTAACCTGG ATATAAACATCTGATGGAAGGCTGCACTGGATGAGGTACAAA
WI-3678	125	G T	TAAATCATGCTTATTTTTCACAAGGTAATCCACTCACAATAGGCAATTGATGTATCTCTTTCTGTAA GAAAAGCTCTCATGCTCTTCTGAACTTCTACTTACTGTGCTGTTATGATGCACCT/GTJCTTTTGG ATAGATGTTGATAGGAGATGGTGTAAAGACACAATTTACCTTGTGTGTTTCAGGCAGAAATAG ACTCTCTGTGTAATCACTGAATGAGTCCAAAAGCCTTTATGCTTAC
WI-3687	67	A C	AAAGCGATGTTGAGATACCACATTCCATGAAAAAGTAAAAACACACACAAAAATATGACATAAAA T/A/CJAAAAACTACTATAGTTTATGAAAAATGACTTCCAAAAATTCAGAGAAAAAGTCACTTAAACAGG ATTCTCAATTCATCCAGAACTCTCTGTCATCTTAACCTTGAAGTGCACAG
WI-3735	72	T C	AAAAC	GGCTCACC CATTGTTTT	TCTAAATGTGAACCAAGAAATCCTGACACGACCTAAGTCCAGTCCCTCAGTTATGTATCAAAATGA AAAACT/CJACACCGTTCAATGAAAAACAATGATTGGTGAGCCATGTCCCTTATTTAATGAAAA GATCTTGGCAATTAACCT

WI-1819	51 C T ...			GAAGAAGCAGGAAGCCAGGACAGCAAACTTTGAAAAAGTCTTTAGCAACAC[CTTTCTGCGATCCG AATTTAGTGTGATTTGGCAGCAATCGGGTAACATGTTCCAGTGTTTTAACTTGCACAGAAATTGC CAGATTAGCGATTGTTGACTTGTCCAATTAATGAATGTGGAAGAAAAAAGGGTGGTAACGTGT AAGCCTGCTGCAATGTTAGACACGAGGGTGGGGGTGGGAGGTGGAATACC
WI-3746	118 G A ...			GGCCTATTACATGACACTGGGCCAAGATCTTGCTCCCTTTCTTCAATAGATAGACTAACTAGAAA ACTGCCCTGGCCAGGAAGATGGTTGCTTCATCATCTCTGCTCTGCG[GA]GCCCCAGGATAAAGCA GGCA
WI-3867	49 T C CAA	ACAGTCATTT AGTCTTCTGTA	TAAGATAACC ATACTAGGTAC ATCCG	AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCTGACAA[TC]CGGATGTACCTAGT ATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTTACTTGAACAAAGACACAGT CATTAAAGTGGAGAAGCCAGCATTCTAATCAGGCTCAGTGATCTGCCAAACCAACCCCTTCTGCTATAG CATC
WI-3898	25 A C G	TGACCAATGTC TTTAGAAGCA	TCGTGGGTGTC CTCTCC	CAATGACCAATGTCCTTTAGAAGCAG[AC]GGAGAGGACACCCAGACACACAGGAAGGAGTGAG GTGAAGATGAAGCAGTGTGACGACCCACAAAGGTGAGGAAGCAAGGGTGTCTGGCCACT
WI-3901	114 A G ...			GGACCAATTGTCCTCAGAAAGTACATTCAGGCCCTGGACGGTGTCTCTAACACTGTGACCTCAGGCA AGTCATGTCGTCTTCTGAACTCGGCTTCTCACCTGACAAGTGG[AG]TATCATGTGTACACTGC AGTGTATTATAATGCTGCAT
WI-3914	99 C T CC	TGATTCTTCTC AAGACTCACA	TCTAGAAGCAA TGAAGGATGG	CTGAGGAGATTGATGCTACTTTACCTGAGGAACTTTTATACCTCCCTGAGTTTGTGCTTGCAA GACATTGCTGATCTTCTCAAGACTCACAGC[CT]ACCATCTTCTGCTTCTAGACCTATAACTAG ACTCAAGTCCAGCAGGCCCTTAAAGGTAAAGTACAAAGTGTGACCCATGGGAGGTATGTTACGCTA CAAAAGAG
WI-4019	33 G A A	CCAGAGCGT CCTATGAATC	AACAGCAATA ACAGGAACAA ATG	CCACTCCAGGCCAAGAGCGTCTCTATGAATCAT[GA]CATTTGTTCTGTTATTGCTGTTACAGAGT GGCAACTCTTGCAAGGGAGGGGTACAAAGTGAATTTTAGATGCTGCAGGAGACGAAGGTC
WI-4091	84 A T	TTGAGGTCTTA GTCATTGCATG	TGAGTTCTCTAT TAAGTGACAAT ATTGTT	TAATTCACATTGCTCTTGTGTCATTATTGCTCTCTTATGTAAACACAAATCACCACCAATTGAGG TCTTAGTCATTGTCATG[AT]TGTATAACAATAATTGTCACCTTAATAGGAACCTCAAGCATAGTTATGTGT ACATTTATTGCTAACAGCAG
WI-4160	117 A G CAACAGAA	CCTATAATTTA GCAACAATAT	TGCAGGTAGAA TTTTCTAATAT AGCC	TCCTCTCTGTAATAGGAAGTCTGATTAGATGCCCTTTTGGGTTAGGTGGCTTCTAAGATGGTAATT ATCTGTCCAAGTTTTTGTTCCTATAATTTAGCAACAATATCAACAGAA[AG]GGCTATATTAGAAA ATTCTACCTGCATCCCTGGATCTGAACGTTCTTCATGATACT
WI-4168	32 A G AAACA	GGTGAGAGTC AAATTGATAC	ATTGCCAAACA GATTTTCAGA	CGTTGCTGGTGAGAGTCAAAATTGATACAAACA[AG]TCTGAAAACTGTTTGGCAATCTATTAAAGG CAAAATATACCAGCAGTGGTGTAGCAATTTCACTGCTGGGCATTACCTAACATAAATGAT

WI-4177	68 T C	TGAATAAGCA CGTATTAAATT TACCTA	AAGGCAGCAA ATCATGATG	ATGCCTGGATATACTTTCCAAATGACTAGTATGAATAAGCACGTAATAAATTTACCTATTATATTT AT/C/CATCATGATTTGCTGCCCTTTCCAAATTTACTACAAATTTGATTGTCACATGAGGCACATG ATCCCATTAACCCAAATAG
WI-4199	51 A C	CTCCCAAGTT AGTCAATATA AAAA	ATATGTTGATT AGGTATAACA ATATGTGTG	GCCATGAGCACAGAGGCTGAAACCACCTCCCAAGTTAGTCAATATAAAAAA/C/CACACACATATTG TTATACCTAATCAACATATAATGTTATAGATTAAACAGTCCACAGCAACAA
WI-5163	24 C T	CTGTCACTGGT CTGCCGTG	AAAGGAACAC AGGAACAGAC C	TTCTGCTGTCACTGGTCTGCCGTG/C/TGGTCTGTTCCCTGTTCTTTCAATGTTCAACTGCTTGAT CTGTGCCACTAAGGTATCAGGTTTATATGGGCACAGGATGAGGGCTTTGTAGACCAGAGTTTCTT GGAATTGCAACATTTGGGCAT
WI-4250b	117 A G	TAAGTGCATTAACTGTACAAGTCCACAAATACCTCTCCACCAGTGCTAAAGCAGTTTTTAATAACA GGTTCAATATGAGTCTTTGTGAACAGGGGTGGGAAGGATCCTGTAAAGG/C/GTTAAATATTGTTTT CCATAATATTGAAGATGTG
WI-4250a	94 G T	TCAATATGAG TCTTGTGAAAC AGG	CTTTTACAGGA TCCTTCCAC	TAAGTGCATTAACTGTACAAGTCCACAAATACCTCTCCACCAGTGCTAAAGCAGTTTTTAATAACA GGTTCAATATGAGTCTTTGTGAACAGG/C/TGTGGGAAGGATCCTGTAAAGGATAAATATTGTTTT CCATAATATTGAAGATGTG
WI-4255	68 G C	TGCTCCCCAT CACCT	AGTTGTGTAAG G	TAAATGCTCTGGGAGATAATAGGAAAGTCCCATCCCTCTGTATACCTTGGTTGCTCCCCATCACCT IG/C/CCTTACACAACTTGAAGTAGGCCCATCCAAACACTGGTCAGAAAGATACTGTGCGAC
WI-4256	57 C T	ACAGCCTCTTCAATGGCACAATCAAAAGCACCAGTAAAGCAGAGGCAAAATCTGG/C/TCTCAC CATTTGAAAAGTCTTCTGAAGGATAAGGAGTGAATGACTGCTAGAGAGAAATGATTGGCCTT
WI-4325b	71 C T	AGTTCACTGCCCTAGATGAGTAGACCATGTTGCTTTTAAATGACTCTTCTTGGTCTCTCAAGATATCACAGCCAC GATG/C/TTACTATAGATAATCTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACAGCCAC CCAGGACACTGCCATATCT
WI-4325a	58 C T	AGTTCACTGCCCTAGATGAGTAGACCATGTTGCTTTTAAATGACTGTCATGGCAGGAC/C/TGGAAA TGGGATGCTACTATAGATAATCTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACAGCCAC CCAGGACACTGCCATATCT
WI-4347	158 A G	TGGGCAGAAAGTCCGGTATGGCAAGTCAGGGTGGTTAACTTGGATGCCACTTCTGCCCTGTACCTTCT CTAGACTTTGACCTGACAGGAGATCCCTGCCCTCCTGAGTTTATCATCTCCACCTCCAGCCGAG GGCCTGTATCTGTTCCAGGCC/C/G/GAATGCTACGGGTCACAACTGTGGGAGGTAGGAATGACGA G
WI-1936	117 T C	CCAGTCTAGGCTGCAAGGACTTCAATCTGGGGCAAGTCTGTTGTTGCTAGGGTCAGAGGCAGCG ACCTGAGGGACACACAAACAGTGGGACACCAGGGGTACTTGTATCACCT/C/CTCCCGCAACCCCA AGCAGCACAGCTTGACAGTCCAGGAAAGACTCCTTACTTCCACTTGAGAAAAGGAGAGGGAAGAGA AAAGAGGACTTTGACACACAACTTGGGA

WI-5204	54	C T	TAGATTTTGTGATGACAATAGGGAAGCCTTTGTTAAATGGGTTTGAAGAA[C/T]GAAGAAAA TGGAAAGGGAAGAAATTGACAGAAACCAAGAGAGTGTGAGGGCGCAAGCAATCCAGTTTGACTGGA ATATAGAGTGATGTCAGGGTTG
WI-5215	70	A G C T C A A A A	GGACCTTAAT ATTTAACAGA	AGATAATTTTG TAAAGATAGTT TTCGC		TTTTCCCTTATTTATTTAGGAAGCAAAATGTTTCATACAGGACCTTAATATTTAACAGACTCAAAAA TAT[A/G]GCGAAACTATCTTTACAAAATTATCTCCATAGCAAGTAGACATTTTAGCACATTTTCCT GTAGTCAAGGTTTTAAAGGCCAAATGAAGTTGACTAAAGACAAAT
WI-4448	112	T G A T A T A A	TTGTATCAAA GAGATGGGT	AATTAAGAA ATCTTTACATG GTTCTTT		CCCTGAAATGTCTTGTCTCTCTCTCCAACTCTCTAGGGAACCTTTTCCATGTCAGGTGAAGGTTTTGA AGAGTACTTTAAATTAACCTGTATCAAGAGATGGGTATATAA[T/G]AAAGAACCATGTAAAGATTT CTTTAATTAGTGAATTTTCATCAGGGCTCTTCCACTGTCTATCAGTAAA
WI-4456	49	C T T A G T T C C	AGTTGAATTA TTCAGAAAAT	TTTCCCTGTTAT GCATGAACCTTG		ACACATTTTCATTTTGTCTTTAAGTTGAATTTATTCAGAAAAATTATAGTTCC[C/T]CAAGTTTCATGCATAA CAGGAACACCAGGTTGGGSCAATTGATTGAATTGT
WI-4461	49	A G C C T T C	TCACTGTTATT TTAAAATTAT	TTTGACCTTC ACCAATTICA		CTGAACTAATGAGGTGCTAAATCACTGTTATTTTAAAAATTATCCTTCC[A/G]TGAAATTTGGTGAAA GGTCAAAGAATGAAATCCCACTTTTAGATTTCTGGAAATTTTATTTGCGATGATAATGCAATGGGC
WI-4465b	75	G A		CTACTGGATTTTACTTTGCTCAAGCCAGACAACACGAAAGT[A/G]TATAAGAAAAACAGTTAGTAAT TCACCTTT[G/A]TATTCTCTCTTCTACCTCAGGGAATC
WI-4465a	41	A G A C A C G A A A G T	AAGCCAGACA ACACGAAAGT	GGTGAAGATT ACTAACTGTTT TCCTT		CTACTGGATTTTACTTTGCTCAAGCCAGACAACACGAAAGT[A/G]TATAAGAAAAACAGTTAGTAAT CTTTCACCTTTGTTATTTCTCTTCTACCTCAGGGAATC
WI-1949b	160	T C T A A T C	GAGTGAATAA ATGAATGCCA	TGAGAGGTGGG GACAAAAA		GGGGTTAGGACCTCGAGATCTTTTCAAGAAAGCACAATTCAAACCATAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT[G]CAAGGCTGCTGACATGGTCATGGCTGAATATATGTTGAAGAAAT GGAGTGAATAAATGAATGCCATAATCT[C]CTGTGTTTTTTGCCCCACCTCTCACACCTTTCCCTGG CACA
WI-1949a	86	T G A T G C T G A G T	CAGTGGTGAG CTATGCTGAGT	CCATGTCAGCA GCTTG		GGGGTTAGGACCTCGAGATCTTTTCAAGAAAGCACAATTCAAACCATAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT[G]CAAGGCTGCTGACATGGTCATGGCTGAATATATGTTGAAGAAAT AAAGGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTTGCCCCACCTCTCACACCTTTCCCTGG CACA
WI-4529	64	T C A A G A T G	CCAAGTAAGT CTATCAITCTG	TTCTAAAAATA ACACTTCCTGA AAAA		TGAGAGAGTTTTTGGATTATTCATCCTCTGCAACACTCCAAGTAAGTCTATCATTTCTGAAGATG[T/C] GAGTCTCTCTTTATATCCTATGATTATTTTCAGGAAGTGTTATTTTAGAATATAAACTCCTGGGT CCCATCCAGGCTAGGGTCAATGGCATCCATGGTGGCTGGACAAGATGGGCTTAGGATCATTTT

WI-4540	110 A G C A T C C	GCACCATGTGG	GACAATGCAGC CATGCA	AGCTTTCCCTTTCTTAAATAATGGTGCCATAGTACTGGCTTCTGTGTGCATCAGGAAGCAAGCCTAT TGCTCGGTAAACAGTACTTTGCAATAAGCACCATGTGGCATCC/A/GJTGATGGCTGCAATGTGCCAGTC AAATGAGACAACCTCCTAT
WI-4582	226 T C	AGCAAGCATCTGGCAAGCCTCGGTGACCAGAACATTAATTCACCAACACCACCTGCTCCAAATGT CCATGTTAATGCAATTATAGAAGACTCCAGTAGCATTCAAGGCCAGTTTAACCTTATCCTGTACACA AATACTTTATGGGAGACAGCATTGTAAATCAATCAATAATGACTCGGTTTGGCTGTACAAGCAT AAACAGAACGCTTGCAAAATATGGTT/C/CCTCCTTGCTAGAAACCATTTGAT
WI-1985	105 G C A G	GCCATTGAGG AAGTGTTTAA	GAATGGATGGG TCATCTCTCT	CAAAGGTAGTTTAACCTGGGGGCAACACAAAAGTTATGAGTACTCAATAACCTATGTTCAAGGG TAACCAACACCTTTTGGCATTGAGGAAGTGTAAAG/GCJAGAGAGATGACCCATCCATTCCTGG GCTTCTTATATGACACCATACTATTCACACAGATGTGGAGTCATTTATTTGGTGGTATGACAGT CATGG
WI-5248b	99 C T T T G	CACTGTTTCT ATTGACCGTAC	AGAAAAGAG AAGAAGGGAA AAA	TGTTTAAACCATACAGTTTGTGCTGCTACGTTGTTAGAGCAACCCAGAAAATTAACACGCTAC CATTTTCACTGTTTCTATTGACCGTACTTG/C/JTCTTTGCTTTTTTTCCCTCTCTCTTTTCTG CCCTCTTTAACTATT
WI-5248a	38 G C C T A C G T G T T	AGTTTGTGCTG CTACGTTGTT	TTTTAATTTTC TGGGGTTCCT	TGTTTAAACCATACAGTTTGTGCTGCTACGTTGTTAGAGCAACCCAGAAAATTAACACGCTAC TACCATTTTCACTGTTTCTATTGACCGTACTTGCTCTTTTTCCTCTCTCTCTTTTCTG CCCTCTTTAACTATT
WI-4596	69 T A A G C A C T G T G A	TGAAGCAGAA AGCACTGTGA	CAGGAGATGGG CCTAATAATG	CATTGGTGGTCCAACTTCTCGGTGACATTACTCTGTTGACTTTGCTGCTGAAGCAGAAAGCACTGTGA CT/A/CATTATTAGGCCCATCTCTGCTGCTGAAGCCTGCTACAGCAATTTGTACATATGGCATTGGG ACATATCTGAGCCCCCACTATTGACAAGATTCTCCTTTTAAACA
WI-5252	119 A C	GAAATAGGGCAAAATTAAGACTTCAATAATTAAGAAGTCTTGGGAAAAGGATTGTGATGATCATTG AATCTGTTTAAATACAGAAATTAATACTGAATACCTGTGTGAATCATTGCTTTT/A/CJTACCATGTACA TATTATGAATTAACAATGTAATAATAGTATGACTAAGAAATATTGGGCCCT
WI-4606	61 A G C T	GCAATGCTAG AAAATTATGC	TTAGGTGCTTA AGTTGTCTACT TGG	TGCAAAAAGGAAAATGATAACCCAGGACTGTTGTTCAAGCAATGCTAGAAAATTAATGCCTA/A/GJC CAAGTAGACAACCTTAAGCACTAAGGCAGAAATGAAAGTTTCTCTCTTGTCAATTAAGTCCCTATTCA ATTACCATTTATCGGGGTAATTAACACTGGAAAGTAATGCCAGGCTAATTGTTAGATTATGATAAT TACACGCTTTGCTATGCT
WI-5257	77 C A G C A A A G A G G	GAGGCATGAA GCAAAGAGG	CCAGGGGCAGA TGAAAG	CAATGAGAAGTTACCAAGATCGGGGCAAAATTAAGCATATGAAAATACCAAGTGTGGCAGAGGCATG AAGCAAAGAGG/C/AJCTTTATCTGCTCCCTGGTGGTTTTTCAGTAACCTGCAACATGCTTTTGCCTCC CGGATGAAAAGATACCCCTTCTATGACTAGCAATCCACTCCTAGGTATGCACCCTAAACATGGGTG GCAAT
WI-4649	50 C T T T C C G A A T G	GAGACCATCT TTCCGAATG	TGACTAGGTG TACTTACAAGA AATCATC	TCACGTGTTAGAAATTTCTTCTCCTCAGTGAGACCATTCTTCCGAATG/C/JTGATGATTTCTTGTA AGTACACCTAGTACATCTATGAGCACACAAATTAACAAGTACTTGCTACCTGAATTTGTTATTTTTTAA AAAATCCTCCCAATATTG

WI-4650	148	A G G T C T C T T	GCACAAAGAA AGTATAAGTT	CTGAAGTGTTA AACTGGATTGG G	AACTGTGTGGTATGTATTGTTGTGATTTTCTGGAGAGTCAGTTACTCTACTAGATCATAAAGGG GACTTGGGAACCAAAAGTATCTCAAGACATTTAATCCTAGAACCAAAAGAAAGTATAAGTTGTCTC TTATATTGCTTTT[A/G]CCAAATCCAGTTTAACACTTCAGTAACGTT
WI-4677	82	T C A A A	TCCAAAGTG ATTAGGTGAA	TTTCAACAGTG TCATTATTCAA CTT	AATTGAGATTTTGAACATACGTGACATTTTGGAAAAAATTTGCCAAAAAGTGATTAGGTGAAAAAAT GAGTTGAAATAAATGTT[C]AAGTTGAATAATGACACACTGTTGAAAAATGATGAATCTGCTTTCAATTCA CATGGAAGGAGACTAGAACACACAGCGTTTATAGGGGAATACTCAT
WI-4698	135	C G ---		---	ATGATGTCATCATGAGGAATTTCTGTAGAAAAATTTTCCCTGGCAATTTGATTCAATAAAGTTTGTC TCACCTGGGAACTGCTTATCTTTGATGTCAGTGACATTTCTTTCTTTTGACGGAAGAAAACTTCAA C/GTTTCGAGAAGGCTTAGATTATATCGCTGAAGCCCATTTCTG
WI-4722	88	G A A A C C C A C A C	TGCACTATGG AACACCACAC	AATATGGAATC TGCATTGAGTT G	CTTCCCATTTCTGCCAGTTAGATGACTGCCTCTCCACCAGCCTAGAAAAAGATGGGAGATTATTATTTG TGCACATATGGAACACCACAC[G/A]CAACTGAATGCAGATTCCATATTGAATCTGGGAAATCAGTGA AAG
WI-2020	145	C A ---		---	GCCACAGTAAAGAGGAAAAATGGAGCCATGTAAACAGAGGAGAGCTTTCTGAAGATCAGTGATTGTCA TAAAGGTGAGTAAATCAGTTTGATGGTTGAGATTTTCAAGAAACGTGAAATTTATTGAGTAACCATGGG TCAACTATGAT[C/A]CCAAACACAGCAGTGTGTCTAAAAAATATGATAGTTCTTCTCTCTGTCACCC GCAATGAAAAAGGAGTT
WI-2028	176	T C C T G T C T C A T C	TGTTACGTTT CCTGTCATC	GGTTGGAACCT CAAATTACCTA GAA	GACTACAGCGCACAGACAGGCAATTTGTGGCTTGACAGGTTTGGTTTGTGTTTAAAGTTAGATT TGAATCCTTTAAAGAAAGAAAGTGCTCTTACGTTTACTACAGACCTCATCTCTCTGTTCTCTTG CACCCAGTCCACTTCACCTGTTTACGTTCCCTGTCATC[T/C]TTCTAGGTAATTTGAGTTTCCAAACC TGTTGG
WI-2033	183	T C A	GGTGCTAGA ACTAATCCCTC	CAGTGGTTCCA CGTTCTCC	ATGTGTATGAGCTCCACATTCGCAGATTCACCAACTATGGATAGAAAAATATAGTATCCCAGATGG GCAGCCCAAGGATCAGAGGGCTAATTTTAAATTTTCCAAGGTTATACAGGACCAGTGTGGAAATTTT AGCATTTCTGGTTTGGCATCCATCAGGGTGCTAGAACTAATCCCTCA[T/C]GGAGAACGTTGGAACC ACTGATATACCAAT
WI-4745	131	T C ---		---	TTATGGATACATGTTTCTGTGGAGGACAAAGAGTTGAAGCAAAAGGACAAAGGAGATCAACTGGG TAGAATAACTCATCGATCCACCCAGGCTCCTTCCACCATTCTCCATCTACTTTCTACTCTGA[T/C] AGGCAGACTTATATGAAAAAAGGGA
WI-2034	150	T C C C A A G G A C	CCACAGTGCA CCAAGGAC	GGGTAAAGAT AGAGTGCAGGT CC	CCACGACTATGTCTTCAGAGTCCCTGGTACTGACAGAGAGAGGCTTTGAGGACCATGTGGGCCCAAGA CCTCCTCTCGGGTTTCAGTGAAAGACGATGAACCTCTTCACTCTTCTACAGCAGCTGGACTTCACCA CAGTGCACCAAGGAC[T/C]GGACCTGCACCTCTATCTTTAACCCTCCGACACACAGATGCTGAGATGCC ACACTCTGAGTG

WI-2038	155	C T	TGTCCTTTAAA GTGTGTAAGT ATTAATTAG	ATTCCTCTTG AAAGAAACAT CA	TCAGGTGACAAAGAAAGTCACATTTCTTCAATCACTCACTGCTGCTCTTGCAGTGT ATCCAAGGATGTCACCTTTTGGAACTCTGTAGATCAGAAAAAAGTGTCTTTAAAGTGTGTAAGTATTA ATTAGATTCTATTTTATGATAC[CT]GATGTTTCTTTCAAGAGGAAATTTGTGTAAGAGGATTCCCAT TGCATTCCATTGGC
WI-4782	113	C T	GATGCAGAAG ATAACTAGAA AATGC	GAACCTCTCTG GTTATTTTCT GTTG	TCATTGACTTTTAGAGTTCTTCCAGTCTTTATGCTTTATTTCTTTAGGAAAAAAGTAGGCTAGGAGAA CACAAATTCAGGTTCTCTCCAGATGCAGAGATACTAGAAAAATGC[CT]GAACAGAAAAAATAACCA GAAGAGTTCAATTATGGTTTCTTCCAGAACGATTAC
WI-4788	65	A G	GCATAGAATC ATCTTGCTAAG TTCC	GGATAAAAT AAAAATTTGGC ATAA	AGGAGAGTTTGGCTCTTTCCGGACTCTTGGAAATTCAGTGCATAGATCATCTTGTCTAAGTCC[AG] JTGAAAAAAATATGCCCCAAATTTTAAATTTATCCAAACTTTAAAGTCGAGATTATAATTGATATTT AAAAAACTATATTGAGTCTTTCTTAAAGAGATGGCGTATCACTCTA
WI-5300	38	T C	TCCAGAGAC CACITTCATC	CTACTCTTTCT ATTCATAATC CAAAA	CTTACTTCCAAAGTGTTCCTCCAGAGACCACTTCTTCTTGGATTATGAAATAGAAAGAGT AGGTGTTATTCTCTCTTTTACCAGGTGAAATGAGGCTCAGAGACAAGGTAGATGATGAGCCCA AGGTCAGTGACAGAGCCA
WI-4818b	121	G T	TGATAATGGG GCCCTGTT	CCTTCTTTTA TATGTATGCCA GA	TATAATGTTTGTTCATAGTTGCCATAGACTAGGTATGTCCACACATGAATAACAATCTTATATA ATAATTTATTCAGAAGGAAATATACATATGGGGTGATAATGGGGCCCTGT[CT]CTCTGGCATA CATATAAAGGAAGGCTAA
WI-4818a	43	A G C	TGCCATAGAC TAGGTTATGTC GC	CATATGTATAT TTCTCTCTTG AATAAAT	TATAATGTTTGTTCATAGTTGCCATAGACTAGGTATGTCC[AG]CACATGAATAACAATCTTAT ATAATAATTTATTCAGAAGGAAATATACATATGGGGTGATAATGGGGCCCTGTCTCTGGCATA CATATAAAGGAAGGCTAA
WI-5317	139	T C	TTCAATTTCTG GTAGCAGGT	GATGCAAGA AGAAATGAGTC C	TTTTCCATTTGTTGATTCTTTTGTCTGAGCCCTTAGATCTCCTTTAAATTAATAGCAAGGTTAAT AATAATAATATGATGTTTATATATACAAATTCAACTCAACAGGAATTCATTTCTGGTAGCAGGT ATA[CT]GGACTCATTTCTCTTTCATCTATTTCTAGGTTATTTGCAGCCCCGAGATCTACCCAGG
WI-4888	56	G A	GCAAGATATA AAGATTAAGA AAAGATAACA	CAATTCACCTA CCTCATTTAT CA	AAATGAGTAACCCCAAGTTACTCGGCAAGATATAAAGATTAAAGAAAAAGATAACAAGA[GA]ATGAAT AAATGAGGTAGTGGAAATGCTTGATAACTGGAGTAGTGCCTT
WI-5328	44	A G	---	---	AACATTTTAAACCATGCTACATTTTACAACACTGAAAAGACAG[AG]AAAAAAGAAATATTTTG CCTCAAAAAGCTCTTAAGAGATTATGTAATAAAGAAAAAATATGAATCAGAAAAAGGAAAGAAAT AGAAACACGTGATACTGGAAGGAG
WI-4897	93	A G	---	---	GCCTTTTGAGTTTAAAGTCTTTTGGAGTGTCTTTTTCCTCCCACTAGGTACTCTCGGCCCAAT CCCCAAAAGAAAAAAGCGCTTGG[AG]GATAAACACATCTTC
WI-5345	29	G A	---	---	CCCTGCTATAGGTCAGTTTAAAAATCCT[GA]CCTGCTATGTTTGGTTGTTGAAGCCACATCCACT GAGGTATATCTGCTGCTATTTCTATATACACACAGCTTCAGATCCACTCCATCAACTTGCAG

WI-5370	143	T C A T A A A C A A	A A T A A G A T G G T A C C T T A A C T A	C A A A G T T G G T A C A G A G A A T T T C A A A	T G C A T G T T A C T C T T G G A A A T C A T A A G G G A T C T G A G A G C C T A C A G T A T A T G G C A A C A T T A A C C A A T C T T T T G A A A A T T A C C T G T A T C C C A T C A T G G T C A T T T G C A A A A A A T A A G A T G G T A C C T T A A C T A A T A A A C A A T T C T T T G A A A T C T C T G T A C C A A C T T T G C T T T T C
WI-9711b	423	T A	---	---	G A T C T C T T C A T C C C T C T C C A G A A G G A G A A G A G A A C A C A A G A A A C G C C T G G T G C A G A G C C C C A A T T C C T A C T C A T G G A T G T G A A A T G C C C A G G T A G G A G A C G G C T T G C T G T A G T G G G A A A G C A C T G G A C C T C A A C A G T T G G A A A A T G T T A G T G T A G C T G C T G T A C C T T G A A G C T G T G C A G C A G C T T C A G T T C T T C G C C T G T G G A A A A T A T T T C C C T G A T A C T C T T A A A A T T T G A A T G
WI-9711a	390	C A	---	---	G A T C T C T T C A T C C C T C T C C A G A A G G A G A A G A G A A C A C A A G A A A C G C C T G G T G C A G A G C C C C A A T T C C T A C T C A T G G A T G T G A A A T G C C C A G G T A G G A G A C G G C T T G C T G T A G T G G G A A A G C A C T G G A C C T C A A C A G T T G G A A A A T G T T A G T G T A G C T G C T G T A C C T T G A A G C T G T G C A G C A G C T T C A G T T C T T C G C C T G T G G A A A A T A T T T C C C T G A T A C T C T T A A A A T T T G A A T G
WI-9702c	345	G A	---	---	G G A G A A T T C A G G G T G A A T G G A C T G C T C C G C T C T G A G T T C A C T G A C T A C G C C T A C G C C T G A G G T T G C A G A C T G G T C T G A A G G T G A C A G G T G C C C T C T G T G C C T A T T C A G C A A T T C C C T A C T G G T A T G T A T C A G G A T A G A G G T G A A T C A A G C T G A T A T T T G C A A C T T C T C A G T T A T T C T A A C T T A A T G A T C T C T G A C T T T T A T A C T A G C T T A A G A G G T T T C A T T C C A G T G T G C T A C A G C A T C T G A T A G
WI-9702b	344	C T	---	---	G G A G A A T T C A G G G T G A A T G G A C T G C T C C G C T C C T G A G T T C A C T G A C T A C G C C T A C G C C T G A G G T T G C A G A C T G G T C T G A A G G T G A C A G G T G C C C T C T G T G C C T A T T C A G C A A T T C C C T A C T G G T A T G T A T C A G G A T A G A G G T G A A T C A A G C T G A T A T T T G C A A C T T C T C A G T T A T T C T A A C T T A A T G A T C T C T G A C T T T T A T A C T A G C T T A A G A G G T T T C A T T C C A G T G T G C T A C A G C A T C T G A T A G
WI-9702a	179	C T	---	---	G G A G A A T T C A G G G T G A A T G G A C T G C T C C G C T C C T G A G T T C A C T G A C T A C G C C T A C G C C T G A G G T T G C A G A C T G G T C T G A A G G T G A C A G G T G C C C T C T G T G C C T A T T C A G C A A T T C C C T A C T G G T A T G T A T C A G G A T A G A G G T G A A T C A A G C T G A T A T T T G C A A C T T C T C A G T T A T T C T A A C T T A T T C T A A C T T A A T G A T C T C T G T A C T T T A T A C T A G C T T T A A G A G G T T T C A T T C C A G T G T G C T A C A G C A T C T G
TGR- A003N21	49	C A	---	---	T A T A G T A T T T A C G A A G C C T A G A A G C A C G G C T G T G G G T G G T A T T T G G T C A J A G C A T A T C T T A G G T A T A T A A T A A C T T T G A A G C C A T A A C T T T A A C T G G A G T G G T T G A T T C T T T T T T A A T T T A A T T T G G G A G G G T T G G A T T T A A C T T T T T A A T G T T G T T A A T A T A A G T T T T G T A A A G G A A A A C C A T C T C T G T G A T A C C T C A A T C T A T T T G T
TGR- A004V30	203	C T	---	---	A G A A T G G C T A C T T C A T A G G G C A G A G C A C C A C T T T T G G C T A A T T T T A A C A T C C A A G C T A A T A A A T A A T C A A G A A G A A A T A G A G A C A T T A A C A A A A T A A A T T A T G T T C T A T T T G G A A T A C C T A A T A T C A G A T A C T A A C A A G T A C A G T G A T A A G A A T A A A A A G A T A A T A A T C A C A C A T A C C T T C T A G G T T A G T A G A A A A G C G T C T C T A G G T T A G T A G A A A A G T T

TIGR- A004W22	232 C A	GGATAATCAGTACAATAATGGGACCTTAAACTGCTGTGATGCAGGAGGGGCTGGCAGTG CCCGAGGAGGGGAGGACAGTGGGACAAAGGATGCTGAGTGGGAGCCACAGCCCTGGGCTCTGGA TGGGCATGGGAATGACCAGGTCCACATCATGCACAGGGGCTGTAGCTTGAGTCCAGACAG GCCTGCCACATTGGTGTGCCGCCCGCTA/C/A/CTGGAGATGCTCTAAAA
TIGR- A005D24 b	138 C T	CATAGAAAGGAGCTTTGAGTATTGTACAGTTTGAAAAATCTCTTTGAGATAATTGATTTCATATT TGTGGCTTCAACCTCCATTACCTCTTGTCATTCCAACATCTTTATAGAGAAATAAACCCAAATTT CTC/TJTTTCAACATTTAGTTGATTATCATCTGGATTTCACTCAAGATGCAGCTCCTAAGATTATT GTTATGTTAAATTCATAAACTCCTTCACTTTAATAAATAAGGAAACAAT
TIGR- A005D24 a	123 A G	CATAGAAAGGAGCTTTGAGTATTGTACAGTTTGAAAAATCTCTTTGAGATAATTGATTTCATATT TGTGGCTTCAACCTCCATTACCTCTTGTCATTCCAACATCTTTATAGAGAAAT(A/G)AAAAACCCAA TTTCTCTTCAACATTTAGTTGATTATCATCTGGATTTCACTCAAGATGCAGCTCCTAAGATTATTG TTATGTTAAATTCATAAACTCCTTCACTTTAATAAATAAGGAAACAAT
U03735	74 C G	TGAGTCTGAGCAGAGTTGCAGCCAGGGCCAGTGGGAGGGGCTGGCCAGTGACCTTCGGGGGC GCATCC/C/GJTAGTTCCACTGCCTCTGTGACGTGAGGCCCATCTTCACTCTTTGAAGCGAGCAG TCAGCATTTAGTAGTGGGTTCTGTTCTGTTGGATGACCTTGAGATTATCTTTGTTCTGTTGGA GTTGTTCAAATGTTCTTTAA
U39840b	42 T C	GGTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAAAT/C/CAACAGCAAAACAAAAACACA CAACCAAAACCGTCAACAGCATATAAAATCCAACAACATTTTATTTTATTTTTCATTTTCATGCACAAC TTGCCCCAGTGCAAAAGACTGTTACTTTATTATTGTTATTCAAAATTCATTGTGTATATTACTACAA GACGGCCCCCAACCAATTTTTTCC
U39840	56 A C	GGTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAAATCAACAGCAAAACAA/C/JACCACA CAACCAAAACCGTCAACAGCATATAAAATCCAACAACATTTTATTTTATTTTTCATTTTCATGCACAAC TTGCCCCAGTGCAAAAGACTGTTACTTTATTATTGTTATTCAAAATTCATTGTGTATATTACTACAA GACGGCCCCCAACCAATTTTTTCC
WI-8997	41 G A CCCC	...	GTGGCCATCGATCTGACCGTCCCTGCCACTTGCTCCCG/A/JTGAGCACTGCGTACAAACATCCA AAAGTTCAACAACACAGAACTGTGTCTCATGGT
WI-7008	180 A G	TATACCCTTCCATTTGATGGAATGCTGCTGTTTCATGACCAACTTTATGGCTAGATGGGTCAGAA AGACCCAGTTTCATGATAGGAGTTGAGGTTCATATGTTGACTGATGACCCAGAGTCAACATTCAG TTTCCACCAAGCCCCAGTACAGGCCAAGAGCTGTCTCTCAAAAG/A/GJAGAGTAGTTATCTGCAGA AGATGGCAGGGCCTTGCTCCGAAAGCCTAGAGACCGCCACTGTGATTCACT
WI-9005	26 C T	...	GGTCCCACGAATTTGCTGGGGAATCT/C/JGTTTTTCTTCTTAAGACTTTTGGGACATGGTTGACTCC CGAACATCACCGACGGTCTCTGTTTCTGGGTTG

WI-7593	46 G A	TTTGTGCTCTGGACACCCCACTGCTCCAGGATGAAAGGAGAG[G/A]AATGAGATCAGTTTTGGA CACTTCCTCTTGAATATAAAGAATCAACAAGTTACAGTCATGTTGGGACTTCTCTCTCTCCAA
WI-6962	78 A G	AGTGCATCTTTGGGGAAAGGCTCCAGTGTTATCTGGACCAGTTCCTTCATTTTCAGGTGGGACTCTT GATCCAGAGA[G/G]GACAAAGCTCCTCAGTGAGTGTTATATCCAGACAGAACCCCAAGTCTCC TGACTCTGGCCTTCTATGCCCTCTATCCTATCATAGATAAGATTCTCCACAGCCTCACTTCATTCAC CTATTCTCTGAAAATATCCCTGAGAGAGAACAGAGATTAGATAAGA
WI-7059	43 C G G C C A T C	AAGGCACCCA GGTCA	GCAGAGAAGAGAACCATGCCAGGGGAGAGGCCACCCAGCATC[G/G]TGACCCAGCGAGGAGCCAA CTATCCCAAATATACCTGGGTGAATATACCAAATCTGCATCTCCAGAGGAAAAATAAGAAATAAA GATGAATGTTGCAACTCTTAAAAAAA
WI-9063	53 A C T T	CACTTCACTGA AAGACACCAT	AGCAGCCATCACATGATCTGTTTTCCACCCTTCACTGAAAGACACCATTTAT[G/C]TACCCAAAGGG CAGAAAGTAGAACTTACTATTCAATTAATGTTTGACACAATGGAAATTGTC
WI-7079	293 T G	AAGGGCATTGAGACTATAAGCAGTAGACAATCCCCACATACCATCTGTAGAGTTGGAACATGCATT CTTTAAAGTTTATATGCATATATTTAGGGCTGTAGACTTACTTTCCATTTCTTTCCATTGCT TATCTTGAGCACAAATGATAATCAATTATACATTTATACATCACCTTTTGTGACATTTTCCAGGCC TTTTACGCTCTGGCACTTTCTCGCTAGGCTGTGAGGTAACCTGGAT
WI-9074	38 A G AAAAG	GATAAGTTT GACCTAGTTCC TT	TGGATGCCGAGGTAAAAGTTCTTTTGCTCTAAAAGAA[G/A]AAGGAACTAGGTCAAAAATCTGTCC GTGACCTATCAGTTATTATTTTAAAGATGTTGCCACTGGCAATGTAACTGT
WI-7104b	249 C T	GGAGTTGCCCTTCTTAAGGGAAGGAGATCTTTATCTTTCTGGTTGCTTGACCCAGTCACGTTGGGA GAAGAGAGAGAGTGCCAGGAGACCTGAGGCGAGCCGTTCTTCTTGGACTGAGAGAAGGAGCC CCAGGCTGGAGCAGCATGAGGCCACAGCAAGAGGCTTGGTTCTGAGGAAGCAGATGTTTCATGCT GTGAGGCCCTTGACCCAGGTGGGGGCCACAGCACAGCAGCATCTTTG[C/T]
WI-7104	157 C A	GGAGTTGCCCTTCTTAAGGGAAGGAGATCTTTATCTTTCTGGTTGCTTGACCCAGTCACGTTGGGA GAAGAGAGAGAGTGCCAGGAGACCTGAGGCGAGCCGTTCTTCTTGGACTGAGAGAAGGAGCC CCAGGCTGGAGCAGCATGAGGC[C/A]CAGCAAGAAAGGGCTTGGTTCTGAGGAAGCAGATGTTTCAT GCTGTGAGGCCCTTGACCCAGGTGGGGGCCACAGCACAGCAGCATCTTTGCT
WI-8974	34 C T AAGAACTCA	TGTAGGGCTGA GCTGGC	CATACAATGAGAGCCCTGAGCCCTCAAGAACTCA[C/T]GCCAGCTCAGCCCTACACCAGTTTCCACC TGGAGTTTCATGCAAGGGCAAAAGGAGTGCCATGCCAAGCTGTTAA
WI-9161	61 C T C C T G G C	GCTACAGGAG AGACTAGACA GGAA	CTGTGAGGGTGACGTTAGCATTTACCCCAACCTCATTTTAGTGCCTAAGCATTCCTGGC[C/T]TC CTGTCTAGTCTCTCCTGTAAAGCCAAAGAAATGAACATTCCA
WI-9014c	93 T C	CCCTGTTCCCATGCTGACCTGTGTTTCTCCCAAGTCACTTTCTGTTCCAGAGAGGTGGGGCTGGAT GTCTCCATCTCTGCTCAACTTTAT[C/G]GTGCACTGAGCTGCAACTTCT

WI-9014b	44 C T	CCCTGTTCCCATGCTGACCTGTGTTTCTCCCGAGTCATCTTC/CTGTTCCAGAGAGGTGGGGCTG GATGCTCCATCTCTCTCAACTTATGTGCACCTGAGCTGCAACTTCT
WI-7023b	206 C A	TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCTCATGGTTGTGACAGACCCCTGGTGCT CAGTGCCCTTAAAGTGCATCCCGCTGTGCTGACTTGTGAGTGGATCAACATCTGTCTACGGGTCCCC TCTTTTGGCCCCAGTATTCATGGCAGGGTTGTGGACACCTACTAGCTTCCCTTCCCATTCACAC A/C/A/CACACATCTTCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7023a	56 A C	TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCTCATGGTTGTGACAGAC/C/CCTGGCT GCTCAGTGCCCTTAAAGTGCATCCCGCTGTGCTGACTTGTGAGTGGATCAACATCTGTCTACGGGT CCCTCTTTTGGCCCCAGTATTCATGGCAGGGTTGTGGACACCTACTAGCTTCCCTTCCCATTCAA CACACACACATCTTCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7093	54 C T	CTGAAATCCCTCTCTGCCCTGGCTGGATCCGGGGACCCCTTGGCCCTCCCT/CTGGCTCCAGCC CTACAGACTTGTGTGACCTCAGGCCAGTGTCCGACCTCTCTGGGCTCAGTTTCCAGCTATG AAACAGCTATCTCACAAAGTTGTGAAGCAGAGAGAAAGCTGGAGGAAGCCGTGGGCCAAT GGGAGAGCTCTTGTATTATTAATTGTGGCGCTGTGTGTGTTA
WI-9171	62 G A	ACATATCTGAAAAATGTTGAAGCCCTAAGCCAGGAATAAAGAAAAAGTAGAGATAATAATCA/G/A/ TTCTTTACAACCGATGGTAATTAAGCTTGTATTCACAAGACTTCATGC
WI-9174	47 T C T	TCTAGAGGGTA TATAGGACAGG ACTG	GTGTGAGACCATCATGGTGCCAGCTAGGACCCCATCTCTCTATTTAT/C/CAGTCTCTGCTCTATATA CCCTCTAGAAACAGAAAGCAATTTTAGGCAGCTATGGTCAAAITGAG
WI-7753	52 A G	CAGAGGTCTTG AAATACAGGG A	AAGGCCAGATGCACATCCCTGGAAGGACATCCATGTTCCGAGAGAAACAGAT/GATCCCTGTATT TCAAGACCTCTGTGCACCTATTATGAACCTGCTCCACAGAACACAGCAATTCCTCAGGCTA AGCTGCCGGTTCTTAATCCATCCTGCTAAGTTAATGTGGGTAGAA
WI-9186	76 G A	AAAGGGAAG TCTGACCTAGG T	AAAGAACTACAGAGGACGATGTCCAAAACAAAAATGGCATCACCTGTCAAAAATGGAGTCCACT TCTCCCGCA/G/A/ACCTAGGTCAGACTTCCCTTTTCATCTT
WI-9193	94 G A CA	AGAAATTGT CTGCCCTTAAAG TAGGGGG	TTGGACAAACCTAGAAATTTCTCCCTTTATGTATCTCTATCGATTGTAGCAATTGACAGAGAATAA CTCAGAAATTTGTCTGCCCTTAAAGCA/G/A/TACCCCTACCACACACCCCTGTCCCTC
WI-9015	48 C T	TTGGATTGATATCGTGAATCCTCAGCCGAGAAATGGGCTGGAATTG/C/CTTTGGTTAATACAT CTTCCCTAAAGAAGATAACACAAAAATCCATTCCAGGTAGCTCGGCACCACTAAGAA
WI-7254	37 A G	GGTCTGAGAG CATTAGGGA	GGAGCCAGGAGACAGCGGTCTGAGAGGAGGCCAC/G/GTCCCTAATGACACCCACTCCTAGCC CTGAGGCTCGTCCCTCAGACTGGGGAAGAGTCCAAAGGAGGAGGCCAGCCACTCCTCAATGC TCAATGGCTCCCTGAAATCAAGACAGG

WI-9231	32 G	CAGTCCCCCA GATTGA	CACCTGCCAC ACTCAGAC	GTGACCCCTGTGAGGTCCGCCAGATTGA[G/C]GCTGAGTGTGGCAAGTGTGTCAAAAGGGGC TGCCCCCAGGAGATGAGGCTGAGAGCAGGGAGTTGAGGCCGAAGTCA
WI-7836	120 T C	CAAATAAACA ATGCAACGTT C	GCTCTCAGAAC CAAGATTAGA AATC	TTGTTGGGAAATAGAGATTGAGATAAACACTCTCATTTCAGTAGTTACTGAAAGAAAACTCTGCTA GAATGATAAATGTATGTTGGTCTATAACTCCAAATAAACAAATGCAACGTTCC[T/C]GATTTCATAAT CTTGGTCTGAGAGCCATTGGTTTCAGTTGAGTGTAGCAATCCCATACCCAGCT
WI-7286	65 T C A	CAGCTTCAGCT TAACTGACAG A	AAACAATCTA ACCAGAAAGCT TTAA	TCCATTCTTTTGGCCCTGCAGCATGTCTGCTCCAGAAATTCAGCTTCAGCTTAAGTACAGATTC GTTAAAGCTTTCTGGTTAGATTGTTTTCACCTTGGTGATCATGCTTTTCCATGTACCTGTATAAT TTCCATCATATCTCAAAGTAAAGTCA
WI-7858	91 T G TAAAT	CTAAGCATGT ACGTGAATTT T	CCCAATTTTA TTAAAGTTTA CATCTAT	CAAACTCTGGAAATATCTCAAATGTTAATAACAATATGAATTTTCTCATGCATACTATTACTACT AAGCATGTAGTGAAATTTTAAAT[T/G]TATAGATGTAACTTTTAAATAAAATTTGGGGTGTGG
WI-7860	50 C G	CGTACCTCCAA ACATAATTGA TTC	GCITGAGTGA AGTCTCGAGA	GAAGATTAGGGAGGGTGTCTGTGGTCTCCTCCCTGCCCTCTCCCA[C/A]GTGGGAGAGACC TGATTTGCCAAGTCCCTGGACCTGGACCACTACTGGGCTTATGGTTGGGGTGTAGGCAGG TGAGCGTAAGTGGGAGGAAATGGTAAGTCTACTCCAAACCTAGGTCTCTATGTGACAGACCAG ACCTAGGTGCTCTCTAGGAGGAAACAGGGAGACCTGGGCTCTGTGGAT
WI-9064	29 A G	CGTACCTCCAA ACATAATTGA TTC	GCITGAGTGA AGTCTCGAGA	CAAGCGTACCTCCAAACATAATTGATTC[A/G]TATCTCGAGACTTACACTCAAGCAATCCTGAGG AATACTGAGGAGGGCTGGCTACTGTCTCTGCACTCTGCTGCTTTG
WI-7307	128 G T	CGTACCTCCAA ACATAATTGA TTC	GCITGAGTGA AGTCTCGAGA	CACACTTGTCTGTTCTCAGTCTGAGGTCTCTGGCAGGTGAGGTGGGTAGCCGGGTTCCACA GGCCCCAGCCCTGGCAGGGGTCTGGCCCCCAGGTAGGGGAGAGCAGTCCCTCCCTCAG[G/T]AAT GGAGGAGGGGACTCCAGGAATGGGAAATGTGACACCACTCCTGAAGCCAGCTTGCACCTCCAGT TTGCACAGGGATTGTCTGGGGGTGAGGGCCTGTCCCAACCCCGCCC
WI-9274	25 C T G	GAAATGTGAC TTCACTTTGGT G	CAGGTAGAATT TTCTGTCCATT G	GAGGAAATGTGACTTCACCTTTGGTG[C/T]CAATGGACAGAAAAATTCACCTGTCTACATAGGAGAA GTTTGGAAATGCACCTAATAGCTGGTTTACACCTTGATTCGAGGTGGAAA
WI-7313e	266 T C	GAAATGTGAC TTCACTTTGGT G	CAGGTAGAATT TTCTGTCCATT G	AATTCCTTTCTGGTAATCAGGCACATGATGAACCTTTGATTAGTGGTGTGATTAAGTTCTTAAAT TGTTTGCAGTCTTTTATGTTTATTATCATAGGTATAGGTGGACCTAAATCCTTATCATATCTTTAT AATTCAGCCAGTGTATCCACCACTTTTGTATGTTTTAAGTAACCTATTATCTCTGGATTTCATG AAGGTGTAATATCGTTTGTAACTGAATAGAAATGTATAGCGATGA
WI-7313c	256 C T	GAAATGTGAC TTCACTTTGGT G	CAGGTAGAATT TTCTGTCCATT G	AATTCCTTTCTGGTAATCAGGCACATGATGAACCTTTGATTAGTGGTGTGATTAAGTTCTTAAAT TGTTTGCAGTCTTTTATGTTTATTATCATAGGTATAGGTGGACCTAAATCCTTATCATATCTTTAT AATTCAGCCAGTGTATCCACCACTTTTGTATGTTTTAAGTAACCTATTATCTCTGGATTTCATG AAGGTGTAATATCGTTTGTAACTGAATAGAAATGTATAGCGATGA

WI-9281	68 G A	---	---	GCTAACACITTT TTAAACCGT CTC	CAITTTATTTG AAAGCTATTCA GACA	ACTGGTGGGAGACTGTGAGGATCCAGGATTTCAGTATTCCTGGCCAGAGGGCCTTGCTGGCTACTGG [G/ATGTTAGTTTGCAGTCTGTGTGCTCCCTCTCTTAAGCTGTGTCC
WI-7848	142 A G	---	---	GTATATTACA ATGATACCG ACTGA	CCCCACAGAAC TATTGTAAAC AA	TTCTGAAATATAACCCAGCCATTGAGCTATTTAAACCTGTAAATTTTTTAATTTACAAAAATATAA AATATGAAGACATAAACCCAGTTGCCATCTGCGTGACAATAAAACATTAATGCTAACACTTTTTTAA ACCGTCTC[A/G]TGTCTGAATAGCTTTCAAAATAAATGTGAAATGGT
WI-9304	70 G A	---	---	---	---	TCACGTTTGGTCTCTCAGATTCTGAGGAAATTCCTTGTATTGTATATTACAATGATCACCGACT G[A/G]AATAATTGTTTACAATAGTCTGTGGGGCTGTTTTTTTGT
WI-7933b	314 C A	---	---	---	---	TTACAGAAACTTGCCCTGTGCCCTGTGTCCTGTCCCCCATGCTAGGGGGGAGGGGTCTTTTCCTCTCTTTCC TACCTACCCCTTTTCTCTTGGCCAGGGCTCGTATCCTTCTCTTCTTGTCCCTGGCTGGCTGCAC AGAGGATTGCCCTTCTCTTTTCAGAGCTGCCCTCGATGCCAAATTAGCATTTAGTATTTGCACAA AGTCTAAGGGACCATTGGCTGCCCTGGTGGGAGGAACCATAGTCCCT
WI-7933	96 G C	---	---	---	---	TTACAGAAACTTGCCCTGTGCCCTGTGTCCTGTCCCCCATGCTAGGGGGGAGGGGTCTTTTCCTCTCTTTCC TACCTACCCCTTTTCTCTTGGCCAGGG[G/C]CTCGTATCCTTCTCTTCTTGTCCCTGGCTGGCTG CACAGAGGATTGCCCTTCTCTTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTGCA CAAAGTCTAAGGGACCATTGGCTGCCCTGGTGGGAGGAACCATAGCT
WI-7374	182 T A	---	---	---	---	CCCAGATGTGCCCATCACGTTTTTCTGAGGCTTTTGTACTTTAGTAAATGCTTCCACTAAACTGAAA CCATGGTGAGAAAAGTTTGACTTTGTAAATATTTTGAATGTAAATGAAAGAAAGTACTGTATATTA AAAGTTGGTTTGAACCAACTTTCTAGCTGCTGTGAAGAATATATTG[T/A]CAGAAACACAAGGCTT GAT
WI-9343	78 C T	---	---	CCAACAACAT CCTCTGCCA	AAATGAAACTT ACGTTTGTG TG	GGTGTGCTCCTGCTACCTTGACCCCTCCCTTCTCCTCTCTCTCTCATCATCATTCCTCCCAACAACAT CCTCTGCCA[C/T]ACACAACAAACGTAAAGTTTCATTTGGGCAAA
WI-7386b	104 T A	---	---	---	---	CTATATGTGAGAGGCGTGATATCTGGATGGAAGTTGGGCTGGATGATCTCCAAGTCGTTTCAACTCT TAAAGACATCTTAATCCTGAATGTAAACAATTGTA[T/A]GTGTTTAGAATCAGAAATTTGATTTTGA ACTTGAGTAATTCATCCTT
WI-9357	75 A G	---	---	---	---	AAGAAGGAGCTCAGTTACGGGGTTTTTAAACCTTCATGAAAACCTGAAGAGTTCACTTTTTGTATTAT GCTCTT[A/G]TGATTACAGACTGATGCCAGACAAACCTTGGGAAGA
WI-9360	79 T C	---	---	CTTTAGAAAA TCTGCTTTAAC TTGG	CCTAGGGAACA CAATTAGAGGA A	TGAAGGGGTGTGGCATCTGTGTTTCTGATGCTTACTACAATATGTGAACCAGTACTTTAGAAAACTGTG CTTTAACTTGG[T/C]ATTTCTCTAAATTGTGTTCCCTAGGAAATGACTGTCCCAAG
WI-7423	107 T C	---	---	TGCTGGGCTGT C GTTC	GGTCCAGAAGA GGCCG	TGCTCCCTGTCCCATCTGCAGTGGACCCAGGCCCCCCCTTTGAGGAGGTGGGGTGAAGTGCCTCT GGCAGGGATTGTGACACTGCATGCTGGGCTGTTCQ[T/C]CGGGCTCTCTGACCTTGCACCGTG GATACCAGGCCATGTGCCATTGTATTTGGTCTCGGAGGGTGGTGAATAAAGGCATACGTCT

WI-7424	131 T A	CAAGAGAGAG AGAGGAAAGA A A A A	TGCAAAAGAAA GAATGAAAGTT G	CCAGGAGCACTAGAGAGGGGGAAGAGCAGAGAGTGTAGAGAAAAAGCCACCGGAGGAAAGG AAAAAACATCGGCCAACCTAGAAACGTTTTTCATTCGTCATCCAAAGAGAGAGAGGAAAGAAAA [T/A]ACAACTTTCATTCCTTCTTGCACGTTTCATAAACATTCATATA
X86400	118 A C	---	---	TCCTGCAAGAAGTTCTCAAGCCTTTTTGATTTTTGTGCAATAAAGTACAGCTTTCGATAAGAGTGAAA TTGGGCTAGCTTAAATGGATCCATAAACTTCTCTAATTTTAAAGTGAGA[A/C]TCTTTTAAACACCT GTTAAATTAATGTAGCAGTCTGAGAATCTAAAAATTATGTACCACCTCGTTTATTTGTTTCATTCATCCA TCCCTTTTCCCATGAATATTTCA
WI-8053	242 T A	---	---	GTGGCCACTACATGTTATAGAAACCATCATCTGTCCACACGACAGTCTATGAATAAAGGCTGAG TTATCACTAAGCAGGAGAAAAAGCATTAAGAGTGCCCATTAAGGGGACTTTTAAATCAACCTAA TAACTCTAATCTGCTGACTTTTAAAGATCTAAGGTCAATTTAATACATGCTGAAAAAGGGTCACA ATTAATCTTTGATCTTTTTTACTCACTGTTAACTTATATA[A/T]TCAGAAAC
WI-8180	165 G A	---	---	TACACAATGAATTGCTTTTATTCGGTATGCATCCACATTCAGCATTTAGTGGTCTGAAACAGCAAG TGGAAAGACGCGCAGCAATTTGCCAGGAGGTCAAGCCACCAATTTGGGGATCTGCTGTGCACACCGG GTTCCCTCTTAATCCCTGCTGAGGATCTTG[A/G]AAGCAGCAGCAGCACCAAAACCAAGGCATGCA CCGGATTCAAGGTTCTTTTGTCCAGTTGTCAGATTCCAACTAGACCCCA
WI-8275	148 G C	---	---	AACAGTACCACCAACCATATGACAACTGCCAGGCAAGGCTTGTCTCCCTCCCTTTCGCTCCC ATGTGCTAGTCAGCAAGGTGGGGAGGCCACCGATGTTAGCTTGCCTCCCAAGGGAGTATTACAGAGA GAGGCTTGGGAA[A/G]CGGAAGGAAACCTGGACAGGCTTTTCAGCACTGAGAAATCACTTAAAACTG ATTTGCTTTCAGTAACCTGGTATGTCTGAA
WI-8421	41 G T	---	---	ACCAAGAGATCAGCTGTCTAAACAGCAGCTTTTTTGTGTTG/TJGGGCTTCTGAAAGAAACCTTGC TGACAGCTTCTCACTGACCTGCAGGAGCGGAACCGTACCTGAGAGGGGATGGGGCTCTCTCACAAAA GAATATTTGGGCAGAACCTCTGGAACCTGGCCACGAGGACATCCCAAATATCCCTCTCTCAGGG CTCACCCCGACATCCTCAGCCAAATGAAGGCTCTGAA
WI-8905	215 T A	---	---	GGGTGAGACGGGTTTATTGTGCACATTTACACAGGTCACAGCGTCTGGGCTGGCAGGGCCATGCTC CTGTGGTCGGGCTGCTCTACAAGGGCGTTCACTTTCTTCCACACACTATGTACAGTCAGTCTCCAA GGTGATGGGCTACAGTGTCTGCATCAGTGAGTCTGTACACACATTTTACATAAATTACACACGACTC ATACATGAAAAA[T/A]JAGAGCCTAAGGGCCTGTATTTTAAATGAGAAAAAAA
WI-9420	202 G A	---	---	AACCTGTTTACAAAAAGGCTTTGCAAACTTCATTACTGAATTTGTAAGTCAATGACTGTGTTGTTT TAAATATGTACCAAGGAAATACAAATGGATAATGATCATTTTTCATGCTCAGGAGAGAACAGCAC AGAAATAAGGATACTGCACAAGGTGCAAGGAAACCCGGAACCCATTGTGTACACTGTCTTTCACACAG [G/A]GCATTCCTTCTACCTTAAGTGCAGCTGTGCAAGATGCCTCAGTGTG

WI-9448	184	G A	TGGGGCTGCTTTTAGACTTCATTCTAGAGCAGAGCACCTAGTGAGAGGAATACCTGGGAGAGAGAC TGCCCTGGCCATGGTGGTTAAACCTACATGAGGGGACTGAAATCTCTTTGGATGCCAGTCCAGATCCC TTTTTAAGAAAAATGGGCTTGTTCCAAAGGCTGAGAGCTGGCACCAC[G/A]CACTGGTTTCTAAA TCTCTGGCTTGGATTTATCCAAGCCATGTTCTTAACGTGCCCGTGAGCAG
WI-9470	204	G A	ATGTCAGAAGAGACACAGCAAGGAGTTTTCCCTTTTAAATGCTAAACAAGTGGCCTAATCCACA GATCTGAAAAGTACAGCTCTCCAGGTTGATAAATCAGATTCCAGGCTTTTCTTGTCAGTCCGCTTA TGAGATCAGGAATATGATCTCCCTAAAGCCCCAGATTCTACTAGACCGCTGGGGACACTGATGAC AA[G/A]GCAATCAACTCATCTCCTCAAGCTCACCAGGGCTCACCTTCCCAAG
WI-1245b	201	G T	GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCTCATAAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTGCCTGATGCAGATCTGCTGAGCCATGTGCTGGCATCACAGGGTGGT TTATTAAATTTCAATTTATCATCTGGACAGCCCTTCTTATAACGTACATCCTTGCCCTCTTCTGAGGC[G/ T]CTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1245a	85	T C	GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCTCATAAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTGCTGCTGATGCAGATCTGCTGAGCCATGTGCTGGCATCACAGGGGT GGTTATTAAATTTCAATTTATCATCTGGACAGCCCTTCTTATAACGTACATCCTTGCCCTCTTCTGAGGC GCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1031	149	G A	TTCAAGTATAAGGACAGGCTAGAACAAAGCGTTCCTAACCCCTGGCACCATGACAGTTTGACCAAA TAACCTCTTGTTCAGGGGACTGCTCTACACATTTGTTGGGATGTTAGCAGCCTCCGTGGCTTCTACCCA CTAGATGCCAGCA[G/A]CACAAACACCCCTCCCAACAATCATGACAATGAAAATGCTCTTTAGACATT GCCAAATATACCTTGTGGGACAAAATGGCCCTGATTGAGAACCACTGGTT
WI-5385	110	G A	AATGAGTCATTGTGGAGTTAGAGGAGGTTACTGAAAATGGTGACTCCAATGGTGGGATTTGAAGAGG GAAGTCTCGATAATTTAACATATGTTTCTTGGCAGGAATCG[G/A]CAATGCTAATCTATTGCTTAA TTCCTTATCAACAGACTCTTTGAATCAATTTAGAGATACTCAGTGACCCCATGGCTAGAGTTCTTGAC CCCTGCTACGGGAACATTGAATGCA
WI-5403	199	T G	ACCAAACCGTTGGCAAAGGCTCCCCAAGACTCACCCCAACTTTGGTGCTTACCCTATGCCGGGTG GGATTGAAGAAATAACCATAAATATAATTGCTACAAATTTTCCAGTAGTTACCAGGCACCCAGCCTAT TGGAAGAAATCATAAATGTAAACCTACAATGTATTGCTCTGCTGCTTGGTGGCAGGCATAGAGTT[G]GGCCTACAACCCATTTTATCATTTGAACCTCAGAAAGCATCCAGTTGGGGCT
WI-5801b	157	G A	TGGTATTTTCTCTTTTCTCTAAAATGTTATGATTAAATTAGTGCTTTGTAGAAATTTGAAAAAATGTAAA TCAGAGAACAGAAAAAATAAGTATAGTTGAAACCTCTAACAAATTTTAGATTTTAAAGGCTTAG GGAAAGAAAGAGAGCCTGGGA[G/A]AGGGAATGAGAAAGCACACCAACGAAAAAAGTGTGT GGCTTAAGGGAAGCCCAAGGAAAGTTAAGT

WI-5801a	48 A G ---	---	TGGTATTTTTCCTTTCTTAAATGTTATGATTAAATAGTGTCTTTGTJGJGAAATTTGAAAAATGT AAATCAGAGAACAGAGAAATAAAGTATAGTTGAAACCTCTAAACAATTTTAGATTTTAAAGGCC TAGGGAAGAAAGAGAGCCTGGAGAGGGAATGAGAAAAGCACACCAAGAAAAAAGTGTGT GGCTTAAGGGAAGCCAAAGGAAAGTTAAGT
WI-5696	61 C A ---	---	TTCTATTTAAATCCTGTGCCCCATTGCAAGACTGCATTAGTGTGCTGATGAGCCTTAGTTTCJCAJTA AAGCCCCCTCACACCGAGGACAATGTTGAGAACTAAATGACTGCAGGTGAGCAATTCCTGTATTA TACAACTGGGACCAAGATGACTTTATAATAGTGGCAAGAGACAATCAGGCAGACTGGGAGGACC TTATAATAGATTATAAGGCTGTGGTGAGTTATTTAAGCTT
WI-7461	153 C T ---	---	TATTACTAGTTTCATAGAGCCCCGTTGTATGATAAATAGCCAAATAGTTAAAGAGGCTGCAGGCC AATCTAACGCTCCTCACTTCCTTCGAAACCCAGCCTCAGAGATGACACTTAGGCTGCACATTCCTG TGGCAGGAGCTGTGCTTCJTGTTCCCTGTGGTCCCGGAACCCAGTGTGGTGCCTGGCACAGAG GAGGCCCTGAGTAGCATGTGCTGCA
WI-9716	221 G A ---	---	AGAAGACAGGAGCACTGGGATCAAGGACTGATAAACTCTGAGGCTTTAATGGTCCCTTGTCTCTAAC GCTTTTGGTACTTCTCTTCTGAAGACCAACCTTTCAAACTCTCAGAACACAGGCAAGATGCAT ATTCTGATGTTTCAGATGTGACTTCTCTACATTCGGAAGACTAGATGATAGGCTCTCTTCATCT CAATTGAAAATTCCTAGAAJGJAJAAACACCTAATTTGGCTCATCTTGGATCA
WI-9760	49 C T ---	---	TTTTCGTTAAGTCTTGAAGCCACACAGAGTGTACTCTCTTACJCTJAAAGTGTACTTTGCA TATATTTATGGGATGATCTATCCCTACTTAAGATTTCTCTCTCAGGTTAAATATCCATTTCT TTGTCAGGAGTTCTTATTTGGCCTTCTTCTAAACCCCTAACCATCTGCTTATTCTCTGCTTGACA CATGCTATTTAATCAAGGTGACATT
WI-9855	31 A C ---	---	GAAAACTCGTTGGCTCAAAGGAAACTGTAGJAJAAATTTCTTTTTTTTATTTTGTGTTTTAACTC AAAGAGTGGAGTTTGCAATTGACCTTGATGGCAGCTGCTCTTTTGTGTTGGTGAATCCTCTAGT GGGCACTTTGCAAAAGCAATTTAGAGCAAAAGGTGGTGGCATGGAGTTGTGAGGTTGCTGAAAAG TAGCAAATGGAAGAAAGGTTAATGGA
WI-10312	41 A G ---	---	AAGGCCAGTGGGAAAGCAGACAAAACACTCCAAGAAATACJAGAGATATAAAACATCATCA GTAGAGATGGGATGACCTAGGAGTCTGCTGATGAGGGCATGTGAGACCAAAAGACATTTGGGTCT TGAGGGTTGAATAGGAGTTGTCTGGTGAGTCTTGCCAGTCCCATAGTAGGTGTTCCATAAATAAC AGTGACTAACTGAGGTAGAGTCACAGAGAAATTTCA
WI-11152	179 C T ---	---	GATCTTTGCGACATGCAGAGCAGATACGGCAAGGCATCTTGGGCATTTGGAAGGAAACGAGCCCTA ATTCATAGAAACAGACTCTACAAAGGACCAGTTAAAGGTCTGCAACCCAGGACTGGGTGGCCAAAG TCAGTCAAGGCATAAAGGGGACAAAGTGGGACAAAAGGCTTGTCAJCTCTGTGCAGAAACATTGAA AACAGCCAGTACATGCCACTGATAGA

WI-1968	167 A G ---	---	TGTTGAGGAGCTGTAAAGCTGAAGAATAGTCTCTGCTCTGCTCTTTCGTTGGAATGGATGAGTCCT TTTACAAAATTTTCTCTCTGCGCATGGGTGTTATGTTAGAAATCATGGAGTTGGAAGACTTAGATTCA ATTTGGGGCTGTACAGTTTACTGGAAGTTGT[A/G]TGAACCTTGAGCAAGTGCTCTTAATGTCTCTCA GCCTCAATGCCCTTCCCTGTAA
WI-4701	198 G A ---	---	GGGTTCAATTAACAGCCTCCCACTGGGTCTCAGATTGCACGGAGATGTAAAAATAGGAAGAGATAG AAAAATGGTGCCCACTATTGACTTGATAACACCTACAAAACACACATTAAACTCCTCCCCACTCTA CCCGCCAAAGTCTACCTTTGGTCTTTTATTTCTGCTAATGACCATACTATTTCCCAATTAGA[G/A] CCATGTCATTTTTCAGAAAAGCAGTATA
WI-4823	164 C A ---	---	TTTATCTTCCAAACCATGTGTGTTTCTTCACATACCTTTACGTAATTTAAATCATGTCAATTAATTA TGCACCTACTGTTGGCTACAGACATTGCTTCCAAATGTAAATCCCTAACACAGCAAGCATAACT GATGTGCCATCTTTGTATTCTCTAAA[C/A]AAAGAAAAGTGCTTTTGTGCATCTGCCCTCTCTGT CTTCTCTGTTTTCACCTCTCTGTTTCCCTATTTCAGCATTCATGATTA
WI-4860	72 A G ---	---	AAAAAACAACTTCATTTGACATCTAAGAAGATAAAGAAAAACACGATCCACTGTGTGTTGCTT GATTT[A/G]GGAGATAAAACCTGATCTTAAGAAAAATTAACCAAGCAGTACACTAAATAGCCT TTGTGTGTTTTCAGGAAAGAAAGCCAACTCAAGTTGCTAAGAAAAATATGTTTCATATCA CTCTAACTTCCACATAGAGCATTAAATAGCA
WI-9705	111 C A ---	---	TGAAGGACCAGTTCGAATGCTTACCAAGGTAAAGTAAATCGAGGGGCGAGGAGTAGGAGTTGCTT CCGGATGTTGCATAAAATTCAGGTTCTTAAGGAGTTCCGCTGCC[C/A]AAAAATGTTAACACTGATGC TGCTCAAAACGCACATAGAAATCGGTGGTAGATTGCGGTTCTCTAGTAAGTAGCTAATGTTTAGATA TGATTGTTGAATTATTGTTGCTGTGTTCTTGGTG
TIGR- A004Z48	177 A G ---	---	CAAAATACTCTGCTTAGAAGTTGCTCTAGGGCCCATGGATTTCATGAAGGGTGGGCGAGGGTGGACTG AAGATCTGTTGGCAGGGCTCACAGAGACGGGGGTGAGGGGAGAGATCGTGGGTTTCATGAGATCCCAT CTTGGGCAATACGGTTATCCCGTGGTCTTCATACGCCACAGA/[G]TCCTCCAATTTTCAGGGGCTCCC GTGGGATGGTGGAGCCCAATGAAGACCAGGTAGATGATGCCACCTAGAGATG
U17579	34 T G ---	---	GGGATTCAATGTGTCTGTCTCATCCAATAAGCACTT[G/C]ATGACCTCAGCCCCATACTCTTTCTCCC TATGTTCCAGAGACAGAAATAGACCTGGCCCTTCTCTAGGGGATCACAATATTGGAAGGATGAG GACTCCAAACAGCCAGCTCCCATGCCAAATAGAACGATGAGTGTCTGGGATCAATTTCTATGGGAGCC TGGGAGAGGGGATCCTTTCTAGTTGA
WI-7747b	88 T G ---	---	GTGAGAGCGAGGCTGAGCCTACAGATGAACCTTTCTGGCCTGCTTTCGTTAACTGTGTATGTACATA TATATATTTTAAATTTGATTT[G/AA]AGCTGATTACTGTCAATAAACAGCTTCATGCCCTTTGTAAGTT ATTTCTGTTGTTGTTGGGTATCTCGCCAGTGTTGTTGTAATAAGAGATTGGAGCACTCTGA GTTTACCATTGTAAATAAAGTATATAATTTTTTATGTTTGTTCIGA

[illegible]

WI-7805	101 A G	TTTCTAGGCTGTACAGTCTGATGCATGATTTTTTATAAATATTTCTACTCTTGGAATTTGGATCTT TTTACTTTGAGCATATATTTAGAAATATGTGTA/GTGTAAAGGATCTCCACAATGTCTGCAGTGTG AAGGCAGGTTTATTGTGGAATAGTTTAAACAGTCAGGAAGGCTAACTGGTCAGTATTAATGTGTAGC CCTACCAAAATAGCCAGTAGTATCTGAAATGAAAAATAATGAAGTAT
WI-7416	137 G T	GGCCAGGAGATTAGCAACAAGGATTCATCTGTTACTTACTTGCCCTTTTATCTTTCCCTCTTGCCC CAGTCCCTTCTCTCCAGCTTCATGTGAAGCTCTGCACAGACAAGACACTAGTGTCTCTGGCAGTGT [G/T]CTACTCTCAGGTGCAGCATACATAACCAAGTAAGAGACTAAATCTGCAATATATAAAGAGCTC CTACAAATCAGTAACATGAAGAACACTCAAAATTTGGCAATGTCATCAG
WI-140	252 C T	ATTTGAAGATTGGAGGGCTTTGCAGAGGAAATAGATTTCAATGGATCCCCAACTATAATGACA AGTTTTTAATTAGGTGATCAAGGCTTCTAAAGTGAATGCAAGTTGTACCAGTAAAGTTTATA TCTTCCATTGAGCCAGCTCATTTGCCAGAAATTCAGGTGAGTGAGTTGGCCAGACTATCTGGCAAG GATGAAATTTTAGTTTAAATGTTGATTTGCTGTATTGGCATTCTC/
WI-198	218 C T	GAGGCTTTTCAGCAACATGGAAGCCCTACTGCTTCAACCCCGAGTCCCGGATCAAGTGTGGCACC CATGATGGAACCTCTGCCATGGTTTAGTACCTGGACCAAGTAGTCAATCCATCTGACITTTAAAA TTCTAAACAGCCTTTGATGGGACAATCTCTGCTAAAGACTAACCACTTCTTATCTTATCTTCAGCTA CCTGCTTCCCTTTC/TGTTTAAACAAGCATAGAATATCTGAACAAC
WI-205c	146 T C	TTATGGTCCCAAGACAGATTTTAAAGAAAGAAATAAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGCTGACTTTTTCAT GCATGAGTTTGT/C]CCAAAGGCTTGATGGGAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAACTGCATATGCCCTTTATTTTGTAGTTCCC
WI-205b	146 T C	TTATGGTCCCAAGACAGATTTTAAAGAAAGAAATAAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGCTGACTTTTTCAT GCATGAGTTTGT/C]CCAAAGGCTTGATGGGAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAACTGCATATGCCCTTTATTTTGTAGTTCCC
WI-234	165 G C	GAAAGACTGAGTTTCCAGGAGGTTGCAGCCGTTTCTCTCGGCCCATATGGCTAATAAGGAGCTTGAGCA GGGATTCAACCTGTTTGCAACCCCAAGTNCCTTCCAAGAGGTCTCAGACTACCTCCTCCATCTCCCCCT CTCCCCCACAACACAAATACAGAGATT[G/C]AATTCAGGAGCCAGTTTCTAGGTGGGCTTGAGC AATCATACACAGTAATCTCTTGGTGTCTTAGTTTCTCAATGGGAAATGG
WI-276b	25 A G	AGCTTTTGAATCCAAAAACCATAT/G]CTTGACTCTCTTATCCTCCTCTTGTTGTAACATCTATCC CTGAGGCAGAAATACAGAACACCCCTGTGGCTGCCTGAACGGAGGAGGATGGGGCGGGGAGACAT CGGTCAATGTATCAAGCATCTCTGCTGCTGAAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGCTTATCCTCTGCTATCCTGATCCCTGATGACTGGGCAAA

WI-276	25 A G ---	AGCTTTGAAATCCAAAAACCATTA/GICTTGACTCTCTTATCCTCCTCTGTTGTAACATCTATCC CTGAGGCAGAAAAATACAGAACACCCCTGTGGCTGCCTGAACGGAGGAAGATGGGGGGGGAGACAT CGGTCAATGTATCAAAAGCATCTCTCGCTGAAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTGTCTTATCCTCTGCTATCCTGATGACTGGGCAA
WI-427	59 G A ---	TTTCCCAATCCACAGGTAAACTAATAATGGATGTATAGAATTTAGAACTACTTC[G/A]GTTT TTCCCTGGGAAAATATTCACAAAACATTTGGTCTGCAATCAGGTTAAAGACATAGTGTGCCA TTTGTCAACAGAGGTAGAGGCTGACTCTGGCAGGATTAGCTACCACTAGCTGTGAGACTTTATGT ATTCAATTTAGAGCCAGGCTTGTCTGTGTCACCCAGCTTTCAGTGCAGT
WI-562c	106 T C ---	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAGCCCAGAAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATTTAAIT/CJAAATGGTCTTTTATTAATAAAAAA AAAGNTATCTAAAGAGAAAACCATATAATCTCAGGTAATTATGGCCACAGCCAAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCCACTTCC
WI-562b	106 T C ---	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAGCCCAGAAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATTTAAIT/CJAAATGGTCTTTTATTAATAAAAAA AAAGNTATCTAAAGAGAAAACCATATAATCTCAGGTAATTATGGCCACAGCCAAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCCACTTCC
WI-562	103 T C ---	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAGCCCAGAAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATTTI/CJAAATAAATGGTCTTTTATTAATAAAAAA AAAGNTATCTAAAGAGAAAACCATATAATCTCAGGTAATTATGGCCACAGCCAAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCCACTTCC
WI-597c	141 A G ---	GTGTAATTTGGTGGCTTTGCAACTTTTCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAAGAAACAAAAGATGCTATGTTGAAGAAGTATCCTTAGGATATCT GATACATG[A/G]TAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTAATAAC TTGATCTAATAATTCTTCACAACTAATATACCTGAGAGAAATAAGTCTATTTAAT
WI-597b	141 A G ---	GTGTAATTTGGTGGCTTTGCAACTTTTCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAAGAAACAAAAGATGCTATGTTGAAGAAGTATCCTTAGGATATCT GATACATG[A/G]TAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTAATAAC TTGATCTAATAATTCTTCACAACTAATATACCTGAGAGAAATAAGTCTATTTAAT
WI-597	136 A G ---	GTGTAATTTGGTGGCTTTGCAACTTTTCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAAGAAACAAAAGATGCTATGTTGAAGAAGTATCCTTAGGATATCT GAT[A/G]CATGATAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTAATAAC TTGATCTAATAATTCTTCACAACTAATATACCTGAGAGAAATAAGTCTATTTAAT

WI-811	66	G C	---			TTCAAAATTAACACCATGGGTATATTATAATTINGCTCTATCCATAGTTCTAACCCCTTCTCTG/ CJACAGTGAGACACCTGCCCTTCTATTGCTCTGACGTATTACGTATTGATCAGTCACCCCATCTGGA ACCAAGTTTCAATTTCTGTGACCCCTCCCTCCTCACCCTACTTGGGCTCTGACTTCTTCTCTGGGCT GAACCTTCTGTGTGGTGTCCGGCTTCCCTGCTGGCTCCCAATAC
WI-881b	156	A G	---			TGAAGCCCTCTCTCTATACCCAAAGTGTCTTTATCTTAAATGCTGTGGTCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTTATACAGGGGAAGCAGCTTTGNCCTGGTATGTATAGCAA TCCATAATTGTTATAGCTATTJAGJTATACTATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCCTTAAGATATGCAGCAAGCACAATCTGTCTGGT
WI-881	156	A G	---			TGAAGCCCTCTCTCTATACCCAAAGTGTCTTTATCTTAAATGCTGTGGTCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTTATACAGGGGAAGCAGCTTTGNCCTGGTATGTATAGCAA TCCATAATTGTTATAGCTATTJAGJTATACTATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCCTTAAGATATGCAGCAAGCACAATCTGTCTGGT
WI-867b	119	G A	---			AATCTTAACAGCCTTTTGTATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCAAGGCTCCCAAGTATCTGGCAGATCTTCCCTTTTATCTCCGJAJTTTGTGTGTTGGC CAAATAATATCTCCCCAGGGACGTCCTCTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC AGTGCTATGGTTGAATGTGTCCTCCCAAGCACAATAGAAAACCTTA
WI-867	113	A G	---			AATCTTAACAGCCTTTTGTATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCAAGGCTCCCAAGTATCTGGCAGATCTTCCCTTTTATCTCCGJAJTTTGTGTGTTGGC CAAATAATATCTCCCCAGGGACGTCCTCTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC AGTGCTATGGTTGAATGTGTCCTCCCAAGCACAATAGAAAACCTTA
WI-867	119	G A	---			AATCTTAACAGCCTTTTGTATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCAAGGCTCCCAAGTATCTGGCAGATCTTCCCTTTTATCTCCGJAJTTTGTGTGTTGGC CAAATAATATCTCCCCAGGGACGTCCTCTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC AGTGCTATGGTTGAATGTGTCCTCCCAAGCACAATAGAAAACCTTA
WI-871b	123	C G	---			TCATCAGACCTGAGATTGAGATGAAATCTACCAAGGTACCACAAATGTAACTTGTCCAAACGA ATCTCAGTTTCTGCATATGTAAATGGGAATGATAAGAGCACCACCTACCTCATGIC/GJAACGTGT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGTATGCACTGTTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGCTGTTTGTACATAA
WI-871	123	C G	---			TCATCAGACCTGAGATTGAGATGAAATCTACCAAGGTACCACAAATGTAACTTGTCCAAACGA ATCTCAGTTTCTGCATATGTAAATGGGAATGATAAGAGCACCACCTACCTCATGIC/GJAACGTGT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGTATGCACTGTTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGCTGTTTGTACATAA

WI-884	198 TC ...	---	AGGTTCTGGACTGATGCTGGGAAACAATTGGGTCCTGGAGAAATTCCTATTTGAGTNTTTCACAGAT CAGTAGAGCCAAATGGGAAAGGTATCCTAGTCCATCCCTTTATTAGGAACCTTCTCCTGATCTATTGGGA ACTTCCTCTAATAGATCAGGAAATCCACCTCATTTAATCATGGACAACNNAAGGAATA[T/C]G ATCCCGCATGCAACATTATTTCAGTGAAACATGATGAAAATGAACATAAT
WI-921b	205 GA ...	---	CACCTCCCAAGGGCTCTGGGGANGAGCGGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGGACAGTTATCTGG CAGTGATGCTCTCAGCCCTGCCGCCCAAGAAAGTCTTNGCCAGGAAAGACGATCCATCTAC TCT[G/A]GGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATTTCTCCGAG
WI-921	205 GA ...	---	CACCTCCCAAGGGCTCTGGGGANGAGCGGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGGACAGTTATCTGG CAGTGATGCTCTCAGCCCTGCCGCCCAAGAAAGTCTTNGCCAGGAAAGACGATCCATCTAC TCT[G/A]GGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATTTCTCCGAG
WI-945c	90 GC ...	---	GGCTGGGATGAGAGGTCTACTTGTTGTTACTGGAGGTTTCACTGGCTTGCTAGAACTAGNAAAGNA GAAAGAGACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGCCCCAAGCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCATGACCAAAACAAGTTCAACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGATCTCTTAAAGGGAATCATGACAGATTTCTTGGCTTTA
WI-945b	90 GC ...	---	GGCTGGGATGAGAGGTCTACTTGTTGTTACTGGAGGTTTCACTGGCTTGCTAGAACTAGNAAAGNA GAAAGAGACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGCCCCAAGCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCATGACCAAAACAAGTTCAACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGATCTCTTAAAGGGAATCATGACAGATTTCTTGGCTTTA
WI-960b	167 CT ...	---	TTGCTTCAAAGAAAGTTCTTGCTCAGGAAGTTATTTCATTAGCAACCTAAAAATGTTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTCTTCTACC CTGAGGAATTTATCAAAGATGTTAAGTTATCT[C/T]CTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-960a	155 GA ...	---	TTGCTTCAAAGAAAGTTCTTGCTCAGGAAGTTATTTCATTAGCAACCTAAAAATGTTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTCTTCTACC CTGAGGAATTTATCAAAGAT[G/A]TTAAGTTATCTCCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-1121	181 TC ...	---	TCCCACTGAGTATGGCTTTTCAGTAGTTTTATTATGATGTCCTAGGTACATTTGTTTTATTGTTCTG CGAATTGTTGTTACTTTGGGAGAAATGCTCAACTATAAATATGCTTCTGACCCCTTTCTGTTCTG CTTCTTAAAGATACAAAATAAATGTAAACATTAGACCTCTCAGTAT[C/G]GCTGTTTTTACTCTCCTCTG ATTTTTTTTCCATTATTTTTATTGCTCTGGCTTCATTTTGTAATNTG

WI-1147b	204	G A	---		TTTGCCATTATTTGAAGATAACCCACACACCTTGGTGTCCAGGGTTTTCACAGGTATTAGTGGTCAGTCA CATAGGCATATAGTACCTGTATGACTTCTATTCAGCCACCGCAAACTTCTCCTCCCTGCTGGCTC CTGAGCCAAAACAGGCATTTACCATAAATCACCTTTGTAGGATGAACCTTATCTGGCCAAACTGATA C/GA/GCATGACCCACAGCCTCAGGTATATAAAACACCTCATCAGGCAGA
WI-1158b	147	C T	---		GCATTGAGGGTTCGTTTAAATGACATTCACCTGAGGCCCTGTCTATGTGAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAATACAATGATGGTCTCCTGAGTGTCTGAATG/C/GGCCAGGT TAAGTGTGGGG/C/TTCTGGGGTCAAGCTGGCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1158a	124	C G	---		GCATTGAGGGTTCGTTTAAATGACATTCACCTGAGGCCCTGTCTATGTGAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAATACAATGATGGTCTCCTGAGTGTCTGAATG/C/GGCCAGGT GGCTAAGTGTGGGGTCTGGGGTCAAGCTGGCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1304	124	T C	---		AAGTTACAGAAAAAATACAGAAAAAGTGACTTCAAGANTCAGCTGAGATAGAAACATATGCCCA TCATCTTCAANGTCCACAGACACTTATCCCTAGACAGCCATTTCTTTTGAATGNT/C/GGNCANT AAAAATGATTTGAAATGGGAATAAGCCCTCCCTCTAATGATTTGACAGTGTAGACCTTGCCTAG GGC
WI-1305d	202	C T	---		TTCTCAATCCAACTGCTGTGTACTTTTATTTCTTTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTNCAGAAAGATAAGGTTTCCCTCACA TCCACTGCTTTCANTAAATNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATA /TAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305c	46	C T	---		TTCTCAATCCAACTGCTGTGTACTTTTATTTCTTTTCCATTCTATGTTGGTAAATATAAAGATG ATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTNCAGAAAGATAAGGTTTCCCTC ACATCCACTGCTTTCANTAAATNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305b	153	T C	---		TTCTCAATCCAACTGCTGTGTACTTTTATTTCTTTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTNCAGAAAGATAAGGTTTCCCTCACA TCCACTGCTTTCANTAAATNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305	202	C T	---		TTCTCAATCCAACTGCTGTGTACTTTTATTTCTTTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTNCAGAAAGATAAGGTTTCCCTCACA TCCACTGCTTTCANTAAATNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATA /TAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA

WI-1306b	248 A G	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNNGCAATAATAAATGGACAATCTTTGTNGNNNNNG GGCTGGGTGACTGTGCCTGGGTCAATTTAGAAGCCATAGAGATGAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAAATCTGAAGCTGTGACCTAAGGNGAGAAGTGCCCTNNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTTCCTA/GJGC
WI-1306	240 A G	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNNGCAATAATAAATGGACAATCTTTGTNGNNNNNG GGCTGGGTGACTGTGCCTGGGTCAATTTAGAAGCCATAGAGATGAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAAATCTGAAGCTGTGACCTAAGGNGAGAAGTGCCCTNNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTA/GJCTTCCTAGC
WI-1307b	118 T C	GACAAGGCTGGTACTAGTTTCCAAATTCCAAATCTATGTACACTTTCCTCTCACTTCTCAAGTGGACA GATTTCTGCATTACTGCTTGGGTTGGGGAGCAGTGGTGTAGGCAAT/CJGTGAGATTGCTTT CCTACCTCTTAATGTATCTTNCATAATATNATGCTAAACCGGTACTGTGATCTATCACTGGTT TCTTTTGGGTGTTGTTGCTGCTGTTGTTTCTCCTGTAAAGNTGTTT
WI-1307	118 T C	GACAAGGCTGGTACTAGTTTCCAAATTCCAAATCTATGTACACTTTCCTCTCACTTCTCAAGTGGACA GATTTCTGCATTACTGCTTGGGTTGGGGAGCAGTGGTGTAGGCAAT/CJGTGAGATTGCTTT CCTACCTCTTAATGTATCTTNCATAATATNATGCTAAACCGGTACTGTGATCTATCACTGGTT TCTTTTGGGTGTTGTTGCTGCTGTTGTTTCTCCTGTAAAGNTGTTT
WI-1325b	169 T C	GAGAGATGGCCAAAGACAAAGCAGAGGGAGAGAGAGCAACCNCTCTGTGGTTTATCGCAGCAAGCN ATGTCGTCTCCATACCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTGCCCTTGTCTCCTT/CJACCCCTCAGAACTTCTTGAGGGGCAGGC ATTATGATCCCACTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1325	165 C T	GAGAGATGGCCAAAGACAAAGCAGAGGGAGAGAGAGCAACCNCTCTGTGGTTTATCGCAGCAAGCN ATGTCGTCTCCATACCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTGCCCTTGTCTCCTT/CJTTACCCCTCAGAACTTCTTGAGGGGCAGGC ATTATGATCCCACTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1327b	162 T C	CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAAGCTGTGTAGTGAAGAAGTCTGTTATTTGTAAA ACACCAAGTGGGTTTAAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTG/CJGAAGTTGGGTAGCTACCGGCCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCCTTACTGAAGAGGCAATGGTTCCATCTCTAAG
WI-1327	175 C G	CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAAGCTGTGTAGTGAAGAAGTCTGTTATTTGTAAA ACACCAAGTGGGTTTAAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGGAAGTTGGGTAG/CJGTACCGGCCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCCTTACTGAAGAGGCAATGGTTCCATCTCTAAG

WI-1341b	136 GA ---	---	TATCAGCATGATTGGCTGTGGACACAAAGTCAATTTGTACTTTTGTGNNNTCCTTTCTNNTT ACCTGATCCACTATCTCTCAAGATCANGTTCAAAATTTGGCTTNCCTTTGTTNAAATATACCCCAAGC [GA]GGATTGTGATGGATCTGTTATTTCTCTGTCTTGGAAACAGCAGAGTCGTCTCTGNGAGTNG GTTTCAGGATTGTCTCTGTTTCCAGCCACCTTGACCTTAGCAAGTGT
WI-1349e	192 GC ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGTGAATTTCCATCTCTGA[G/C]JTTCAA ATAATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAAAATA
WI-1349d	264 CA ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGTGAATTTCCATCTCTGAGTTTCAAATA ATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAAAATATGAT
WI-1349c	192 GC ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGTGAATTTCCATCTCTGA[G/C]JTTCAA ATAATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAAAATA
WI-1349b	264 CA ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGTGAATTTCCATCTCTGAGTTTCAAATA ATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAAAATATGAT
WI-1349	264 CA ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGTGAATTTCCATCTCTGAGTTTCAAATA ATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAAAATATGAT
WI-1403b	57 CT ---	---	TGGTATTTGGAATGGGTTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTG[C/J]TCCGAAT GCCACTTTATAAGTTAGAGGTATTACCTTGGAGGGGGACGTAGAGTAAGCCATAAAATATACGT AAAGTTTACATCAACATAATCTTGGCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCCTCA TAATCCCCAAAGTGCCAAAAGGGTTGTATCTGATTGT
WI-1403	58 T C ---	---	TGGTATTTGGAATGGGTTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTG[C/J]TCCGAA TGCCACTTTATAAGTTAGAGGTATTACCTTGGAGGGGGACGTAGAGTAAGCCATAAAATATACG TAAAGTTTACATCAACATAATCTTGGCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCCTC ATAATCCCCAAAGTGCCAAAAGGGTTGTATCTGATTGT

WI-1417c	31	C T	---			CAGCCGGAAGAGATTACGTGGAGAGATGTC/JTTGGCCAGGGCGGCGAGATGTAGCCACCGG GGTGACAGCATGCTGCTGGCAATTTGGAGGGCCCCAGGAATCCAGTGGCCCTCTCAATGACTTG GGGTCTCGACTCGGAAGTTTAAGGGCTCGCTTCAAAAGCTGGTCCGTTTGAGGCGGTTGC AGCGAGGCCCTTAGTCCGTATTTAATGTTTGTCTTTAGAAAAAGTCGC
WI-1417b	31	C T	---			CAGCCGGAAGAGATTACGTGGAGAGATGTC/JTTGGCCAGGGCGGCGAGATGTAGCCACCGG GGTGACAGCATGCTGCTGGCAATTTGGAGGGCCCCAGGAATCCAGTGGCCCTCTCAATGACTTG GGTCTCGACTCGGAAGTTTAAGGGCTCGCTTCAAAAGCTGGTCCGTTTGAGGCGGTTGC AGCGAGGCCCTTAGTCCGTATTTAATGTTTGTCTTTAGAAAAAGTCGC
						CCATGAGCAACAGCATGTTTCTACTCTGTGATGTGTATGTTAGGGGCGATGTATCTGTATTTCTT TTTTATTCTCTCCAAAAGAAATTTCAATTATGCAAAACATTATCAGGCAATGCAGCTCGTAATAAGA TGTGGAGAACTGAAAAAGAGAGCTTACATGACCCCAATAGCAAACTCTCCACACATTTCCAGCA GATGATGTCTCTCCGTGGTNACTTCTCTCCACCACATCACCTGTGTTTT
WI-1729	172	A	---			TGCCCTACTTCTTTGTTTCAATCCACCATTACATTTTGTAAATTTGAACTTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAGGAGTNTCCCTGGGTCAACCTTTT/JATTCACTCT CTGCCACATGCTAGTAAGTGTGAGTGATGGTGCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTCACTACTATTCATCATATTGGCTAAGGTATTCATCATATTGGCTAAG
WI-1732b	122	T C	---			TGCCCTACTTCTTTGTTTCAATCCACCATTACATTTTGTAAATTTGAACTTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAGGAGTNTCCCTGGGTCAACCTTTT/JATTCACTCT CTGCCACATGCTAGTAAGTGTGAGTGATGGTGCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTCACTACTATTCATCATATTGGCTAAGGTATTCATCATATTGGCTAAG
WI-1732	114	C T	---			GCGAATTTAATGACTCCAAAGGTAGTAATTCCTTCCCCCAAAAGGTTTAAATCTGTGTGGA CATAATGTTTGAATTTGCAGTTCACCTTGG/JGTTTAAAGTGTGCTGTTTTCTGGCAAGAGTCAG TGGAGTGTCCGGGAAAGGGCTAAAGTCTTTGTAGTCAGACAAACCGGCTTGCACTCCTGACTGAG CTACATTCACTTTATGATCTCCAGCAGGTTCTTCCA
WI-1750	97	A G	---			GGTACACAAAGAAATGCTTCTGGAAATCTAC/JGTAGGCCCTTAACATTTTGGCTGAGTATTAATC TGTACATGTGTAATGTGAACCAACCATGAAGCTGGGCAAAAGAACAAATTCCTAGGAAAGTACAATTAC TGGGAACTGTAGAACAATAATTCATAGTTTACACATAGCTGGGAATCACTCATGTTTCCCATCA ACTGGAGAGACCTTGTGAGTACAGAGGACATTCAGAATAATCATAAAAAT
WI-1780	31	A G	---			CCACTCAGTAATAATAGTGTGGAGATAAGTATATGGTAGGCACATAATAATTATTTTCAGGCAGAA CCATTATGAT/JAGTAGGGTAGAGCATCACACTTGGGAGGACATAATTCTGGAGTNAGATATCCTG GGTGCTAATTTCAAATATATCTACTAAAGCATGACTTCTAGAAAAATTAATTACTCTTGTCTCAA GGAAATGGGAATACCTATAATACAGTCTTATTGAGGAAAAATAACTGGAATCA
WI-1803c	77	A G	---			

WI-1803b	77 A G	---	---	CCACTCAGTAATAAGTGTGGAGATAAGTATATGGTAGGCACATAATAATTTTCAGGCAGAA CCATTATGATGAGTAGGTAGAGCATCACACTGGGAGGACATATCTGGAGTNAGATATCCTG GGTGCTAATTTCAATATATCTACTAAGCATGACTTCTAGAAAATTACTTATTACTCTTGCTCCTCAA GGAATGGGAATACCTATAATACAGTCTTATTGAGGAAAATACTGGAATCA
WI-1837b	112 C T	---	---	TTTACTTGGGATTTTCATAGCTGATCATAATTTACCAATTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAAATAGACCCGTTTATAC/C/TCTGTCCCCAGTTTATTTTT AAGGTTTTTTTCATTGCACCTGATGCCAAAACAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACTGGGAAGTCTGGGAACGTTTAGCTTTCTGCTGTGGCT
WI-1837	112 C T	---	---	TTTACTTGGGATTTTCATAGCTGATCATAATTTACCAATTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAAATAGACCCGTTTATAC/C/TCTGTCCCCAGTTTATTTTT AAGGTTTTTTTCATTGCACCTGATGCCAAAACAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACTGGGAAGTCTGGGAACGTTTAGCTTTCTGCTGTGGCT
WI-1840b	79 G T	---	---	TCACCTAGGGAGGTCGCTAAAAATGTAGCTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACCT[G/T]GAGAACTCTGAATATTCAGCACATACAAAGTGTGACAAACCACTTGTTTAGTAT ATTTTATCTCCAGAGTGTTTGAATTTACTAAAAAGTTCCTAAAGAGCCATGAAGAATTATAAGACT ATCGCA
WI-1840	79 G T	---	---	TCACCTAGGGAGGTCGCTAAAAATGTAGCTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACCT[G/T]GAGAACTCTGAATATTCAGCACATACAAAGTGTGACAAACCACTTGTTTAGTAT ATTTTATCTCCAGAGTGTTTGAATTTACTAAAAAGTTCCTAAAGAGCCATGAAGAATTATAAGACT ATCGCA
WI-1879b	110 C T	---	---	GGGCTCACTTTTCATCAGAGCACATATCAGGTGATAGTCTGTTTCTCTTTTCATAACTTACTCCCCCG CACTGTAGGNTTTCTTTTGAGGTNAAGGACCTGCCNTTTTAC/C/TGTCTGCNAAATAAACTCCCAAAA AAGTGTTTAGTCCACAGGGTTTAAATAGTCTTGTGTAATGAATTTCTGTGCGACCCCTGTGCCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1879	110 C T	---	---	GGGCTCACTTTTCATCAGAGCACATATCAGGTGATAGTCTGTTTCTCTTTTCATAACTTACTCCCCCG CACTGTAGGNTTTCTTTTGAGGTNAAGGACCTGCCNTTTTAC/C/TGTCTGCNAAATAAACTCCCAAAA AAGTGTTTAGTCCACAGGGTTTAAATAGTCTTGTGTAATGAATTTCTGTGCGACCCCTGTGCCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1900b	119 C T	---	---	TGTTCTCTGGTCCAGGCACCGGGCTAAGTCTTGTCTGCATAATGGAATAATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGG[C/T]GCTCTGAGAGGT AAAGTGCCTGCCCCAACCGCACAACTAGAGAGAGCAACAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTGCTTAAGTGCATGAGAAACCACTTTCTTTGCTOC

WI-1900	119	C T ---			TGTTCTGGTCCAGGCACCGGGCTAAGTCTTGCTGCATATGAATAATCAACTGGACAAACCCOING CTNAGGTAGGNTACCTNGGCAATTAGCCCATTTACAGCTGCAAGAGGG[C/T]GGCTCTGAGAGGT AAAGTGCCCTGCCCAACCGGCACAACTAGAGAGCAGCCAAACAGGTGTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGCTTAACGCCATGAGAAACCACTTTCTTTGCTCC
WI-1943c	165	C T ---			ATTCAGTTTACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAAATGGTAGGAAAGACCAGCC[C/T]CTCTGAANCTGGTCCACGCTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943b	165	C T ---			ATTCAGTTTACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAAATGGTAGGAAAGACCAGCC[C/T]CTCTGAANCTGGTCCACGCTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943	164	C T ---			ATTCAGTTTACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAAATGGTAGGAAAGACCAGCC[C/T]CTCTGAANCTGGTCCACGCTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1960c	270	A T ---			CCAGGTGAGGCTGAAAGAGGAGGAGGCAATTGCTGTTGGAGTGAGGGATTCTGGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAGGTGCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAAACTTAAAAATGCACCTCCCAACTTT
WI-1960b	270	A T ---			CCAGGTGAGGCTGAAAGAGGAGGAGGCAATTGCTGTTGGAGTGAGGGATTCTGGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAGGTGCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAAACTTAAAAATGCACCTCCCAACTTT
WI-1977	203	T C ---			CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTTGGATCTGGTAAGTAGGAGTCA TTCTGGGCATTTCTCATAGAGTNTGTTTTAGTCTCGTAATAATACTGTTGCCCTAGGAAGGTTGTT TTTCTACTGCGTCTGTGAAAGCCCTTCCCCATCGAGTGATACAGTACTTTCCAGTTATGGAGATTTT /C/TAAACAATCAACACTGGCTGAGGCTGTTGG
WI-2012	102	T C ---			AAATCTAGAAGCCAGAGTCAGCTCAGCTACGATTATAAAGTTGAAGTAAATGCATTGTAGTTTCATGT TTTCTCTTAATTCTGCACAAAACCTAGCTAAAAATC/TCTTTAAATCAGTTACCAGAGGCAATACCT GGGTTAATGTAGCACTCAAAAGTTATGTAGAGTAGCTGTCTCTGAGTCACTTTTCTTCTACTCTCATT GGCTTACCAATGCTTCCACTGGATC

WI-2013	127 C T	---	---	---	CTTTAGAGTGGTCAATTCGGTCCCTTCTGGAAAGTGATTCGTGTTAAGAAAAATAGATGCAACG TTGCTAAGTACACCTAACATTTAAACAGTCTCCAGCAGATAAATGCTGATCTGACACTC/TCTCA CCAGAAAAAGAGAAATACCCATCATGAGGAAGAGAAATGACTTTTGTTCAGTTATGCTCCCGGGTCC CCTTCACTGGAGGGATATCTCAGCTTCTGAGCCCTGGTACTGCAATCC
WI-2032c	166 G A	---	---	---	ACCAGACATCCCATCAGGAGTATGCTCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAACC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAAACC ACATCACCCAACTGGTTTCTAGATGTACAC[G/A/TGTGGACCTCTGTCTCAACCTCCGACTTTCAC AGATCATTTGGTGGCTCACCTTCTGTAAATGCTTCTGTTTTTCAAAGGG
WI-2032b	219 C G	---	---	---	ACCAGACATCCCATCAGGAGTATGCTCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAACC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAAACC ACATCACCCAACTGGTTTCTAGATGTACACGTGTGGACCTCTGTCTCAACCTCCGACTTTCACAGA TCATTGGTTAGGCTCA/C/G/CTTCTGTAAATGCTTCTGTTTTTCAAAGGG
WI-2032	219 C G	---	---	---	ACCAGACATCCCATCAGGAGTATGCTCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAACC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAAACC ACATCACCCAACTGGTTTCTAGATGTACACGTGTGGACCTCTGTCTCAACCTCCGACTTTCACAGA TCATTGGTTAGGCTCA/C/G/CTTCTGTAAATGCTTCTGTTTTTCAAAGGG
WI-2054b	188 C T	---	---	---	CGTTTTCTTCTACATCTTGGGNACATAAAGANGAAAGNAGCTGTCTTTTGTGGTAGTTTGCT CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAATACCTTACAGACTTAGGATTTGGA TTTTCATGGTGGTGGCACAGCCAGGCTCAACAGAACTAATACCTGCT/C/G/TTCTCTGCCTCCAC CAGCCCTATCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGTCTTT
WI-2054	183 T C	---	---	---	CGTTTTCTTCTACATCTTGGGNACATAAAGANGAAAGNAGCTGTCTTTTGTGGTAGTTTGCT CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAATACCTTACAGACTTAGGATTTGGA TTTTCATGGTGGTGGCACAGCCAGGCTCAACAGAACTAATACCTGCT/C/G/TTCTCTGCCTCCAC CAGCCCTATCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGTCTTT
WI-2573d	129 T C	---	---	---	TGGGATTAACCCCTGTTTTCTTCTCCAGTTCAGTGGCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTGCCGTTACAAAGGTGTTTCCGTCTT/C/T/GA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCCTAGGTAAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTTGCTTGCACAAGGTATATGGCTGGGCTTGGACGAG
WI-2573c	165 A/C	---	---	---	TGGGATTAACCCCTGTTTTCTTCTCCAGTTCAGTGGCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTGCCGTTACAAAGGTGTTTCCGTCTTGTATAT CATCTGATCTTCCCAACAGGGCTTATTTA/C/T/GCCTAGGTAAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTTGCTTGCACAAGGTATATGGCTGGGCTTGGACGAG

WI-2573d	129	T C	---	---	TGGGATTAAACCCCTGTTTCTCCCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTTGCCGTTCAAGGTGTTCCGTGCTTT/CJGA TATCATCTGATCTCCCAACCAGGGCTTATTTATGCCTAGGTAAAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAAGGTATATGGCTGGGCTTGGACGAG
WI-2573c	165	A C	---	---	TGGGATTAAACCCCTGTTTCTCCCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTTGCCGTTCAAGGTGTTCCGTGCTTT/CJGA CATCTGATCTCCCAACCAGGGCTTATTT/CJTGCTAGGTAAAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGACAAAGGTATATGGCTGGGCTTGGACGAG
WI-2573b	165	A C	---	---	TGGGATTAAACCCCTGTTTCTCCCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTTGCCGTTCAAGGTGTTCCGTGCTTT/CJGA CATCTGATCTCCCAACCAGGGCTTATTT/CJTGCTAGGTAAAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGACAAAGGTATATGGCTGGGCTTGGACGAG
WI-2573a	129	T C	---	---	TGGGATTAAACCCCTGTTTCTCCCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTTGCCGTTCAAGGTGTTCCGTGCTTT/CJGA TATCATCTGATCTCCCAACCAGGGCTTATTTATGCCTAGGTAAAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAAGGTATATGGCTGGGCTTGGACGAG
WI-2868b	60	A G	---	---	GACTTCATGCTCATGAACAAGCATTTGCTTAATTTACAGACATTAAAGCAAGCTTTCCJAGJCTC CCACTTCCCTCCCACTATCACCTCAACCTCTTCCATCCACTTTAAAGAGGTTCTTTAGGTCCTCTGCAT ATCATGGAAGCCCACTACTCTATTAAACGCTTTCCCAATGATGCAGCCCAAGTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAACACAGCTGAAAAATGAAATATCGATATAC
WI-2868	60	A G	---	---	GACTTCATGCTCATGAACAAGCATTTGCTTAATTTACAGACATTAAAGCAAGCTTTCCJAGJCTC CCACTTCCCTCCCACTATCACCTCAACCTCTTCCATCCACTTTAAAGAGGTTCTTTAGGTCCTCTGCAT ATCATGGAAGCCCACTACTCTATTAAACGCTTTCCCAATGATGCAGCCCAAGTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAACACAGCTGAAAAATGAAATATCGATATAC
WI-2870b	131	T C	---	---	CATGCTGTGTAAACCTCTGTGCTGCTGCTGCGGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGAT/CJ AGAAATGAATAGAGCCCCATTTAAATTATATCACAGCTTTATGTCCACTTCTGTTCCCTGCCATCAC TGGGCTTTTACAAAGGAGGGCTTT
WI-2870	131	T C	---	---	CATGCTGTGTAAACCTCTGTGCTGCTGCTGCGGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGAT/CJ AGAAATGAATAGAGCCCCATTTAAATTATATCACAGCTTTATGTCCACTTCTGTTCCCTGCCATCAC TGGGCTTTTACAAAGGAGGGCTTT

WI-2954c	49 T A ---	---	TTAGCACACATATCTGTTGGGACTTAAGTGAGACAAGGCATAAAAAAT/A/CAGCACCTGGGGCA CAGAGGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2954b	41 A G ---	---	TTAGCACACATATCTGTTGGGACTTAAGTGAGACAAGGC/A/GTAAAAATCAGCACCTGGGGCA CAGAGGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2954a	38 G T ---	---	TTAGCACACATATCTGTTGGGACTTAAGTGAGACAAGGCATAAAAAATCAGCACCTGGGGCA CAGAGGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2971b	62 T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGA/T/C/G CTGCCAGCACCAATAAGCTTTCTTCAAACAATTGTGAACCTCCTCTCCTTAATAAACCTAAC ATTTCCCTTTGTTCCCTGACATCTGAAGGCCACGCTGTAGATGTATGTCAGATTGCAATCCT AGTCTTTAATGTTATCTGAAAGAAAACCTTTTACTTAGGGATTGTCT
WI-2971	62 T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGA/T/C/G CTGCCAGCACCAATAAGCTTTCTTCAAACAATTGTGAACCTCCTCTCCTTAATAAACCTAAC ATTTCCCTTTGTTCCCTGACATCTGAAGGCCACGCTGTAGATGTATGTCAGATTGCAATCCT AGTCTTTAATGTTATCTGAAAGAAAACCTTTTACTTAGGGATTGTCT
WI-2995d	133 A T ---	---	TTCTGGGAAAGAAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTTA /AAATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT
WI-2995c	151 G C ---	---	TTCTGGGAAAGAAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTTA AATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
WI-2995d	133 A T ---	---	TTCTGGGAAAGAAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTTA /AAATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT

WI-2995c	151	G C ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTNNATCAAGATAAGACCTGGAAGACCCGAGCCAAAGGAAGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAAATGGGTAAAG AATGAGACAGAACTAGCAGAAAAGTGTT
WI-2995d	133	A T ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTNNATCAAGATAAGACCTGGAAGACCCGAGCCAAAGGAAGAGCTGGANTTTTTTNA /TAAATCTTTCTTTCTGGT[G/C]TTTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAAATGGGTAAA GAATGAGACAGAACTAGCAGAAAAGTGTT
WI-2995e	151	G C ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTNNATCAAGATAAGACCTGGAAGACCCGAGCCAAAGGAAGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAAATGGGTAAAG AATGAGACAGAACTAGCAGAAAAGTGTT
WI-2995b	151	G C ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTNNATCAAGATAAGACCTGGAAGACCCGAGCCAAAGGAAGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAAATGGGTAAAG AATGAGACAGAACTAGCAGAAAAGTGTT
WI-2995a	133	A T ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTNNATCAAGATAAGACCTGGAAGACCCGAGCCAAAGGAAGAGCTGGANTTTTTTNA /TAAATCTTTCTTTCTGGT[G/C]TTTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAAATGGGTAAA GAATGAGACAGAACTAGCAGAAAAGTGTT
WI-3147	85	C T ---	---	GTGGTGCAGTTTCATCCTCTGGAGCTCCCTGTGAGATCAGACTGGAGCCAGTCTCCAGCTTGAGACCAC ATCTCAGTTAGTCTCCTT[C/T]CCTGCCATATCCTGTTTTCCTTACTCCTATCTCCTGAGACTTCTCCT GAATGAATTACATGCACCTCAATCCCTGCCTCAGTCTCTGCTTTNAGGGAACCTTGACCTAAGACAGAA ATCTTAGTACCAATACTTTGCAAGG
WI-3234b	68	T C ---	---	ATTCTGTAATGTTTTCACTGCTTCCAGTAAATCTTTATTGAGGTCCATGTCCATTACCTCTACTTA[T/C]GACAAGCAAGAACACACAGAAAAGCCTCTGTTTGCAATCTGGCCTCTTATAAATACCTTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATTCATCCTTAAATAGCATATCAAAAATTTTAC TCAGTAATTCAGAAAGAAAGGACAATGGAATGTACTTATTTTATATCTTAT
WI-3234	68	T C ---	---	ATTCTGTAATGTTTTCACTGCTTCCAGTAAATCTTTATTGAGGTCCATGTCCATTACCTCTACTTA[T/C]GACAAGCAAGAACACACAGAAAAGCCTCTGTTTGCAATCTGGCCTCTTATAAATACCTTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATTCATCCTTAAATAGCATATCAAAAATTTTAC TCAGTAATTCAGAAAGAAAGGACAATGGAATGTACTTATTTTATATCTTAT

WI-3292b	106	G A	---			GTTTGCTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACATCC TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCT[GA]TGGTATTGGATTGGGATGGATTACTT GCCATGAATATTTCCATTGTTCTCATTAATGATTAATAATTAAGTAAAAATATTATTTNCCATGA GACAAATGGAAAAATGGAAACATTTCATGGAAAAAACCCATTTCATC
WI-3292	106	G A	---			GTTTGCTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACATCC TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCT[GA]TGGTATTGGATTGGGATGGATTACTT GCCATGAATATTTCCATTGTTCTCATTAATGATTAATAATTAAGTAAAAATATTATTTNCCATGA GACAAATGGAAAAATGGAAACATTTCATGGAAAAAACCCATTTCATC
WI-3355	19	G C	---			CCATGAACCATGGGCTACA[G/C]ATATTCTTAACTTCAGAGTCCCTCTACTGGAGAGGGATCCA CTTTTAAATATGATTTCTTGAAGTGGCTGCATACCTTCCCAAGCACCTTAAACTCATCAGAA AAAAATCATCAAAAGTGAAGTGAAGTTAGTTTNAATACCTTCACCTTTTCAATGGAAAACTTTATAA ACTGTGGATCAATTTATATTACTTTTGGATCAGTTTAGATGACTTTNAGTTG
WI-3408	194	G A	---			CCATGAAGAATGAGTTCCCTCCCTCCCTGGTCAAGTCTAAGAAATAGCACACCTTGAGAAATTTNACT TAGCACGTGGCATTTGTAATGGCTGGATTTCTCCGCTCTAAGACACACCTTTATGCTTTNAGCTTT CTGGAATTGGGATGAATCTNACATTCATGTGACCCCTCGTGTGGGATCACTTCTCC[GA]TGGCCC ATCTCGNAGAACCACTGGGAAGTCGAAGGAGTGACTTCAATCAGG
WI-3505b	131	G A	---			TAACTTATGCTCATCTGGCTTACTGCTTAGTCCCATTTTGTCACTAGTGCACCTTAAAAAATATTTT GAAAAATTGCCATTTTAAATATCTTTGGAACTTCTTAACACATTACCTATTTTNAACCAAC[GA] AGGTATTCCTTATGGGAAAAATATATACAGCAAGAAAAAANANNGAAAAAATGTTGATGATACCT GTTTAAATTGGGAAATATGTTGCATAT
WI-3505	131	G A	---			TAACTTATGCTCATCTGGCTTACTGCTTAGTCCCATTTTGTCACTAGTGCACCTTAAAAAATATTTT GAAAAATTGCCATTTTAAATATCTTTGGAACTTCTTAACACATTACCTATTTTNAACCAAC[GA] AGGTATTCCTTATGGGAAAAATATATACAGCAAGAAAAAANANNGAAAAAATGTTGATGATACCT GTTTAAATTGGGAAATATGTTGCATAT
WI-3564b	177	C T	---			GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGAGTCACTAAATGTTTGGAGAAATAAAGT GAAATCAATGTGCTTCCAGTGTATTCACATGGCACAGTGCACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGGTTGACTAACGTTAACATGCATGCTGTT[CT]AACAAAGTGTGTTGTGGTGTCTC AGTGTCACACATGCTACCTTCCCTTCACAAAAA
WI-3564	177	C T	---			GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGAGTCACTAAATGTTTGGAGAAATAAAGT GAAATCAATGTGCTTCCAGTGTATTCACATGGCACAGTGCACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGGTTGACTAACGTTAACATGCATGCTGTT[CT]AACAAAGTGTGTTGTGGTGTCTC AGTGTCACACATGCTACCTTCCCTTCACAAAAA

[illegible]

WI-4110	130 TC	---			GAAAAATGATGTTTTGATTCCCTCCTATCTCAGATTATTGGAGTGTCAATTAGAAAACTGATAGT AACCTTTTATTGATGAAACTCTGTCTATAATTAAACCTTCTCTCCTGCTTTATTTTGCCCT/CJACA GTTAGGTAATAAAGATGCCAAGAAATTCAGTATTCAGGTACAGTAAAAAGTAGCAACCATGGG GTAGGGACAAGTNCAGAAAAAGGAGGAGGTNGGGGTTTTCTGGGAAGA
WI-4119b	168 GA	---			ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGTGGGAAAAAGTAATAAATAG AATGGAAGGATAAATAAGGTAACTACGGGGGAAGAACAGGACAGAACAGACAGAAAGGGGT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTTCTTTCA TGAGACCGTCTGCATCTTTGTTTTTAAAGGGCTCTGTTGATCATCATCTTCA
WI-4119	168 GA	---			ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGTGGGAAAAAGTAATAAATAG AATGGAAGGATAAATAAGGTAACTACGGGGGAAGAACAGGACAGAACAGACAGAAAGGGGT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTTCTTTCA TGAGACCGTCTGCATCTTTGTTTTTAAAGGGCTCTGTTGATCATCATCTTCA
WI-4123b	51 TG	---			CAAAGTCAGATTTTGATTATTCAGGATAACAATTTTGAATAAGAAAGTG[T/G]TTTAAACTATTT CAAATAACAATAAAGAAACATGATGAAATTTCTCGTTACATAATTGTATAGAAATTTAGTGGG TTCTCCATGACATTGGCTTGTCTTCTCAACAGTGGGTGGTGGATGTTTCTATGCTTTCTC AGGCACAAACAACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4123	51 TG	---			CAAAGTCAGATTTTGATTATTCAGGATAACAATTTTGAATAAGAAAGTG[T/G]TTTAAACTATTT CAAATAACAATAAAGAAACATGATGAAATTTCTCGTTACATAATTGTATAGAAATTTAGTGGG TTCTCCATGACATTGGCTTGTCTTCTCAACAGTGGGTGGTGGATGTTTCTATGCTTTCTC AGGCACAAACAACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4149b	145 GC	---			TTGTACATGTTCAATTCATCCCTCCCAATCTTTCTGTCTTATAAGAACCTCGCTTCTTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTTTATTTCCATCAAAGCTTCTCAGCATCTTCTATATACT GTGCTG[T/G]CCTTGTGAAGAACCCAGAGCCGAGCATACCAACATGATCTTTTGTGAACTGTAGT AGGAGAGACAAGACAGATGTGCGGGTCCCAATGATATAAGGTAATTG
WI-4149a	137 TC	---			TTGTACATGTTCAATTCATCCCTCCCAATCTTTCTGTCTTATAAGAACCTCGCTTCTTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTTTATTTCCATCAAAGCTTCTCAGCATCTTCTATATACT T/C]GTGCTGTGCCCTGTGAAGAACCCAGAGCCGAGCATACCAACATGATCTTTTGTGAACTGTAG TAGGAGAGACAAGACAGATGTGCGGGTCCCAATGATATAAGGTAATTG
WI-4182	188 GA	---			TAACACACTTTTCAATTTGGTTTCTTACTGAGTTAAAGGACCATCCATTATATACAATTCCTC AGTTCTATGCTTTAGAGTNCATATAGGACTACTGTAAATTTTCAAGGGAAATTAATCTCTGGAGTA GGGGAATGAGTTAAATAATCTACCACATGCCAATTCAGGGACTGTGGTTAA[G/A]ATGTCCTCTCT TGCCCCCTTCCCAAGTTCTTAAATTCCTAG

WI-4230	93 T ---	---	AGAGACGTTGAATGGGACATCTTTCTATTTTCGATTTTAGTTTAAACATTTGATAAGAATTGATGAAA GTTTGTACATTCCAGATTTATCTTTATAGCAGCAGAGTGGCAATAATAACAGCACACTGACT TTCCATGGTAAAAAGAGTTAGAGAAAAACAGCCTATTTTCTTAATGTTAAATGTAATCTGAAT ACATTTAAATGGAGAGATAGTGACCTTTGAAATTTGAATTTATGG
WI-4241	118 C T ---	---	GAAATCCATTGAAGTTTGAACCTTGAACCTGATCTCATTAACTATTTNCTTGTAGTGGTTGATTT CATTTTGAACAAGAACAGACGAAATTTCCACTTAAATTTAAATCTC/TCTAGTATCTATGAT TTAGCACTGTTAGCACCAAGAACTGTGAAATTTATCTCTAGATATCTTCAGAACTAGGATGGAAG AA
WI-4271b	151 A ---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGGAGCCCCCAACCCCTCCCTTTGTCTCAGG CTCTAGAAGGTCCAGTCAGGGGC
WI-4271	151 A ---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGGAGCCCCCAACCCCTCCCTTTGTCTCAGG CTCTAGAAGGTCCAGTCAGGGGC
WI-4389b	156 G A ---	---	AATCGAAACATTGATTTTGTAAAGGAACCCACATTTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGAAATAGAAAGGATATTATGCTAACCTTTGGA AGGTAAGATGTGAACCTATACA[G/AT]NGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
WI-4389	156 G A ---	---	AATCGAAACATTGATTTTGTAAAGGAACCCACATTTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGAAATAGAAAGGATATTATGCTAACCTTTGGA AGGTAAGATGTGAACCTATACA[G/AT]NGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
WI-4488	31 A G ---	---	GATGACAATTATTGTGATTGGCATTTTAA[A/G]GTACCATTCATTTCTTCTGGCTTCGTGTGTT TGTTGTTGAGAAGTCAGGGGTTAGTCGTATTGCTCTCTTTCTAGTTCTCTCAGTAGGAAGACTGATC CTAAACAACCTAATTACCCATGCCAAAGTACGTCCAAACTGATCTTTAAAGAACATAAATCAAATTG TATTATCCTATGCTTAAATGCTCAG
WI-4491	145 G C ---	---	ACCATCAATGTATCACCTCTAAATTTATTAGATGATTAACTGGCTCTGTTAAAAAATAAAAAACCT GTCTTGGACATTGAAATAAAACATTACTATTGGTCACTTTCTGCTACTTACAAAGGTACTGCACATA AACAAAGTTAAG[G/C]GTTTTTGGAGGGGAAAAATCATAAAAATGCATAAAATTTCTACCACTGTCA TTTCTGTGCCATAAATAAATTTTACATGCCT

WI-4584	144 A G ---	---	---	TTGGTTGGCATTAGCCTCATAACAACATATTACAATCATAATTGTTACTCTTATTTACAAACAAG AAAAATGAGGCTTAACATCACACTCTGCTTAGTCGCAGAGCCAGGATTTGAACCCAGGAATCCATT CACCGGTAC(A/G)TGCTACCTGGGTAATAATGTTTAAATTAATCTATGGCATTAGATTTCAAAGA GTCCTAATGTGGTTTGAATAAGGTGCTTTAATTTGTTTATCAGTATGC
WI-4639	185 C T ---	---	---	TTTCTGCATTTGAATGTGTATGGTCAGACTTCAGAGGAACCCAGGAATCTCAATTTATCAGTACAATA TGGTGGCCAGGTGCTCAGGCCCTATTATCAGAGAGATCTCAGTTTAACTTTCCAAATCCACCAATTTAG TGACCATATGACTTGGGGAACATTATCTCACTATCTGAGTCTGTATCC(C/T)CATCTTTAAATTTGTA AATTTAAGGACACCTATCATAGTAATATTGTGAGGATAAAATGAAATAA
WI-5327	63 A ---	---	---	AAATGAATCCGCTTTAGAGCAATACCAGTAAGGGCTGGTGCAGGATGGTGGCTGAGAGA(A/-) JGATTACTCATAAAGCATATTAAATTTTATAATATGAAAAATTTAACTAGATAATTAATGTGAAT TGAGTTGAAGTTGCATGAGAGTAGGAGGAGGTAGTTCTACTTATAGGTTTATATAAGTNTGCT TCAATAGAATGGCTCTTTCCGATGACAATGATGAACGTGTTCTAAGCAGACAG
WI-5390	87 C T ---	---	---	GCCTTGAGAAATGAAAAAGGGAGCCTGGACCATTCAGGGCTTCTTCATCTCTGATTATTTTGTGTAT TTATTGTTACCTTATTAT(C/T)GTCTGTCTCCCTTCTGGTATGCTTGTGCATGAACAATGAATTC CCCAGTGCTGGCCGATTCGTGGCTCCTAGAGGTGCCAGAAAAAGTTTCGGTGAATAGAAATTG ACGAATGGTTTCAGAAATGAAACCTGTGAATCTATGGAAGACAAAAACGAAT
WI-5404b	87 G A ---	---	---	CCCTGCCTGCTTATGCATAATGAGAAATAGAGTTGACTCTCTGTCAGAAATCAATTTAAGCAGT GCAACATTAATTTAATTT(G/A)AAAGAAACTTGTTCGAACTTTGTACTCTTTGTAGTNAATTG AATCTTCCCTTCAGCAGTTCCATGTCGTGAATCCACCCCATCTCTTTCCACGATAGCAAGATT GCTACTTATATGGAAGGGTTTAGAGTTTATAACAA
WI-5404	87 G A ---	---	---	CCCTGCCTGCTTATGCATAATGAGAAATAGAGTTGACTCTCTGTCAGAAATCAATTTAAGCAGT GCAACATTAATTTAATTT(G/A)AAAGAAACTTGTTCGAACTTTGTACTCTTTGTAGTNAATTG AATCTTCCCTTCAGCAGTTCCATGTCGTGAATCCACCCCATCTCTTTCCACGATAGCAAGATT GCTACTTATATGGAAGGGTTTAGAGTTTATAACAA
WI-5545b	77 A C ---	---	---	TAGGAAAGGGGATGGTGATGGCTCTGAGACATTTAAATCTATCTTTCCACCACTCACACTGCCGCCA TATCTCCTC(A/C)CCAACACCTCTGTTTCTGACAGCCCAAGTTCCATCAGTTGATGGGACTATTT GTTGCAAAACAATGTTAAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACACCATGAATTTTATTTCATTCA
WI-5545	77 A C ---	---	---	TAGGAAAGGGGATGGTGATGGCTCTGAGACATTTAAATCTATCTTTCCACCACTCACACTGCCGCCA TATCTCCTC(A/C)CCAACACCTCTGTTTCTGACAGCCCAAGTTCCATCAGTTGATGGGACTATTT GTTGCAAAACAATGTTAAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACACCATGAATTTTATTTCATTCA

WI-5860b	134 A G	---	---	ACTCAAGTTGGGGATAAAATCAGAAGTTCTATGTACAACTTAAATTTTGCTAAGATTTTATTGT TTCTTTTATATAAATATGGATTTGTTTACTTCCCTAACCAACCTTCTAACTGAGGAACAC/A GTTTACTGGAATCATGTGAAGACATTCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTTCCAAATCATCAACTTCTGTAT
WI-5860	134 A G	---	---	ACTCAAGTTGGGGATAAAATCAGAAGTTCTATGTACAACTTAAATTTTGCTAAGATTTTATTGT TTCTTTTATATAAATATGGATTTGTTTACTTCCCTAACCAACCTTCTAACTGAGGAACAC/A GTTTACTGGAATCATGTGAAGACATTCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTTCCAAATCATCAACTTCTGTAT
WI-6106	208 C G	---	---	GCAACAACCTATTATACCTGATCCCAACCCAGGTTCTACTAACATTAATCAACCCTAACCAATAC TATATTGCTGTTCTGAATTTATTTTCAATTTAGAACTGATGAGATTTAGCATGGGATAAGTGCAG TGCAGAGATAGTAACACTGCTCTTTTGTCCAGGAGTCTCAATGTGAAGTATAATTTCTTACAGAG TAATTC/GTATAGTAGGTCACCACAAAGTCTATATTGTATGTGAAGGAAAG
WI-6109d	129 T C	---	---	AAGATAGACAAACATATGCCAGACCAACAAAAACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAAACGAAAGGAAAAAACCT/C AAACCCTATATTNCTGCTTGTGTCATACCTTAAATGTATAATGTGGGAGAGAGGAAATTTTGATGT GNAAAATTATCCCTGAAATTTTATACCA
WI-6109c	147 T C	---	---	AAGATAGACAAACATATGCCAGACCAACAAAAACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAAACGAAAGGAAAAAACCTAA ACCTATATTNCTGTC/CCTTGTGTCATACCTTAAATGTATAATGTGGGAGAGAGGAAATTTTGATG TGNAAAATTATCCCTGAAATTTTATACCA
WI-6109b	147 T C	---	---	AAGATAGACAAACATATGCCAGACCAACAAAAACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAAACGAAAGGAAAAAACCT/C AAACCCTATATTNCTGCTTGTGTCATACCTTAAATGTATAATGTGGGAGAGAGGAAATTTTGATGT GNAAAATTATCCCTGAAATTTTATACCA
WI-6109a	129 T C	---	---	AATGCCTATCACCTCCATCATGCTGCATAACTGATTGATCATAATGCTTATTGTTAGCACCTGTC TTCCAACACATGCTGTTTTGTTCAATGAT/CJGCATATCCCAAGTGCCTTAGACAATGCCTCCCATAC AGTGAACAGTATTGACTAAACATACCTTGTTAAATCAATAAAATTAATCAACTTGGCATATGCAGG GAAC

WI-6244	103 T C	TAATTGCACAACTTACATATCAGGGTTCTGATTGAAGGAAGAGAATAATTCCTTTCTTTAGTGATT GCTTAATATTAATTCAATAAAGTGCACCATCTCTTCGCTCCTTATAAATGTGTTTGAAGAAGG AAATTGAGTGTGGGAATTAAAGCAACCAGGAGACATTTTATATACTCTACAGTGGGGAAGACTT CCTATTCTCTTCCCAAGGATGGATACATTCTAC
WI-6268	124 C T	CTGGCCTTATAATCCAAGTTAGGATTATCTTACCCCACTTAATAGACTCCAGACAGTTGCAGTT GTCTACAAGATTCTCTAGTAGGGCTTTGGGTGGCACCCTTTGGCTCATTC/TACTCTCCCT GGGTCTATTGACTTTCAGGAGCCTAGAAAGAGCTGGACAAACCTGCTTCTTGCAGAAAGAGTCG GGGTCCAAGATTTCGTTACGATTTTITA
WI-6336b	234 C T	AGGTGCCATTTAATCCATTCAAATTTGAAGCTACATCTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATAATCCCTTTACATGTTTCTTATAAGACATACAGTTTAAATCAATTAACAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTAATAGATCAGATGAATGGACCATGTG GTACCCAGTGCAATTATGCTTGGTAGAGCC/CTTJGAGGACACTGACAGT
WI-6336	234 C T	AGGTGCCATTTAATCCATTCAAATTTGAAGCTACATCTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATAATCCCTTTACATGTTTCTTATAAGACATACAGTTTAAATCAATTAACAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTAATAGATCAGATGAATGGACCATGTG GTACCCAGTGCAATTATGCTTGGTAGAGCC/CTTJGAGGACACTGACAGT
WI-6381	92 C A	TTGGATACAAAATTCAGTTACACAATCAGTAGCATTCAAAATAGTTATGAGTATTTATACAATTA CAAAAATGNNTTTCATGTTTAAACAA/C/AJGTAATTTAAAGCTCAACATTTTAAACAGGCACAAT ATTCTAANGGCATATGCATTCACCATGGGCTTTGAATGTCCTCACTCCCAACTTCACAATCAAAATC TACAGANGCGGCAAAAGATCAGAGTTTCAAG
WI-6436	198 C G	GGTTGAGGCATTGGGAAGGCAGAAATTTGAGGCAAGTAGAAAATGGACATTTTAGGAAAAGAGAAGT TCAGAGGCAAGTCATGACAGACAGGAAATACAAGGCTTAGGAAGACAGTAGTCTCTGTGGTTGAA ATTTGGTGTATAATAAGAAGTTTAGACTTTGGTGGTTGAGTAGTTGAGTAGTAGGTAGCGTT/C/ G/ATTGGGTGTATCCACAGACAAGGIGATGTTCTAAGATTGATATTATTGT
WI-6449	186 C T	GAGGCTCTTTGCTTTTCTCAGTCAAGGCTGTATCCAGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTTCTGATTGGTTGGTGTGCTCACACTGCCAGATTGTTAAATATTTGAAAATC GTATCTGTTCTATTCACTGCTGCTGATCTTATGTCGGCTCTATT/C/ATCCCTATTCTCTGA TCTTATGTGACAGCTGAAGTTCTCTAAITTTCTGTGGTGTATTATA
WI-6449	186 C T	GAGGCTCTTTGCTTTTCTCAGTCAAGGCTGTATCCAGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTTCTGATTGGTTGGTGTGCTCACACTGCCAGATTGTTAAATATTTGAAAATC GTATCTGTTCTATTCACTGCTGCTGATCTTATGTCGGCTCTATT/C/ATCCCTATTCTCTGA TCTTATGTGACAGCTGAAGTTCTCTAAITTTCTGTGGTGTATTATA

WI-6463	72 T C	---	---	GCTGGAGAGAAAAGACCTCCAAAAGAGAAACTAAATCAGAGTCTCTTGAGCAAGAGGAATTGAAA AGAACA[TC]TGAAAAAAATTAAGTAGAAGTCAAGAGCCAAAAGTCCCAATTTGTCTCCATTA TAAGAAATATTTGAATGGAAATCTTAAGAAATGATTTTATTGATCAGTTAAATGTTCTCTCTCCTC CAGTCCCATTTATATGACATTCGCATGCTG
WI-6474b	76 C T	---	---	AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGGTAATGTTATAGAAACTTCAGAGGANAC AGAGGCAAA[CT]GTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAAGTAGGATTTGAAAGGCACAGAGAAAAGGGGTGACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACTAAAGTATAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6474	76 C T	---	---	AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGGTAATGTTATAGAAACTTCAGAGGANAC AGAGGCAAA[CT]GTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAAGTAGGATTTGAAAGGCACAGAGAAAAGGGGTGACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACTAAAGTATAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6478b	175 T A	---	---	GAAGTATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG GAAGTATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG GAAGTATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG GAAGTATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6478	175 T A	---	---	GAAGTATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG GAAGTATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG GAAGTATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG GAAGTATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6559	149 G A	---	---	CACATTTGAATGCAACTGAGAAANTGGTTTNTAGGCCTACCTTTATTTAAGAGTACATCTGGCTC CAATGTTACCCCAACATGCAAAACATAAGGCAACAATCTGATCATTTTATAGGNTCCCAAGCCCA TTAGCAATATCTTA[G/A]TCAAAATTTTAAAAAGAGAACAGGAAATAGGAAAGGCCTAACAGAGGAG TTAAATAATTGTGCAAAACTTATCAGTTCTTC
WI-6564b	54 G A	---	---	TTCTTTATTGGTCTACCAATGTGACTCTTTACCCAGGCCACTGTTCTATGC[G/A]CACTGGCTTTG TAGGCATTACATCATATGCTGTGCTGCTGAAATCTCAATTAATTTCTCCTNCCTATTCTTTCCAT GCTCTGCCTCATTNCTCAGAAATGGAAGGCAATTTGATTATNATTTTTTTGGGTCTGTGTAAG GTTCTTGGCAGGAGAACATGCATATGACTTTAAAAATAAGACCAACA
WI-6564	54 G A	---	---	TTCTTTATTGGTCTACCAATGTGACTCTTTACCCAGGCCACTGTTCTATGC[G/A]CACTGGCTTTG TAGGCATTACATCATATGCTGTGCTGCTGAAATCTCAATTAATTTCTCCTNCCTATTCTTTCCAT GCTCTGCCTCATTNCTCAGAAATGGAAGGCAATTTGATTATNATTTTTTTGGGTCTGTGTAAG GTTCTTGGCAGGAGAACATGCATATGACTTTAAAAATAAGACCAACA

WI-6608b	46 C	CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGGCTCAGT[C/- JAGTTACGGCAGCTAAAGGAGGGGATTCCTCTAGTCTCTCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGTAATTTCTAGAGGAAAAAGAACTGAACCTCCAGCACTAG GTAAAACTGCAAAAAGAAAAACACCTGTGCCAGGCACTAGCTACAAGGCCACACAGAAAAAGGAA AGC
WI-6608	46 C	CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGGCTCAGT[C/- JAGTTACGGCAGCTAAAGGAGGGGATTCCTCTAGTCTCTCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGTAATTTCTAGAGGAAAAAGAACTGAACCTCCAGCACTAG GTAAAACTGCAAAAAGAAAAACACCTGTGCCAGGCACTAGCTACAAGGCCACACAGAAAAAGGAA AGC
WI-6666	68 C A	GTAGACAGTATCCAGCAAAAAAGGTTATTTATACCTCTACTTTTCCAAAAAGAGGAAACCTCCCC A[C/A]AAATCCCATCAACACACAGTCATGCTGGAAGGCATTCTGTCTTACTCTGTGGTTTCATGTAA ATGTTGGGGTGACTCATTCGGCTCTCTNTTCTCAAGTTCCAGGCTCTTGGGTAGACCAAACTA ATACACAATGTTAGAGCACACAAGAGA
WI-6670b	120 A G	AGATTACATAATTACTGGGGCCATTGTAGGGTTNGGAGGAGTGTCTTTCTATCTGCAGCCAAA CAGAAATACTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTTAGCCA GCATTGCCATTACGGCCGAGTCAAGGTTGTGGGCCAGAAAGTTAGACAATTTGGGGAATCTGA AAAAAAAAGAAATACAGAAATTGTAACACAGACACAGAATCTTAGAAGGGAT
WI-6670	120 A G	AGATTACATAATTACTGGGGCCATTGTAGGGTTNGGAGGAGTGTCTTTCTATCTGCAGCCAAA CAGAAATACTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTTAGCCA GCATTGCCATTACGGCCGAGTCAAGGTTGTGGGCCAGAAAGTTAGACAATTTGGGGAATCTGA AAAAAAAAGAAATACAGAAATTGTAACACAGACACAGAATCTTAGAAGGGAT
WI-6704c	33 T C	TTTGAAAAATAATTCATGCACCAATGTTTAACT[C]CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAGTTTTTCATGACACACCGNCA CTATTGCTCTTTAAATATGTTGTACATGTCAATTAATCGATTGTTCTTCCACATGGTTATT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704b	33 T C	TTTGAAAAATAATTCATGCACCAATGTTTAACT[C]CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAGTTTTTCATGACACACCGNCA CTATTGCTCTTTAAATATGTTGTACATGTCAATTAATCGATTGTTCTTCCACATGGTTATT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704	28 T C	TTTGAAAAATAATTCATGCACCAATGTTTAACT[C]AACTCACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAGTTTTTCATGACACACCGNCA CTATTGCTCTTTAAATATGTTGTACATGTCAATTAATCGATTGTTCTTCCACATGGTTATT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG

WI-6710	106 G A		CCATGGACAGTTTAAATTAGGAAGCTTCGACTTGTTAGATAACAGAGGAAGTCCAGTTATCTACCT ATTCCTTAAACACATTTTGTCCAGGCTGGAATGATTCCTC[G]ATAGTAAACCTCAACATCCACACCT GCATAACATCGCCTCCCAAGTACTATTTACTAGTGCACACAGGATGTCACCAGTGAGCCTC ATCTCCAGTCCAATGGAGGAGTTGACTTAGACCTTCCTTGGACAGGAAGGGTC
WI-6766b	148 G C		AAACAAATGGTGCAATTGCATAATATTGTGGTCACAGTATAAAACAATAACAATTAGTTCATATAAC ATTGGATATGGACAAAATAACACANGATCCTTTCTTGTCTACGGAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTTAGGNTCTGCACACATATTATCACTGA GAATTTGGTCAACAGTGGAGNGAACTTACCCAAATCCAGTCCCTTCTTC
WI-6766	148 G C		AAACAAATGGTGCAATTGCATAATATTGTGGTCACAGTATAAAACAATAACAATTAGTTCATATAAC ATTGGATATGGACAAAATAACACANGATCCTTTCTTGTCTACGGAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTTAGGNTCTGCACACATATTATCACTGA GAATTTGGTCAACAGTGGAGNGAACTTACCCAAATCCAGTCCCTTCTTC
WI-6787b	97 A G		ACAGATAAAAGTCTTTATCCCTGTATGTTTACATAAGAAAGTCTTTACAGACTTTTTTTTATACA ATACCTGTGCAGCAATGTTCAAATTCAC[G]JTCTTACTGCATAAGATATCTTCATGTACAACTGT ATGCTTTGTCTTCTGGGAAGGACGCTTAAAGACCTATGATAAACACACATCCACATGACAAAAGGA GAGTGCAATAGGGCAGAGTAGANTACTACAGGAAAGAGTAAATTCAGGT
WI-6793	105 C G		GAACCCACAGGTCCTGTTATTTTAAAGGAGCATTTACATTATGATAGCAAGTTTCAACACATTCA TCAACAAGGCGGCTTCAAATCAATCAGTCAACCCCTC[G]GAGTTAGAAAGTAGAGTCATGAGGAA GAGCTGCTTGCTGTAGGAAGTAGGTTAATGCCCTCTAATCCCCGAAAGGGCAGACTGAAGCCA GAGCCAGANTCCTGGCAATTCACCAGTTTCTCATCACAGGTAAAGGCAAC
WI-6810b	37 T C		CACAATAATAAAATCACTCCCTACCTTGAAACCTTTAT/CJAGAAGCATTTTTTAATTTACAACACA AAGCTCAACCGNACCTACAATAAGTCTAGTGTCTGTACGNGCCAAAGGATAAGGCTGAACAATA AATTAACCCCTTAAAAATGCTATGNACAAAGTACAAATTTCTTTTGAGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAATCCAGCGGCAATGAAGTTAAT
WI-6810	37 T C		CACAATAATAAAATCACTCCCTACCTTGAAACCTTTAT/CJAGAAGCATTTTTTAATTTACAACACA AAGCTCAACCGNACCTACAATAAGTCTAGTGTCTGTACGNGCCAAAGGATAAGGCTGAACAATA AATTAACCCCTTAAAAATGCTATGNACAAAGTACAAATTTCTTTTGAGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAATCCAGCGGCAATGAAGTTAAT
WI-6817b	145 C A		GCATGATTAAACCAGTGCAGAAAAATACCAAGTACATGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTAAATCCAGTTAAGACCATCAGGATATACAACATCATCACTAACTCAACAATGTAGCT GCAGGGTAAAC[C/A]TGTGGATACCCGTGTGCTCTACTNGCCCTCCAAAGGCATTCAGGGGATCATCA AAGATGTTGGACACCTTGTTTCAATCTTGTTTCAGGTGCGGCCTGTGCAG

WI-6817	145 C A ---	---	GCATGATTAAACCAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTTGTAAATCCAGTTAAGACCATCAGCATATACAACATCATCACTAACTCAACAATGTAGCT GCAGGGTAAC[C/A]TGTGGATACCCTGTGTCTCTACTNGCCTCCAAAGGCATTGAGGGGATCATCA AAGATGTTGGACACCTTGTGTTCAATCTTGTTTCAGGTGCGGCTGTGCAG
WI-6819b	221 C ---	---	GATGGAAGGCCATTTATTTTCTCTAAATTTAAATAGAAGACITTTAATGGAAAAACATTTAGTAC CATCATGTCACCCCTGAATGCCAGCAATACCTCGACTTTACACACGCGAGGAGCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTTTCATATACAAAATTTTCTGCTATTTTG CTTAGCAACAGCAATAACTTTTGTTTCTCTATATGACACCTAATATCCAG
WI-6819a	175 G T ---	---	GATGGAAGGCCATTTATTTTCTCTAAATTTAAATAGAAGACITTTAATGGAAAAACATTTAGTAC CATCATGTCACCCCTGAATGCCAGCAATACCTCGACTTTACACACGCGAGGAGCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTT[G/T]CATATACAAAATTTTCTGCTATT TTGCTTTAGCAACAGCAATAACTTTTGTTTCTCTATATGACACCTAATAT
WI-6826b	154 A G ---	---	GCAAAAAGCTTTATTGGCTCCAAACAAATTTATCCCTTTTAAAACTCCTCTCTCTCTGGTCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTTCCTAAGAACCATATAAATAC ATGCAAAACCTTGTACAT[G/G]GAGCTTAAATAATCAAAATGCAAAATAGATTGGGTGCACGTG TAAGCTGAATTGCAAAATTTATGGCAACACACACTGGACTGGGTATACGTTG
WI-6826	154 A G ---	---	GCAAAAAGCTTTATTGGCTCCAAACAAATTTATCCCTTTTAAAACTCCTCTCTCTCTGGTCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTTCCTAAGAACCATATAAATAC ATGCAAAACCTTGTACAT[G/G]GAGCTTAAATAATCAAAATGCAAAATAGATTGGGTGCACGTG TAAGCTGAATTGCAAAATTTATGGCAACACACACTGGACTGGGTATACGTTG
WI-6857a	122 T C ---	---	AGTGCAAACTATTTGAACAAAAGTAAACTATGAGTCACAGCATTGCAAGACATCAGACACGGA AGAGTGAACAAATATTCACATAAGTAAATACAGCAGATGAGATGCTCTCACATGTA[T/C]ATTTAAT TATTCATGCTTTTCAATAGTCTCTAGTCAACTTTGAGTAAATTCACAAATATATAGCAGCTCA AACACAAATGCAGGACACAAATGGCAAAAGTTTGCAACTGTTTGGGCTAATT
WI-6865	153 G A ---	---	TTATAGAATACTTATGGGCATACGNGTAAATGAACCTGTCAACCTTAAATCTAAACAAACAGCTTG TTTGTTGTTGCTGAAATCCTCCTGCTCACAAAACAGCCAGCTACTNGGTTTTCTAAAGACGTA ATTTTGCAAGGCAAACTT[C/G]ATAGAGCCATTCTGTGCAGAGAAGGGAAGGAGCTGTTTGT TTACCTGTAGTATGAAGATATTTCTTGGCTGTAGAACTGAGCTCAATTA
WI-6909	73 C T ---	---	ATTGAAACTGGTTAGCAACAGATAAATTACAATAGAGCCTGGATATAAAAATGAGAGAAGATGC AGACTTAC[T/A]AGCTTATAGAGAAAGTCAAAAAGGAGCAAGTTTTTGAATCAGATTTTATGATAC GGAATAAAATTTCCTTTTTTGGCAACAGGATATTTCGAATAATAAATCTGCCAGTGCCCAATCAG AAACACCAATTTCCACAATATTTGCATGCCCTAGTTGCCTATTTTATACATATC

WI-6910b	163 G T	CACTCAAAACCCTTTATTCATTGATTTACAAACTGTACAATATTTACAAAGTTTAGGCATTATCCCA TATTGACATGAATGCTGTGGAGAGTCTAAATAATATATGTGGCACATAGCTTAATATACACATCAT GGCTCTTTACACTTAAGCCATTACCAATA[G/T]TGAGATGTAATGGAGAATTTAATGTGGTAGAAAA GTCAGAGTGGCTGACCAGTCCCGACCTTCCATGTGAATGACTCTTCCTTGGC
WI-6915	144 A	GCTGTTTTTTTTGTTGTTTTTAAGTGACACCTTGGCCTTGTTGGCATTTCTTCACTTATCTTACCC AAAGTGCCCTTGGCCAGCCACTGACTGATTTAAACCAGAAATGTGTTTAAACAATGTGGT CGTGGTAATTCAGGTGATTTTCTATTTGGTAGTATTTTCAGATTTCCACAAAAGAACATG TATTGCTTTGTAATTTGAAAAAAAATCAACACAGGATAGTAAAGATAT
WI-6928b	175 T C	CAATCAAAAGTTCCAAGTTTCAAAGCTGGGATGAAAGCCAGGCTTCTGACTTGCACCTGTGCAC ACTGGATTTNCCCTCTGATCCAGCTGCAGCTCCCATAGAAAGTTCACTCTTAATTTCAATGCCCATG CTTTGCTTGGTCCCTGTGAGGAAAGGGTCAAGTAAAGGT/CJAAGTGTCTATAAGGATGGGTAGG TATCCTGGCAAGATATTTCCCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6928	175 T C	CAATCAAAAGTTCCAAGTTTCAAAGCTGGGATGAAAGCCAGGCTTCTGACTTGCACCTGTGCAC ACTGGATTTNCCCTCTGATCCAGCTGCAGCTCCCATAGAAAGTTCACTCTTAATTTCAATGCCCATG CTTTGCTTGGTCCCTGTGAGGAAAGGGTCAAGTAAAGGT/CJAAGTGTCTATAAGGATGGGTAGG TATCCTGGCAAGATATTTCCCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6955b	79 G A	TTTTATGAACAATTTCAAGATTCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCTCAATCCCAATCCTAGGTAAGATATCAAGTTACAAANTAC AAGTCCGNTAATTAACCTATAGGTAGTATTAANCAAAAATGNGTTTTTNGCAATTTATGTGAAAT AAGGCTTTAACCAAGC
WI-6955	79 G A	TTTTATGAACAATTTCAAGATTCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCTCAATCCCAATCCTAGGTAAGATATCAAGTTACAAANTAC AAGTCCGNTAATTAACCTATAGGTAGTATTAANCAAAAATGNGTTTTTNGCAATTTATGTGAAAT AAGGCTTTAACCAAGC
WI-6957	47 C G	AAACTAAAACCCTTATTGTCTCCAAGTGTGGGCAAAATAGAAAATC/GJTTTCAATTACATTAGG AAATCGGGTGGATAACGGAGTATAGTTATTCACCTTAAGAAGCATTCAGTCAATAATCACAAAA ACAAATTCAGATTGCTTGGATCTTGGTCAATTTATGGCTTGAAGAACTGGATTGAAAACCACTTTAGG CTAAAATAATGTATATGAATAATGCATAGACTGTGTATCTAGAAAATCATGC
WI-6996c	242 G T	ACTTCTAGTGCCTCTGTTACCACCACTCTAATGCCTCTGGTCGCCGACTTCTGATGTCCGTAGGCCT TAAATCTGCCTGGCTCCCTCTGCTTTCAGCACCCAGAGGAGGAGAGCGCGGAGTTCCCTG CAGGAGAGAGGGGGCTGCTGGACCCCAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCTGACT CTCTCCTGATGTGGGGCCCTCTGIGCTTCTCTCTCCG/GTGTGGATC

WI-6986b	242 G T ---	---	ACTTCTAGTGCCTCTGTTACCAACACCTCTAATGCCTCTGGTCGCCGCACTTCTGATGTCCGTAGGCT TAAATCTGCCTGGCGTCCCTCCCTCTGCTTTCAGACCCAGAGGAGGAGAGCCGGCAGTTCCTG CAGGAGAGAGGAGGGGCTGCTGGACCAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGCTGCTGACT CTCTCCTGATGGTGGGCCCTCTGTGCTCTTCTCTCCG/GTGGGATC
WI-6996	228 T G ---	---	ACTTCTAGTGCCTCTGTTACCAACACCTCTAATGCCTCTGGTCGCCGCACTTCTGATGTCCGTAGGCT TAAATCTGCCTGGCGTCCCTCCCTCTGCTTTCAGACCCAGAGGAGGAGAGCCGGCAGTTCCTG CAGGAGAGAGGAGGGGCTGCTGGACCAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGCTGCTGACT CTCTCCTGATGGTGGGCCCTCTG/GIGCTCTTCTCTCCGGTCCGATC
WI-7021b	112 G A ---	---	TGGGAGGACAGGGAGATGCTGCAGTTCACAAAGAGAAGGTTCTTCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGCTCTGAAGCCACAGACAATATGGTCCCAATG/AJCCGACTGCACCTTCTGTG CTTCAGCTCTTCTTGACATCAAGGCTCTCCGTTCCACATCCACACAGCCAATCCAATTAATCAAACC ACTGTTATTACAGATAATAGCAACTTGGGAATGCTTATGTACAGGTTA
WI-7021	108 A G ---	---	TGGGAGGACAGGGAGATGCTGCAGTTCACAAAGAGAAGGTTCTTCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGCTCTGAAGCCACAGACAATATGGTCCG/A/GJAATGCCGACTGCACCTTCTGTG CTTCAGCTCTTCTTGACATCAAGGCTCTCCGTTCCACATCCACACAGCCAATCCAATTAATCAAACC ACTGTTATTACAGATAATAGCAACTTGGGAATGCTTATGTACAGGTTA
WI-7056c	118 C T ---	---	GGCAGTAGGACCACAGTGTGGGTTCTGCTGGGACCTTGGAGAGCCTGCATCCAGGATGGGGTGG CCCTGCAGCCTCCTCCACCTCACTCCATGACAGCGTAAACGTTGGTGA/C/TGGTGGGAGCCTCT GGGGCTGTTGAAGTCACCTTGTGTGTTCCAAAGTTCCAAACAACAGAAAGTCATTCTCTTTTAA ATGGTGCTTAAGTTCAGCAGATGCCACATAAGGGGTTTGCCATTGATA
WI-7056b	118 C T ---	---	GGCAGTAGGACCACAGTGTGGGTTCTGCTGGGACCTTGGAGAGCCTGCATCCAGGATGGGGTGG CCCTGCAGCCTCCTCCACCTCACTCCATGACAGCGTAAACGTTGGTGA/C/TGGTGGGAGCCTCT GGGGCTGTTGAAGTCACCTTGTGTGTTCCAAAGTTCCAAACAACAGAAAGTCATTCTCTTTTAA ATGGTGCTTAAGTTCAGCAGATGCCACATAAGGGGTTTGCCATTGATA
WI-7091b	153 A C ---	---	AATTCGCTGAAAAGGAACCTACCTATCCTTACATTTACCTTACCTTCTTCTTAACATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACATGTTTATCTGCTCTATAAATAGTATTCOAATCACTGTG CTTAATTTAAATAGCATT/A/CJTCTTATCATTTATCAGCCTTTTATGTTATTTCCAAAGTAAATATTA ACATATTATTCATGGTCTCTCTTTTATCTGGTCTATGAATGCTAT
WI-7091	153 A C ---	---	AATTCGCTGAAAAGGAACCTACCTATCCTTACATTTACCTTACCTTCTTCTTAACATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACATGTTTATCTGCTCTATAAATAGTATTCOAATCACTGTG CTTAATTTAAATAGCATT/A/CJTCTTATCATTTATCAGCCTTTTATGTTATTTCCAAAGTAAATATTA ACATATTATTCATGGTCTCTCTTTTATCTGGTCTATGAATGCTAT

WI-7136	58 TC ---	---	TGTGAAGCCACATTTCCACATGAGCCTCATGAAGCCAACTAAGTGTATTGAACCTGT/CJAATTC TCTCAATAACTCAGTGACACTTTAAAGCTGAAGACGACCAATGAAAGAGCATATCAATGATG GTGGAGAAAGGGAAGGGTTGGCTTTTAAATTTATTTTCTTCATCTTTATAACAAGAAAGNNNN NNNGTAGCTTTCTATATATG
WI-7146c	210 AG ---	---	GGGACGCCCTGTTGTTGGCTCAATTTGGGTTGTTGGTCACATGGAGCTCTTCCATTTGTTAGCTG AATAATGAGTTGTTCTAGAGGAGACAGCCTGCTCTCTCTGTTGCCCCAAAGCCCATGCCCTGCCG TGGTGGCAGCTGGGCTGTGGATGGAGGGTCCCAACATGGATGTTGGCCCTCTCTCGCATGCC AACGC/A/GJTTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAAATTA
WI-7146b	210 AG ---	---	GGGACGCCCTGTTGTTGGCTCAATTTGGGTTGTTGGTCACATGGAGCTCTTCCATTTGTTAGCTG AATAATGAGTTGTTCTAGAGGAGACAGCCTGCTCTCTCTGTTGCCCCAAAGCCCATGCCCTGCCG TGGTGGCAGCTGGGCTGTGGATGGAGGGTCCCAACATGGATGTTGGCCCTCTCTCGCATGCC AACGC/A/GJTTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAAATTA
WI-7146	202 GA ---	---	GGGACGCCCTGTTGTTGGCTCAATTTGGGTTGTTGGTCACATGGAGCTCTTCCATTTGTTAGCTG AATAATGAGTTGTTCTAGAGGAGACAGCCTGCTCTCTCTGTTGCCCCAAAGCCCATGCCCTGCCG TGGTGGCAGCTGGGCTGTGGATGGAGGGTCCCAACATGGATGTTGGCCCTCTCTCGCATG/A JCAACGCAGTTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAAATTA
WI-7153	161 AT ---	---	ATATTACAACCTGCTTTTAGCTGATCTTCCATCCTCAAAAGACTCTTTTCTTTATATGTTAAACATA TATAAAATGGCAACTGATAGTCAATTTGATTTTATTCAGGAACATCTGAAATCTGCTCAGAGCCT ATGTGCATAGATGAACNNNNNNN/A/TJAAAAAAGTTATTTAACAGTAATCTATTACTAATTAT AGTACCTATCTTAAAGTATAGTACATTTTACATATGTAAATGTTATGTT
WI-7155	156 TG ---	---	TAGAATAGATCGGTCATATCTCTTTGGCTCTGTTCTCCAGCCCTCATGGTTGGCATCACATAT GCCTGCATGCCATTAAACACAGCTGGCCCTACCCCTATAATGATCCTGTGCTCAAAATAATACAC CAGTGGTCTCTCCTCCCTGT/GTJAAAGACTAATGCTCAGATGCTTTACGGATATTTATATTCTAG TCTCACTCTCTTGTCACCCCTCTCTCTCTCCCATCCCAACTCCAG
WI-7169b	161 AG ---	---	AGCTCCACAGATGCAGATTTGTTGTTTGTGTTGTTATCACTGTCACACAGCTTATAACATGTAT GCTTTTCAGAAATACAGTTGTCTAGCCAAAGCCATCAAGTGTGAAATTCAAATTTGTTTATGCAAAAT ACAGCAAACTTTTATTTAAGTAGAT/A/GJGGAGAAATATGTTTAAATATTAGGAATCCTAGACCATA TTTTCAAGTCACTTAGCAGCTAGGATCTCAAAATGGAAGTGTATATATA
WI-7175b	194 CT ---	---	CTCTAGACTAGTGCCTTTACCTTTTAAATGAACGTGTGACAGGAAGCCCAAGGCAGTGTTCCTCACCA ATAAATTCAGAGAAAGTCAGTTGGAGAAAATGAAGAAAAGGCTGGCTGAAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAAATATATAATGTTTACTGCTGCTATTGTCATGCTGCTA/CJTJAGAT AAITTTTTTGTATTTTGAATAAAAAACATTTGTACATTCCTGATACJGGG

WI-7175	194 C T ---	---	CTCTAGACTAGTGCCTTTACCTTTATTATGAAGTGTGACAGGAAGCCCAAGGCAGTGTTCCTCACCA ATAACTTCAGAGAAGTCAGTTGGAGAAATGAAGAAAGGCTGGCTGAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAATATATAATGGTTTACTGCTGCTCATTTGCCATGCCTA/C/TJAGAT AATTTATTTGTATTTTGAATAAAAACATTTGTACATTCCTGATACTGGG
WI-7178b	273 G A ---	---	TGTATCAGGTCAGGGAATTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCAGCTGCCTGGAG AGGGTCTGGCTGTCAGTGGCTGGCTCTAGGGGAACAGACAGTGAACCCAGAAAGCATAACACCA ATCCCAGGGCTGGCTCTGCACCTAAGAGAAAATTGCACCTAAATGAATCTGTTCCCAAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
WI-7178	273 G A ---	---	TGTATCAGGTCAGGGAATTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCAGCTGCCTGGAG AGGGTCTGGCTGTCAGTGGCTGGCTCTAGGGGAACAGACAGTGAACCCAGAAAGCATAACACCA ATCCCAGGGCTGGCTCTGCACCTAAGAGAAAATTGCACCTAAATGAATCTGTTCCCAAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
WI-7182b	116 A C ---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCAACAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATCACCAGTTCCTCTGCAACCCAC/C/ATCTGAGCCTATCTCTCCCTATTT TACTTGAGGCTGCAATACCAGCCCCACGTTTCAGCTCAAGAGATGCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGAATGGCAGCTATTTCCCTGAAGCCTAGTACCCCAATT
WI-7182	106 C A ---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCAACAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATCACCAGTTCCTCTGCAACCCAC/C/ATCTGAGCCTATCTCTCCCTATTT TACTTGAGGCTGCAATACCAGCCCCACGTTTCAGCTCAAGAGATGCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGAATGGCAGCTATTTCCCTGAAGCCTAGTACCCCAATT
WI-7191b	273 T A ---	---	ATAATTGCTTGTCTAGCCTGGCAAGATATTTTCATAAAGAGGGATAACAATGCTGATTACTAC CTTTTAAATATTTAGATAAATGCACAGCACCACAGCACCACATCTAAGCATTAGTGATGGTAGC TGATGTCAGCTTCATGTGGATTTAAGCACTCTAGAAACAATGAAGCTTCTTGGCATAATTTAAGGAG CTCCCAAATGTGTACCTATTAAATTGTAACTCAGCAAGTAGAAGACCATTT
WI-7199c	112 T C ---	---	CCCAGTGGTGAACAGAACCTCCCAAATTTGAGTTGCACCCCTTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTCAGCTCCTTGACCTATGAGC/C/CGGGGCCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATTAGCATTCTTAATGTTTTGTTGGTGCTGCTGAATTTCTCTTTATTAT AGTCTATAGTTTTACTCTCAGTTCTCACCATCATCTGTCTAA
WI-7199b	112 T C ---	---	CCCAGTGGTGAACAGAACCTCCCAAATTTGAGTTGCACCCCTTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTCAGCTCCTTGACCTATGAGC/C/CGGGGCCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATTAGCATTCTTAATGTTTTGTTGGTGCTGCTGAATTTCTCTTTATTAT AGTCTATAGTTTTACTCTCAGTTCTCACCATCATCTGTCTAA

WI-7216c	237	T C	---			TGACACTAACACTCTAATTAAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGCTCTTCTCCCC AAGGACAAAATGTAGAAAGATGTAGATAAATTAAGTAAAGTCCCTCCAGAAAATACGTATGT TTAAAACCCCTTCTGTCTATACATAGGAAAAGACACACATCCACCTAAAATTGACTGTACTGTTTAA CTGTCAATTCCTCTGAGGCTAAACACAGTTTGTCTTCTGTAATCACTT
WI-7216b	237	T C	---			TGACACTAACACTCTAATTAAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGCTCTTCTCCCC AAGGACAAAATGTAGAAAGATGTAGATAAATTAAGTAAAGTCCCTCCAGAAAATACGTATGT TTAAAACCCCTTCTGTCTATACATAGGAAAAGACACACATCCACCTAAAATTGACTGTACTGTTTAA CTGTCAATTCCTCTGAGGCTAAACACAGTTTGTCTTCTGTAATCACTT
WI-7220b	147	A T	---			AGGATGATGCTCCAAAAGGGGACCTTGAACCTATTACCAATTAATTTGCTCTTTAAGCTGGCAACCCA TCATTAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAA[AT]AATCTTGAGCACAGTGAATGACCTATCTGCAACATCTAATGGATCTCTA AAGGTAACAAAACCTATAAATCTGGCTTACTGCACATATTAGTGTGTT
WI-7220	140	A T	---			AGGATGATGCTCCAAAAGGGGACCTTGAACCTATTACCAATTAATTTGCTCTTTAAGCTGGCAACCCA TCATTAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGC[AT]CTAGAAAATCTTGAGCACAGTGAATGACCTATCTGCAACATCTAATGGATCTCTA AAGGTAACAAAACCTATAAATCTGGCTTACTGCACATATTAGTGTGTT
WI-7226	232	C	---			GATCGAATTTTCAGATGATTCGGAATTTTCATTCAGGTAATTTGTAATAGTGACATATATGTATA TACATACACCTCTATCTCTAATTTTGTAAAATGTTAACTGGCAGTAAGTCTTTTGTGATCATTT CCCTTTCCATATAGGAAACATAATTTGAAGTGGCCAGATGAGTTTATCATGTGTCAGTGAAAAATAA TTAGCCACAAATGCCACCAGTAACGATTCCTCACTTCTGGGGTTT
WI-7228b	254	G A	---			ATAGCTTCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACCAGTAATTTGGCTCCAAATTCATAA TATGTTCCACGAGGATACAAATTTTGTCTCTTGTCTTTGTAATCTATTTAGTTGATTTTAATTA CTTTCTGAATAACGGAAGGATCAGAAGATATCTTTGTGCTAGATTGCAAAATCTCCAATCCACA CATATTGTTTAAATAGAAATGTTATCCAACATTAAGATATCTCAATGT
WI-7228a	163	G A	---			ATAGCTTCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACCAGTAATTTGGCTCCAAATTCATAA TATGTTCCACGAGGATACAAATTTTGTCTCTTGTCTTTGTAATCTATTTAGTTGATTTTAATTA CTTTCTGAATAACGGAAGGATCAGAA[G/A]ATATCTTTGTGCTAGATTGCAAAATCTCCAATCC ACACATATTGTTTAAATAAGAAATGTTATCCAACATTAAGATATCTCAA
WI-7233c	213	C T	---			CGATCGTACTGCCAGTAGCATTTGTCTGTCTGCGGCTTTGTTGATCATTCATTTCAATTTGTACA GATGTGAACCTTTATCTCTGTCACTAATTAATTTAAATTAATTTCTAGGAAGTCAAAAAATATAA TAAAGGTTGAGCCCTCTACTTTCTTCTGCCACCTTTTGTGGCAATATTAAAGTGAAGTGAAGTGA GTGTAAGT[AT]GTGCACAAAACCACTGCCAGATAACCCAGAGGGGCTG

WI-7233b	213	C T	---	---	CGATCGTACTGCCAGTAGCATTGTCTGTCTGTCGGTCTTTGTGTACATCCATTTCAATTGTTACA GATGTGAACCTTTATTCCTTGTCACTAATTATATTTAAATATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTTCTCTTGCCACCTTTTGTGGCAATATTAAAGTGAAGTGTCTAATA GTGTAAAGTATCTGTGCACAAAACCACTGCCAGATAACCCAGAGGGGCTG
WI-7233	211	T C	---	---	CGATCGTACTGCCAGTAGCATTGTCTGTCTGTCGGTCTTTGTGTACATCCATTTCAATTGTTACA GATGTGAACCTTTATTCCTTGTCACTAATTATATTTAAATATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTTCTCTTGCCACCTTTTGTGGCAATATTAAAGTGAAGTGTCTAATA GTGTAAAGTATCTGTGCACAAAACCACTGCCAGATAACCCAGAGGGGCTG
WI-7238	128	T C	---	---	GGTCTACAGACAGCTCACCATTTTGTCTGTATCTGTAAACACTTTTGTCTTAGTCTTTTCTTG TAAATTGATGTTCTTTAAATCGTTAATGTATAACAGGGCTTATGTTTCAGTTTGTCTT/CJCCGTT CTGTTTAAACAGAAAATAAAGGAGTGAAGTCTCTTTCTCATTTCAAAGTGTCTACCAGTGTAT GCAGTAATTAGAACAAAGAAACAATTCAGTAGAACATTTTATTCGCTA
WI-7252f	520	T C	---	---	CCACGAGGATCCAGCCCAAGCGGCCCCCTCCCGCCCCCTCCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCCCGGCGCCAGCCCGGGCCCTGGCTGGAGGCTGCCCGGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGAGCCCTAGAGCCTGCCTGGAGCGTTCTAGCAAGTGAAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACTCAGTCAATTAGACTCCTCTCCA
WI-7252g	552	T C	---	---	CCACGAGGATCCAGCCCAAGCGGCCCCCTCCCGCCCCCTCCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCCCGGCGCCAGCCCGGGCCCTGGCTGGAGGCTGCCCGGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGAGCCCTAGAGCCTGCCTGGAGCGTTCTAGCAAGTGAAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACTCAGTCAATTAGACTCCTCTCCA
WI-7252d	540	T C	---	---	CCACGAGGATCCAGCCCAAGCGGCCCCCTCCCGCCCCCTCCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCCCGGCGCCAGCCCGGGCCCTGGCTGGAGGCTGCCCGGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGAGCCCTAGAGCCTGCCTGGAGCGTTCTAGCAAGTGAAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACTCAGTCAATTAGACTCCTCTCCA
WI-7252c	552	T C	---	---	CCACGAGGATCCAGCCCAAGCGGCCCCCTCCCGCCCCCTCCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCCCGGCGCCAGCCCGGGCCCTGGCTGGAGGCTGCCCGGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGAGCCCTAGAGCCTGCCTGGAGCGTTCTAGCAAGTGAAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACTCAGTCAATTAGACTCCTCTCCA
WI-7252b	540	T C	---	---	CCACGAGGATCCAGCCCAAGCGGCCCCCTCCCGCCCCCTCCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCCCGGCGCCAGCCCGGGCCCTGGCTGGAGGCTGCCCGGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGAGCCCTAGAGCCTGCCTGGAGCGTTCTAGCAAGTGAAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACTCAGTCAATTAGACTCCTCTCCA

WI-7252a	520 T C ---	---	CCACAGATCCACGCCAAGCGGCCCTCCGCCCTCCCACTCGCAGACGCGCGGGACAGAG GCCTGCCGGCGCGCCAGCCCGGCCCTGGGCTGGAGGCTGCCCCGGCCCCCTGCTCTCTGGTCOG GACACTCCTAGAGAACGCGAGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCACTAGACTCCTCCTCCA
WI-7265m	252 T A ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCTTCTGTGGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATATTTATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCTT
WI-7265l	231 T A ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCTTCTGTGGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATATTTATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265k	121 T G ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCTTCTGTGGTTCAATTGTA GTTTAAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATATTTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265j	174 T A ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCTTCTGTGGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATATTTATGTAATAATAACGATCTCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265i	227 T C ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCTTCTGTGGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATATTTATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265h	80 T A ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCTTCTGTGGTTCAATTGTA GTTTAAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATATTTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265g	170 T G ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCTTCTGTGGTTCAATTGAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATATTTATGTAATAATAACGATCTCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT

WI-7265f	231 T A	AAC TTGGTATGTGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGATGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATTATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTT/AAGGGAGTAAAGATTGTCCT
WI-7265e	227 T C	AAC TTGGTATGTGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGATGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATTATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTT/CCTTTAAGGAGTAAAGATTGTCCT
WI-7265d	174 T A	AAC TTGGTATGTGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGATGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATTATATGTAATAATAACGATCTCTT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGTCCT
WI-7265c	170 T G	AAC TTGGTATGTGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGATGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATTATATGTAATAATAACGATCTCTT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGTCCT
WI-7265b	121 T G	AAC TTGGTATGTGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGTA GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATTATATGTAATAATAACGATCTCTT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGTCCT
WI-7265a	80 T A	AAC TTGGTATGTGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTT/AJTATTTGCCACCAAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGTA GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATTATATGTAATAATAACGATCTCTT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGTCCT
WI-7281b	183 C	GATCACCCAGCCACAAAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGAGCCAAAGC ATCTTCCTGGGAAGTCTTTCTGGCCAAAGTCTGGCCAGCCTGGCCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTCCTTGGCAAAAACGGAGTCCGCGAGGCCGAG GTGTTGTGAAGACCACCTGTTCTGTGGTGGGGTCTCTGCAAGAGGCCCTCCTC
WI-7281	171 C A	GATCACCCAGCCACAAAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGAGCCAAAGC ATCTTCCTGGGAAGTCTTTCTGGCCAAAGTCTGGCCAGCCTGGCCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTC/AJTGGCAAAAACGGAGTCCGCGAGGCCG CAGGTGTTGTGAAGACCACCTGTTCTGTGGTGGGGTCTGCAAGAGGCCCT

WI-7282b	159	GC	---			TGTCACCTGGCACATTCTTCAGTTGAAGAAGAGAAAAATTTGAAAAATGTCCTTATGCTTTTAGA GTTGCAACTTAAGTATATTTGGTAGGTGAGTGTTCCCACTCAAAATATGTCAACTNNNNNNNT AGGCCCTTTCATAAAACCAAACCTG/CJTAGCAAGATGCAAAATGCATGGCAAAATCTGTCGGTCTCCA GTTGGTTATCTGAATAGTGTACCAAAATCCACCAAGACAGTGTGAGATTGG
WI-7292	92	TC	---			CTTGATTACTCCACTGAGGTGGGAGCATCTCCAGTGTCCCAATATATCTCCCCACTCCACTAG TCTCTTCCCTCCACTTCAITTTCC/CJTTGTCTTCTCTCTAATTCAGTGTTTGGAGGCTGACTTG GGGACAACGATTTATGATATATTGCTGTTTCTCTTCCCAATAGAATAAGTGCATGGAGCC TGAAGGGTGCCTAGTTGACTTACTGACAAAAGGCTAGTTGGGCTGA
WI-7301f	133	AG	---			AACTATGGCAGTGGTCTGTTATAGTAGTAGAGGGGGTATGGTGGTGGACCAAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTG A/GJCGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCA ATCAAAATTATGGACACATGAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301e	94	TG	---			AACTATGGCAGTGGTCTGTTATAGTAGTAGAGGGGGTATGGTGGTGGACCAAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTG/CJTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTT TGACGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301d	138	AG	---			AACTATGGCAGTGGTCTGTTATAGTAGTAGAGGGGGTATGGTGGTGGACCAAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGTG/CJGTAACTATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301c	211	AC	---			AACTATGGCAGTGGTCTGTTATAGTAGTAGAGGGGGTATGGTGGTGGACCAAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAATCA AATTATGGAC/CJCATGAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301b	182	CT	---			AACTATGGCAGTGGTCTGTTATAGTAGTAGAGGGGGTATGGTGGTGGACCAAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301	88	GT	---			AACTATGGCAGTGGTCTGTTATAGTAGTAGAGGGGGTATGGTGGTGGACCAAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTG/CJCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTT TGACGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG

WI-7301	205 A C ...			AACTATGGCAGTGGTCTGGTTATAGTAGAGGGGGTATGGTGGTGGACCCAGGATATGGAA ACCAAGTGGTGGATATGGTGGCGGTGTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTGA CGGTAGTAACATATGGTGGTGGGAACATAATGATTTTGGAAATACAGTGGACAACAGCAATCA AATTACITGGACACATGAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7314c	49 G A ...			CTCTCTTTTTTCTTCAGATCTGCTCCTGGGTTTAAATTTGGGAGGTCA[G/ATTTGTTCTACCTCACTG AGAGGAAACAGAAAGGATATTGCTCTCTTTGCAGCAGTGAATAAAGTCAATTAATAACTTCCCAGG ATTTCTTTGGACCCAGGAAACAGCCATGTGGTCTCTTCTGTGCACATGAACGCTTCTTTCCCAGGA CAGAAATGTGTAGTCTACCTTATTTTTTATTACAAAACCTGTTTTT
WI-7314b	49 G A ...			CTCTCTTTTTTCTTCAGATCTGCTCCTGGGTTTAAATTTGGGAGGTCA[G/ATTTGTTCTACCTCACTG AGAGGAAACAGAAAGGATATTGCTCTCTTTGCAGCAGTGAATAAAGTCAATTAATAACTTCCCAGG ATTTCTTTGGACCCAGGAAACAGCCATGTGGTCTCTTCTGTGCACATGAACGCTTCTTTCCCAGGA CAGAAATGTGTAGTCTACCTTATTTTTTATTACAAAACCTGTTTTT
WI-7314	36 A G ...			CTCTCTTTTTTCTTCAGATCTGCTCCTGGGTTTAA[G/ATTTGGGAGGTCAAGTTGTTCTACCTCACTG AGAGGAAACAGAAAGGATATTGCTCTCTTTGCAGCAGTGAATAAAGTCAATTAATAACTTCCCAGG ATTTCTTTGGACCCAGGAAACAGCCATGTGGTCTCTTCTGTGCACATGAACGCTTCTTTCCCAGGA CAGAAATGTGTAGTCTACCTTATTTTTTATTACAAAACCTGTTTTT
WI-7321b	199 C T ...			ACTCAGGGAAGGGATGCCCCATTAAAGTGACAAAAGGGTGGGTGGGCACCATGGCATGAGGAAG AAACAAGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGACTGCTTTGGCATCCAGGGCCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNNAGGGTGGCACACCCATC[C /T]GTTGCTGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7321	199 C T ...			ACTCAGGGAAGGGATGCCCCATTAAAGTGACAAAAGGGTGGGTGGGCACCATGGCATGAGGAAG AAACAAGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGACTGCTTTGGCATCCAGGGCCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNNAGGGTGGCACACCCATC[C /T]GTTGCTGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7336b	248 A C ...			AGACATTCTCGTTCCTGAAAGACTGAAGAAAGTGTAGTGCATGGGACCCACGAAACTGCCCTGGC TCCAGTGAACCTGGGCACATGCTCAGGCTACTATAGTCCAGAAAGTCCCTTATGTTAAGCCCTGGCAG GCAGGTGTTTATTAAATCTGAATTTGGGATTTTCAAAGATAATATTTACATACACTGTATGT TATAGAATTCATGGATCAGATCTGGGGCAGCAACCTATAATCA[A/C]CA
WI-7338c	221 A G ...			CTCTTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTAAACTCTACCATGGATAATGCA AACAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGCAGAGAAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTGTTCTCTTTACACAC[A/G]TATACACACAGACATCAGAAAATTTCTGTT

WI-7338b	125 A C ---			CTCTTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATAATTGGCAAAAGGTGCTTT[A/C]CCTTG AGCCATTATTTGTGTGAGAGAACAAAGAAACAGAATCAATATATAAATCAAAGACTATCTGCAG CTAGTGTCTTCTCTTTACACACATATACACAGACATCAGAAAATTCTGTT
WI-7338	125 A C ---			CTCTTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATAATTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTGAGAGAACAAAGAAACAGAATCAATATATAAATCAAAGACTATCTGCAGCTA GTGTTCTCTTTACACACATATACACAGACATCAGAAAATTCTGTT
WI-7338	221 A G ---			CTCTTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATAATTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTGAGAGAACAAAGAAACAGAATCAATATATAAATCAAAGACTATCTGCAGCTA GTGTTCTCTTTACACACATATACACAGACATCAGAAAATTCTGTT
WI-7384c	146 T A ---			CCTATGTCATGAATGCTAGGGGCCAGGGAACAAAATTTTAAATAATAAATTCACCATAG CAATACAGAAATACCTTTAAATACCATTAATACATTTGATTTTCAATTTGTAACAGGTATTTCTTCA CAGATCTCATTTT[A/J]AAATCTTAAATGATTATTTTACTTACTGTTTAAAGGGATGTTA TTTTAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7384b	146 T A ---			CCTATGTCATGAATGCTAGGGGCCAGGGAACAAAATTTTAAATAATAAATTCACCATAG CAATACAGAAATACCTTTAAATACCATTAATACATTTGATTTTCAATTTGTAACAGGTATTTCTTCA CAGATCTCATTTT[A/J]AAATCTTAAATGATTATTTTACTTACTGTTTAAAGGGATGTTA TTTTAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7384	145 T A ---			CCTATGTCATGAATGCTAGGGGCCAGGGAACAAAATTTTAAATAATAAATTCACCATAG CAATACAGAAATACCTTTAAATACCATTAATACATTTGATTTTCAATTTGTAACAGGTATTTCTTCA CAGATCTCATTTT[A/J]AAATCTTAAATGATTATTTTACTTACTGTTTAAAGGGATGTTA TTTTAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7388c	106 A T ---			TGAAATCTGGGTCTCTGGCCTGCTGTAGCTGTTATTTTACTTTGCCCTCCCTCTTTT TGAGATCCATCCTTTATCAAGAAGCTGAAGCGACT[A/T]TAAAGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAAGGTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTGA CTTGTGCTGTCCAGAAGCTTTCCCTCCAAAGATGTATAGTTATTGG
WI-7388b	106 A T ---			TGAAATCTGGGTCTCTGGCCTGCTGTAGCTGTTATTTTACTTTGCCCTCCCTCTTTT TGAGATCCATCCTTTATCAAGAAGCTGAAGCGACT[A/T]TAAAGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAAGGTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTGA CTTGTGCTGTCCAGAAGCTTTCCCTCCAAAGATGTATAGTTATTGG

WI-7388	94 T A ...	---	TGAAATCCTGGGCTCTTGGCCTGCTGTAGCTGGTTATTTTACTTTGCCCCCTCCCCACTTTT TGAGATCCATCCCTTTATCAAGAAGT[A]CTGAAGCGACTATAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAAGTTACCTCTATTTGCCACAAGCGTCTGGGATTGTGTTGA CTTGCTGTCTGTCAGAACTTTTCCCCCAAGATGTGTATAGTTATGG
WI-7438	64 A G ...	---	TTAGATTTTAAATGGCAACCACTCACTGCCACCTTCCACTGCAGATCTNCTATTCTCTGG[A/G] GTTGATATGACAAGGAACCTATTGGAACCAAGTCTTCAGATTGNCCTGTGCAGACAGGCTCCT TGCTGTAGGTGTAGTAGCATGTACACTGTACTGTCTACTGTAACATAGTTGTNCTGGTATTTGTTA TTGGAATGAATATCGCTTCCACTGACTTTTACCA
WI-7454b	152 T C ...	---	CCATGATCCCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAGCCCCAAACC CAGTACAAACTGAGAAATGAGAGAACCCCTGATAGCACTGTCTGAATGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTCTT[C]GTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCATTTGTCTACTTCTCAAAATGTTTTTGACA
WI-7454	152 T C ...	---	CCATGATCCCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAGCCCCAAACC CAGTACAAACTGAGAAATGAGAGAACCCCTGATAGCACTGTCTGAATGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTCTT[C]GTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCATTTGTCTACTTCTCAAAATGTTTTTGACA
WI-7464c	177 G C ...	---	AATTTGAAAATCTGAAAAAAGTGCATAAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACAATGCATAAATTAATTTTAAATTCCTATGTA CAACAGAGCCACAGCAAGAGGGTGGGCATAAGCAGTTGCCA[G/C]CCAGAAGAGCTTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGGCAACGTTCAACCAAAATTAT
WI-7464b	168 C A ...	---	AATTTGAAAATCTGAAAAAAGTGCATAAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACAATGCATAAATTAATTTTAAATTCCTATGTA CAACAGAGCCACAGCAAGAGGGTGGGCATAAG[C/A]AGTTGCCAGCCAGAGAGCTTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGGAGCAACGTTCAACCAAAATTAT
WI-7464a	103 C A ...	---	AATTTGAAAATCTGAAAAAAGTGCATAAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACAATGC[A/A]ACTAAATTAATTTTAAATTCCTAT GTACAACAGAGCCACAGCAAGAGGGTGGGCATAAGCAGTTGCCAGCCAGAGAGCTTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGGAGCAACGTTCAACCAAAATTAT
WI-7499b	134 T G ...	---	CAATTCCTCAATCCAACCTAGTCTGTNTGCCATAACCTTCCAGACAACCTCCACTCGAAGGTTTTA AATGCATAAGTCAGATAGCAATCCTTCAGTTGCCAGAGGCACATCACGTTCTTTGAATGCTTCAIT /GJTATAGTCTCTTCATTAGCAATCAGTGAGGCAATACACTGGCATCATGCCCTTTTTTTAGGA ACTCTGTACAAAAATCCCTTTGAAAAATATAAAATTTTGGAAATGAGTGATGA

WI-7499a	33 A G ...				CAATTCTCAATCCAACTAGTCTGNTGCCTAA[A/G]CCATTCCAGACAAACTTCCACTTCGAAGGTT TTAAATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCAGCTTCTTTGAATGCTTC ATTATAGTCTCTTCATTTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTTAGGAA CTCTGTACAAAATTCCTTTGAAAATATAAAATTTGGAAATGAGTGATGA
WI-7506b	118 A C ...				TGGGAATAGTAAGAGAAAGATGGGAAAGGTGACCAAAACAATATAGAGGCAGAGGCCAAAGTGAAT GCATCCCAGCAGCAGACCACTTNAAGTAGTCTGGTCTGATTGCCTAGC[A/C]GGAGAGTTGAG TGCCACAGGTAAGATGAGTGAAGAGGAAATAATCATGATGTCATGATGCAGTAATTACTATGTCA GAAGAAAATATTTTAAATATTGGACCACCTCTTGTCTACCATCCCTACCCACT
WI-7506	118 A C ...				TGGGAATAGTAAGAGAAAGATGGGAAAGGTGACCAAAACAATATAGAGGCAGAGGCCAAAGTGAAT GCATCCCAGCAGCAGACCACTTNAAGTAGTCTGGTCTGATTGCCTAGC[A/C]GGAGAGTTGAG TGCCACAGGTAAGATGAGTGAAGAGGAAATAATCATGATGTCATGATGCAGTAATTACTATGTCA GAAGAAAATATTTTAAATATTGGACCACCTCTTGTCTACCATCCCTACCCACT
WI-7534b	143 C T ...				TGTGAATCTTAGCTCTGGAAGGTGTTATGCCCTTTCGGGTTCTTGATGTTCCGAGTGTCAACCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCCGTGGAACACATCCCGGTGATAGAAATGCT AAATTGT[C/T]GTGAAATAGGTAGAAATTTCTTTAAATATGTTTTCTTATTTCGTGAAAAATTCGG AGAGTGTCTGCTAAAATTTGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7534	135 T C ...				TGTGAATCTTAGCTCTGGAAGGTGTTATGCCCTTTCGGGTTCTTGATGTTCCGAGTGTCAACCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCCGTGGAACACATCCCGGTGATAGAAATGCT /C/JAAATTGTCTGTAATAGGTAGAAATTTCTTTAAATATGTTTTCTTATTTCGTGAAAAATTCGG AGAGTGTCTGCTAAAATTTGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7543b	162 G A ...				GGGAAAGAAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACC AGTCTGTTTGCAGGGAAGCCCCACTTGAAGGAAGTCTAAGAGTGAAGTAGGTGACTTTGAAC TAGATTGCATGCTTCTCTCTTCTCTTGAAGAACCCAGCTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTTCTCTGGCTCCTTGGATGTAGTCAGTTA
WI-7543	162 G A ...				GGGAAAGAAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACC AGTCTGTTTGCAGGGAAGCCCCACTTGAAGGAAGTCTAAGAGTGAAGTAGGTGACTTTGAAC TAGATTGCATGCTTCTCTCTTCTCTTGAAGAACCCAGCTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTTCTCTGGCTCCTTGGATGTAGTCAGTTA
WI-7555c	60 T C ...				GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTC/JCTA AAAAGAAAGTGGTATGTTGTGTGATGATCAGCACTAAGTCTGATTCCTGTTAAAGCCACTTGGGTC ATAAGAGGGGAAGTAAATAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTGATTTTGAATTCAG

WI-7555b	60 T C	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATTCTCCCTCAAAATTTGTAGAGGTCCTCTA AAAAGAAAGTGGTATGTTGTGATGATCAGCACTAAGTCTCGCATCTCTGTTAAAGCCACTTGGGTC ATAAGAAAGGGAAGTAAAAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTGCAATTTGAATTTGAG
WI-7555	60 T C	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATTCTCCCTCAAAATTTGTAGAGGTCCTCTA AAAAGAAAGTGGTATGTTGTGATGATCAGCACTAAGTCTCGCATCTCTGTTAAAGCCACTTGGGTC ATAAGAAAGGGAAGTAAAAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTGCAATTTGAATTTGAG
WI-7567b	290 G T	TGAGCCATCACTAGAAAGAAAGCCATTTTCAACTGCTTTGAACTTGCCTGGGCTGAGCATGAT GGGAATAGGGAGACAGGGTAGGAAAGGGCGCTACTCTTCAGGGTCTAAAGATCAAGTGGCCTTGG ATCGCTAAGCTGGCTGTTTATGCTATTTATGCAAGTTAGGCTCTATGTTATTTAGGATGCGCTAC TCTCAGGGTCTAAAGATCAAGTGGGCTTGGATCGTAAAGCTGGCTCTGTTT
WI-7569b	63 T C	AATGTATCCCTTTCGGTCCAAACAGGAAACCTGACTGGGCGAGTGAAGGAAGGGATGGCA(T/C) AGCGTTATGTGTA AAAAACAAGTATCTGTATGACAACCCGGGATCGTTTGCAGTAAGTAACTGAATCCAT TGGACATTTGTGAAGCTTAAATGAGTTTAGTGGAAATAGCGTTGTTATCGCCTTGGGTTTAAAT ATTTGATGATTCACITGTATCATGCGCTACCGAGGAGAGAGGATTTG
WI-7574c	216 A G	GCCACAGCAGAATGGAGCGGTGTGAGGAAGTCCCTTTCTCTGTTTGTGTTGCCAAGGCCAAAC TCCCACTCTGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAATCATTTTG TACCACCTTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTTCTTG ATAGCCCAGGGC(A/G)TCTGCTGGGCTGACCACGTTACTCATCCCCGTTA
WI-7574b	216 A G	GCCACAGCAGAATGGAGCGGTGTGAGGAAGTCCCTTTCTCTGTTTGTGTTGCCAAGGCCAAAC TCCCACTCTGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAATCATTTTG TACCACCTTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTTCTTG ATAGCCCAGGGC(A/G)TCTGCTGGGCTGACCACGTTACTCATCCCCGTTA
WI-7574	216 A G	GCCACAGCAGAATGGAGCGGTGTGAGGAAGTCCCTTTCTCTGTTTGTGTTGCCAAGGCCAAAC TCCCACTCTGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAATCATTTTG TACCACCTTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTTCTTG ATAGCCCAGGGC(A/G)TCTGCTGGGCTGACCACGTTACTCATCCCCGTTA
WI-7576c	168 A T	AATGATGATGATAATGATGATGACGACGACACGATGATGCTTGTAAACAAGAAACATAAGAGAGC CTTGGTTTCATCAGTGTAAAAATTTTGAAGGGCGGTACTAGTTGACACACTTTGGAAGTTTGTGT TCTGTTTGTAAACTGGCATCTGACACAAAAA(A/T)GTTGAAGGCCCTTATTCTACATTTACCTAC TTTGTAAAGTGAGAGACAAGAACGCAANNNNNNNNNNAAGAAAAAATAAAC

WI-7576b	168 A T ---	---	AATGATGATGATAATGATGATGACGACGACACGATGATGCTGTAAACAAGAAACATAAGAGAGC CTTGGTTTCATCAGTGTAAAAAATTTTGAAGGCGGTACTAGTTTCAGACACTTTGGAAGTTTGTT TCTGTTTGTAAACTGGCATCTGACACAAAAAAAT/GTTGAAGGCCCTTATTCATATTCACCTAC TTTGTAAAGTGAGAGACAAAGCAAAANNNNNNNNNNAAGAAAAATAAAC
WI-7577g	77 T C ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTAA AAATATGCAAT/CJCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577p	50 G C ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTAA TAAAAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577o	157 G A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAATAA AGAAGTTCAATTTGGTTTACAC/GJTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577n	48 A G ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTAA TAAAAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577m	84 G A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTAA AAATATGCATCAAAATC/GJATCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577l	93 T C ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577k	154 C A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAATAA AGAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC

WI-7577j	117 A G ...	---	AACCATGTTCCCTTCTTCTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTA/GJACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577i	77 T C ...	---	AACCATGTTCCCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTTAA AAATATGCAT/GJCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577h	50 G C ...	---	AACCATGTTCCCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTTAA TAAAAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577g	157 G A ...	---	AACCATGTTCCCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AGAAGTTCAATTTGGTTTACAC/GJATAGGAAGAAGAGAGAGCATCAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577f	48 A G ...	---	AACCATGTTCCCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTTAA TAAAAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577e	84 G A ...	---	AACCATGTTCCCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTTAA AAATATGCATCAAAATCG/JTCTCTCATTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577d	93 T C ...	---	AACCATGTTCCCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577c	154 C A ...	---	AACCATGTTCCCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AGAAGTTCAATTTGGTTTAC/JACGTAGGAAGAAGAGAGAGCATCAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC

WI-7577b	117 A G ---	---	AACCATGTTCCCTTCTTACACACAAATATCAAAACCCCAACATAAGTGTGCTTCCCTTAA AAATATGCATCAATCGTCTCATTTCTCTGAGGTTTGTAGTA/GJACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATGACTGATTTTC
WI-7577	107 G A ---	---	AACCATGTTCCCTTCTTACACACAAATATCAAAACCCCAACATAAGTGTGCTTCCCTTAA AAATATGCATCAATCGTCTCATTTCTCTGAG[GJA/GJTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATGACTGATTTTC
WI-7619q	106 C G ---	---	ACAAGCGGACTTGAAGAGGACGCGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAGGGCCAAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATAC ATGGCAGGAAGATGGGCCCTTAAGGGAGTGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCT CTCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619p	150 T C ---	---	ACAAGCGGACTTGAAGAGGACGCGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAGGGCCAAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGCCCTTAAGGGAGTGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCTC TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619o	228 A G ---	---	ACAAGCGGACTTGAAGAGGACGCGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAGGGCCAAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGCCCTTAAGGGAGTGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCTCT CGCTTCTTCTTACACAGAAACAT/GJACATACCGAGAAACCTATTTC
WI-7619n	237 G C ---	---	ACAAGCGGACTTGAAGAGGACGCGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAGGGCCAAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGCCCTTAAGGGAGTGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCTCT CGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619m	99 C T ---	---	ACAAGCGGACTTGAAGAGGACGCGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAGGGCCAAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACAT TGGCAGGAAGAAATGGGCCCTTAAGGGAGTGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCTC TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619l	189 T A ---	---	ACAAGCGGACTTGAAGAGGACGCGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAGGGCCAAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGCCCTTAAGGGAGTGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCTC TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619k	90 C G	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCAATCCG/GTCCCTAACGAGACTCTGTGCTGGGGTGTCTAATTAC ATGGCAGGAAGAAATGGGGCTCTAAGGGGAGTGTGGGTGTCTCTCCCTTTTCCATCTTTTCTCT CTCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619l	206 T G	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGTGGGTGTCTCTCCCTTTTCCATCTTTTCTCTCTCT CGCT/GTTCCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619i	106 C G	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTGCTGGGGTGTCTAATTACATGG ATGGCAGGAAGAAATGGGGCTCTAAGGGGAGTGTGGGTGTCTCTCCCTTTTCCATCTTTTCTCTCT CTCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619h	150 T C	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGTGGGTGTCTCTCCCTTTTCCATCTTTTCTCTCTCT TCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619g	228 A G	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGTGGGTGTCTCTCCCTTTTCCATCTTTTCTCTCTCT CGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619f	237 G C	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGTGGGTGTCTCTCCCTTTTCCATCTTTTCTCTCTCT CGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619e	99 C T	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTGCTGGGGTGTCTAATTACATGG TGGCAGGAAGAAATGGGGCTCTAAGGGGAGTGTGGGTGTCTCTCCCTTTTCCATCTTTTCTCTCT TCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619d	189 T A	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGTGGGTGTCTCTCCCTTTTCCATCTTTTCTCTCTCT TCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619c	90 C G ---	---	ACAAGCGGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGTATCC[C/G]CTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCT CTCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619b	208 T G ---	---	ACAAGCGGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCTCTCT CGCT[G]TCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619	189 T A ---	---	ACAAGCGGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCTCTCT TCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7626d	105 A G ---	---	CCTTTGATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACCAAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTTGGC[G]TTAAACCAATCATGGACCAATGTG CCATACTAATGATGAGCAATTTAGCACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTTATTTATAGTAACCATTTTCCCTTGGACTGTTCA
WI-7626c	155 C T ---	---	CCTTTGATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACCAAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTTGGCATTAAACCAATCATGGACCAATGTGCCA TACTAATGATGAGCAATTTAG[C/T]ACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTTATTTATAGTAACCATTTTCCCTTGGACTGTTCA
WI-7626b	28 T A ---	---	CCTTTGATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACCAAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTTGGCATTAAACCAATCATGGACCAATGTGCCA TACTAATGAT[C/G]GAGCAATTTAGCACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTTATTTATAGTAACCATTTTCCCTTGGACTGTTCA
WI-7626	144 T C ---	---	TCCCATACCCGCTGATTCTCAGGGTCTGTCTGCCGCCCAACCCAGATGGGGAAAGCAGAGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTTCTCTAAAT /GJTAAGGGGAGAGTCACACTGGGCAGCTGATACAAATTCAGACTGTGTAAAGAGAGAGCTTAAT GATAATATTGGTGGCCCAAAATAAAATGGATTATTAGAAATTCATAIGAC
WI-7689c	134 A G ---	---	

WI-7689b	134 A G ...				TCCATAACCGCTGATCTCAGGGTCTCTGCTGCGGCCCCACCCAGATGGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGTTCTCTAAAJA /GJTAAGGGCAGAGTCACACTGGGCGAGCTGATACAAATTGCAGACTGTGTAAAAAGAGAGCTTAAT GATAATATTGTGGTGGCCACAAATAAATGGATTATTAGAATTTTCATATGAC
WI-7689	121 G A ...				TCCATAACCGCTGATCTCAGGGTCTCTGCTGCGGCCCCACCCAGATGGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGTTCTCTAA AATAAGGGCAGAGTCACACTGGGCGAGCTGATACAAATTGCAGACTGTGTAAAAAGAGAGCTTAAT GATAATATTGTGGTGGCCACAAATAAATGGATTATTAGAATTTTCATATGAC
WI-7690	45 G A ...				TGGAGAACATTCAATCTTCCGTCACATTCATCAATGAAGATTAGJACACTGAGATCCAGAGAGG CTGGATGACTTGTCAAGTTCCAGCATGTTAGTGGCAAGAGAGGTCAGAGTCTGGCCCTTGAT GCCAGCTCAGTCCACAAAGCTCAGTAGGAGGATGTTCCAGTGATGAGGCCACCCAGGAAGCAC AGGTCCAAGGCTGGTCCACACTTATCAGCAGCAACAACCTGTCAGTTTCATCC
WI-7703b	164 T C ...				ACAGAAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTTCACATTTGGAACAAGTCAGTCATTGATGATGATTCAAA TGCTATAAACCAAACTGATGTAAGTAAATJ/CJGGTCTCTCAGTTGTTTATTTAACCTCTAAATTCT TTCATTTAGGGGTAGCATTTGTGTTGAAGAGGTTTAAAGCTTCCATTGT
WI-7703	158 T C ...				ACAGAAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTTCACATTTGGAACAAGTCAGTCATTGATGATGATTCAAA TGCTATAAACCAAACTGATGTT/CJAGTAAATGGTCTCTCAGTTGTTTATTTAACCTCTAAATTCT TTCATTTAGGGGTAGCATTTGTGTTGAAGAGGTTTAAAGCTTCCATTGT
WI-7743e	106 C A ...				TAAATGAGTGTGTTTGTACCCGTTGGGATTGGGAAGACTGTGGCTGCTGGCAGTTGGAGCCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC/CJ/CJCCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATCTGCTACCTCAGTGGGTCTCTGGGGCTCGGAGCCTCATCCGAGGCGGGTCAGGA GAGGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743d	275 C T ...				TAAATGAGTGTGTTTGTACCCGTTGGGATTGGGAAGACTGTGGCTGCTGGCAGTTGGAGCCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC/CJ/CJCCAGGAGTCCCTGGTAATAAGTACT TACAGAAATCTGCTACCTCAGTGGGTCTCTGGGGCTCGGAGCCTCATCCGAGGCGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743e	106 C A ...				TAAATGAGTGTGTTTGTACCCGTTGGGATTGGGAAGACTGTGGCTGCTGGCAGTTGGAGCCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC/CJ/CJCCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATCTGCTACCTCAGTGGGTCTCTGGGGCTCGGAGCCTCATCCGAGGCGGGTCAGGA GAGGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC

WI-7743d	275 C T ---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCAGCACTAAGCAGTGGAGCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743e	106 C A ---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCAGCACTAAGCAGTGGAGCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GTGTACAGAAATCTGCTACCTACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGGCC
WI-7743d	275 C T ---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCAGCACTAAGCAGTGGAGCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743c	106 C A ---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCAGCACTAAGCAGTGGAGCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGGCC
WI-7743b	275 C T ---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCAGCACTAAGCAGTGGAGCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743	106 C A ---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCAGCACTAAGCAGTGGAGCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGGCC
WI-7743	275 C T ---	---	---	TTAAATGAGTGTGTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCAGCACTAAGCAGTGGAGCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7758	144 A G ---	---	---	TGACATTTATTCAAAGTTAAAGCAACACATTACAGAAATTATGAAGAGGTATCTGTTTAAACATTCC TCAGTCAAGTTCAGAGTCTTCAGAGACTTCGTAATTAAGGAACAGAGTGAGAGACATCATCAAGTG GAGAGAAATC/GJTAGTTTAACTGCATTATAAATTTTATAACAGAAATTAAGTAGATTTTAAAA GATAAATGTGTAATTTTGTATATTTCCCATTTGGACTGTAACTGACTGCC

WI-7765b	126	GC	---	---	ACAGGGCCTTTGGCAGGTGCAGCCCCCACTGCCCTTTGACCTGCCCTCCCTTCATGCATGGAATTCCTCTCATCTGGAACCATCAGAAACACCCTCACACTGGGACTTGCAAAAAGGGTCAGTATGG[G/C]TTAGGGAACAATCCATCCTTGAAGTCAAAAATCTCAATCTCCCTATCTTGGCACCCCTCATGCTGTGTGACTCAAAACCAATCACTGAACCTTTGCTGAGCCTGTAAATAAAAGGTCGGA
WI-7773b	237	CG	---	---	TTAATTTACTGATTCCAGCAAGACCAATCATTTGTATCAGATTATTTTAAAGTTTTATCCGTAGTTTTGATAAAGATTTTCTATTCCTTGGTCTGTGAGAGAACCTAATAAGTGTACTTTGCCATTAAAGGCA GACTAGGGTTCAATGTCTTTTACCCCTTNNNNNNNNNTTGTAAAGTCTAGTACCTACTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTCAAGCA[G/C]TTTCGACGTTTGA
WI-7774b	170	TC	---	---	TGCAACCTCTTTTCGTGATGGGAGCCTGCTGGTGCAGCACTCCAGTAGCGAGAGACGGCACCCAGAATCAGATCCAGCTTCGGCATTGTATCAGACCAACAGTGTCTTCCGGGGAGGAAACACTTTTTTAA TTACCCCTTTGCAGGCACCACCTTTAATCTGTTT[C/JATACCTTGCTTTATAAATGAGCGACTTAAA ATGATTGAAAATAATGCTGTCTCTTAGTAGCAAGTAAATGTGCTTGCT
WI-7785c	165	G	---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATCTGTAAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATCTGTAAATGCATTGGAATAAACTGTCTCCCATTTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANNNNNNNNNNNGCCAAAGGCTAATCCAATTATTATCACATTTACCA TAATTTATTTTGCCATTGATGTATTATTTTGTAAATGTATCTTGGTGCTGC
WI-7785b	165	G	---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATCTGTAAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATCTGTAAATGCATTGGAATAAACTGTCTCCCATTTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANNNNNNNNNNNGCCAAAGGCTAATCCAATTATTATCACATTTACCA TAATTTATTTTGCCATTGATGTATTATTTTGTAAATGTATCTTGGTGCTGC
WI-7785	156	T	---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATCTGTAAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATCTGTAAATGCATTGGAATAAACTGTCTCCCATTTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANNI- /TNNNNNNNGCCAAAGGCTAATCCAATTATTATTCACATTTACCATAATTTATTTTGCCATTGA TGTATTTATTTGTAAATGTATCTTGGTG
WI-7789c	84	GA	---	---	TCCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCATCTTACAGAGACTCTCC TGACGGTGGAAATTTAA[G/A]TTAGGGTCCCTAAAAGCATTGACACACAGTTGTTGAATGACTGAC CAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCCTGGTGACTCGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT
WI-7789b	84	GA	---	---	TCCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCATCTTACAGAGACTCTCC TGACGGTGGAAATTTAA[G/A]TTAGGGTCCCTAAAAGCATTGACACACAGTTGTTGAATGACTGAC CAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCCTGGTGACTCGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT

WI-7789	73 GA ...			<p>TCTCCCTCATCCAACTCGAAAGTGTGAATCTCCAAAGGAGGACCACCTCTTACAGAGACTCTCCC TGACG(GA)GTGGAATTTAAGTTTAGGGTCCCTAAAGCATTTGACACACAGTGTGTTGAATGACTGAC CCAAA'GTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTCAGGCCGCTGCOCTAGGATAT GCCCTCCTGGTACTCGGGGCTGTCTCAGAGACTAGCCAGGACCCATCT</p>
WI-7790b	190 CT ...			<p>AATTGTCAGTCACCTCTTCAAACCTTACAGTCTTCTCCTAAGGTACTCTTCATGAGATTCCATT TACTAATAGTATTTTGGTGACTAGGCTTGCCTATGTGCTTATGTAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAAGTTGTGTTCTATTTCTTGAAGTCTC(T)TCTATACTTT AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC</p>
WI-7780	190 CT ...			<p>AATTGTCAGTCACCTCTTCAAACCTTACAGTCTTCTCCTAAGGTACTCTTCATGAGATTCCATT TACTAATAGTATTTTGGTGACTAGGCTTGCCTATGTGCTTATGTAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAAGTTGTGTTCTATTTCTTGAAGTCTC(T)TCTATACTTT AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC</p>
WI-7795b	81 CA ...			<p>CAGATGTTCTGGTAAACTGATTGCTGGCAACACAGATTCTCTGGCTCATATTTCTTTCTTCAT CTTGATGATGATC(A)GTGATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCACATATAAATGACTTTTCTCCAGAAAAATTCCTTGAGGAAAAATGTCCAAA TAAGATGAATCAC(T)TAATACCGTATCTTCTAAATTTGAAATATAATCTG</p>
WI-7795	81 CA ...			<p>CAGATGTTCTGGTAAACTGATTGCTGGCAACACAGATTCTCTGGCTCATATTTCTTTCTTCAT CTTGATGATGATC(A)GTGATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCACATATAAATGACTTTTCTCCAGAAAAATTCCTTGAGGAAAAATGTCCAAA TAAGATGAATCAC(T)TAATACCGTATCTTCTAAATTTGAAATATAATCTG</p>
WI-7814c	41 GA ...			<p>TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCG(GA)TTTCAATTTAGTCATGTGACCACTC TGCTTTGTGTTTCCACAGCCTGCAAGTTGAGTCCAGGATGCTAACATCTAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAACTTTAGAGAAGTATACATAAGTTAGGATAAAATAATGGGATTTTC TTTTCTTTCTCTGTAATATTGACTTGTATATTTTAAAGAAATAACAGAA</p>
WI-7814b	41 GA ...			<p>TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCG(GA)TTTCAATTTAGTCATGTGACCACTC TGCTTTGTGTTTCCACAGCCTGCAAGTTGAGTCCAGGATGCTAACATCTAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAACTTTAGAGAAGTATACATAAGTTAGGATAAAATAATGGGATTTTC TTTTCTTTCTCTGTAATATTGACTTGTATATTTTAAAGAAATAACAGAA</p>
WI-7814	28 GA ...			<p>TTCTCTCATTTTATCCCTCACCTGT(A)GATGCCAGTCCGTTTCAATTTAGTCATGTGACCACTC TGCTTTGTGTTTCCACAGCCTGCAAGTTGAGTCCAGGATGCTAACATCTAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAACTTTAGAGAAGTATACATAAGTTAGGATAAAATAATGGGATTTTC TTTTCTTTCTCTGTAATATTGACTTGTATATTTTAAAGAAATAACAGAA</p>

WI-7830d	150	C T	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAACG ATCCATAACTTTAGT[C/T]TAATGTACACATTGCATTTTGATAAAATTAATTTGTTGTTCCCTTTG AGTTGATCGTTGTGTTGTTGCTGCACTTTTACTTTTTGCGTGTGGA
WI-7830c	54	G A	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGATGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTGTTGTTCCCTTTG AGTTGATCGTTGTGTTGTTGCTGCACTTTTACTTTTTGCGTGTGGA
WI-7830b	134	G A	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAAC[G/A]ATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTGTTGTTCCCTTTG AGTTGATCGTTGTGTTGTTGCTGCACTTTTACTTTTTGCGTGTGGA
WI-7830	44	A G	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGATGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTGTTGTTCCCTTTG AGTTGATCGTTGTGTTGTTGCTGCACTTTTACTTTTTGCGTGTGGA
WI-7865e	25	C T	CCACTTCCTATCTGATTTTCCAG[C/T]AATGAGGAGGCAATTTCTAGTCTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAAGATTCAGGGTGTCTTCCAACTGAAATCTCAATCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTCTATTACCCAGTAAACCCAAA
WI-7865d	191	C T	CCACTTCCTATCTGATTTTCCAG[C/T]AATGAGGAGGCAATTTCTAGTCTCCACAAAACATCTA ATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGGGT ATGCTACTCATAAGATTCAGGGTGTCTTCCAACTGAAATCTCAATGTCTCAGT[C/T]GAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTCTATTACCCAGTAAACCCAAA
WI-7865c	25	C T	CCACTTCCTATCTGATTTTCCAG[C/T]AATGAGGAGGCAATTTCTAGTCTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAAGATTCAGGGTGTCTTCCAACTGAAATCTCAATGTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTCTATTACCCAGTAAACCCAAA
WI-7865b	191	C T	CCACTTCCTATCTGATTTTCCAG[C/T]AATGAGGAGGCAATTTCTAGTCTCCACAAAACATCTAGCC ATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGGGT ATGCTACTCATAAGATTCAGGGTGTCTTCCAACTGAAATCTCAATGTCTCAGT[C/T]GAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTCTATTACCCAGTAAACCCAAA

WI-7865	25 C T	---	---	CCACTTCTATCTGATTTTCCAGC/C/TAATGAGGAGGCAATCTAGTCTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCATTTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTATAAGATTTAGGGTGTCTTCCAACCTGAAATCTCAATGTTCTCAGTAGCAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865	191 C T	---	---	CCACTTCTATCTGATTTTCCAGCAATGAGGAGGCAATCTAGTCTCCACAAACATCTAGCC ATCTAAATGGAGAGATGAATCATTTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGGGT ATGCTACTATAAGATTTAGGGTGTCTTCCAACCTGAAATCTCAATGTTCTCAGTAC/C/TAAGAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7867c	92 A C	---	---	TTCAACACCTGTCTTCCACCTCCACCATCTGTGCAATCACTTACCCCTCAGCCTCAGTCTCCCC CTAACAATACCTGTCAAGAGG/C/AGAGTCAGCTCAGGTGGATTTAATGGGTTTAAATATGGC CTGTTGAGTTTAAATGTTAATGTTGATTTCTTTAAGTAACCATTTCTGTTCTGCTATAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7867b	92 A C	---	---	TTCAACACCTGTCTTCCACCTCCACCATCTGTGCAATCACTTACCCCTCAGCCTCAGTCTCCCC CTAACAATACCTGTCAAGAGG/C/AGAGTCAGCTCAGGTGGATTTAATGGGTTTAAATATGGC CTGTTGAGTTTAAATGTTAATGTTGATTTCTTTAAGTAACCATTTCTGTTCTGCTATAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7868c	173 C T	---	---	TTGATCGATCTTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGCTTT CACCCAACTGCTCCCTCTGATCTCCATCAGGGCCAGATCTCCAGTCTCCATCTCAGTACACAAT CAITTAATTTCCCTGTCTTACCCCTATTCAAGCA/C/TTAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7868b	173 C T	---	---	TTGATCGATCTTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGCTTT CACCCAACTGCTCCCTCTGATCTCCATCAGGGCCAGATCTCCAGTCTCCATCTCAGTACACAAT CAITTAATTTCCCTGTCTTACCCCTATTCAAGCA/C/TTAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7868	66 T C	---	---	TTGATCGATCTTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGCTTT /C/TCACCCAACTGCTCCCTCTGATCTCCATCAGGGCCAGATCTCCAGTCTCCATCTCAGTACAC AATCAITTAATTTCCCTGTCTTACCCCTATTCAAGCAACTAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7870b	85 T C	---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTCTGCAGTGATTAGAAGGG GTGGGTGGCGGGAATCC/C/TAATATCAGACTCTGTAATTAATTAATTAATGTTTACTCAGAGGA GCTGCAAAATGGCTGCAAAATGAATCCAATCAGCACTAGAAATTTAAACATCATTAATGCCCAT CITTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTTG

WI-7870	76 C T	---	---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAAGAACACTATTAACTACTCTGCAGTGATTAGAAGGG GTGGGGTGGG[C/T]GGGAATCCTATTATCAGACTCTGTAATTGAATATAAATGTTTTACTCAGAGGAG CTGCAAAATTGCCTGCAAAATGAAATCCAATGAGCACTAGAAATATTTAAACATCATTACTGCCATC TTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATCAATTG
WI-7889c	54 C	---	---	---	TTAGTCTCATGCCACTCCCCAGGAGCAGCTGGCACTGACAGCTGGGGGGCGCTCTCCCCCTG CAGCCGTGAGGACTCTAGCTCATGAGTGGAAAGTCACTACAGGACTGGGGCGGGCCAGGGCCTCT GGCTTCCCTGCCCAATCCTCCTGGAGAGGGACATGGGAATGAATTGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGCTCCCTCCAAGGCTGCTTCTCCAGAGCACAAAG
WI-7889b	54 C	---	---	---	TTAGTCTCATGCCACTCCCCAGGAGCAGCTGGCACTGACAGCTGGGGGGCGCTCTCCCCCTG CAGCCGTGAGGACTCTAGCTCATGAGTGGAAAGTCACTACAGGACTGGGGCGGGCCAGGGCCTCT GGCTTCCCTGCCCAATCCTCCTGGAGAGGGACATGGGAATGAATTGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGCTCCCTCCAAGGCTGCTTCTCCAGAGCACAAAG
WI-7894c	142 A G	---	---	---	AGCCACCCCAATATAACTGTTATCCAGAGCTGTTATGTCCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGCTCTATTGTTTGTGAATTTATTTGCGTATAC ATTATC[A/G]TATGTAATAATTTGCAATTTTTTATTGAAATTTATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCAATCGTTAATTTAACCGCTATAGAGTATTCCATA
WI-7894b	142 A G	---	---	---	AGCCACCCCAATATAACTGTTATCCAGAGCTGTTATGTCCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGCTCTATTGTTTGTGAATTTATTTGCGTATAC ATTATC[A/G]TATGTAATAATTTGCAATTTTTTATTGAAATTTATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCAATCGTTAATTTAACCGCTATAGAGTATTCCATA
WI-7900e	84 C T	---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCCTCAGATTTGAACCCAGTGAAA TATGATGTTTCTGAGCTAAAACCTCAACTATAGAAGACATTAAAGAAATC
WI-7900d	128 C T	---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCCTCAGATTTGAACCCAGTGAAA TATGATGTTTCTGAGCTAAAACCTCAACTATAGAAGACATTAAAGAAATC
WI-7900e	84 C T	---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCCTCAGATTTGAACCCAGTGAAA TATGATGTTTCTGAGCTAAAACCTCAACTATAGAAGACATTAAAGAAATC

WI-7900d	128	C T	---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACACAGTGATTAAAGTTTGATCAAGCCATGGTGA/C/TJACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900e	84	C T	---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACACAGTGATTAAAGTTTGATCAAGCCATGGTGA/C/TJACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900d	128	C T	---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACACAGTGATTAAAGTTTGATCAAGCCATGGTGA/C/TJACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900c	84	C T	---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACACAGTGATTAAAGTTTGATCAAGCCATGGTGA/C/TJACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900b	128	C T	---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACACAGTGATTAAAGTTTGATCAAGCCATGGTGA/C/TJACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900	84	C T	---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACACAGTGATTAAAGTTTGATCAAGCCATGGTGA/C/TJACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7901c	33	C T	---			AGACTTAGGTACAATTGCTCCCTTTTATATA/C/TJAGACACACAGGACACATATATTAACAG ATTGTTTCATCATTCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGAC CCTTTAAACAAACTCCAGGCCCTTGGTGGGTCGCTGGGTTATTGGGCGAGCGCGCGTGGTCGT CACTCAGTCGCTGCTGCTCTCTGTCTATACAGACAGGTAACCTAGTTCT
WI-7901b	33	C T	---			AGACTTAGGTACAATTGCTCCCTTTTATATA/C/TJAGACACACAGGACACATATATTAACAG ATTGTTTCATCATTCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGAC CCTTTAAACAAACTCCAGGCCCTTGGTGGGTCGCTGGGTTATTGGGCGAGCGCGCGTGGTCGT CACTCAGTCGCTGCTGCTCTCTGTCTATACAGACAGGTAACCTAGTTCT

WI-7901	33 C T ---		AGACTTAGGTACAAATTGCTCCCTTTTATATAJC/TJAGACACACAGGACACATATATTAACAG ATTGTTTCATCATTTGCATCTATTTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGAC CCTTTTAAAAACAACCTOCAGGCCCTTGTTGCGGGTCGCTGGTTATTGGGCGAGCGCGCTGGTCGT CACTCAGTCGCTCTGCATGCTCTCTGTCTATACAGACAGGTAACCTAGTTCT
WI-7901	271 T G ---		AGACTTAGGTACAAATTGCTCCCTTTTATATACAGACACACAGGACACATATATTAACAGATT GTTTCATCATTTGCATCTATTTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGACCOO TTTTAAAACAACCTCCAGGCCCTTGTTGCGGGTCGCTGGTTATTGGGCGAGCGCGCTGGTCGTCA TCAGTCGCTCTGCATGCTCTCTGTCTATACAGACAGGTAACCTAGTTCTGTGT
WI-7926c	150 C A ---		CATTCCGCATCTGTCAACAGGACAGAAAGCATGGACAAGGATGAGCTTTACAAAGATGATGCAC TTGGAGATCAGAAAATTCATATTTAAGCAAAGTGATACAAACACAGTGATTTGGGAATGCCTTCATT TACAAATGCAATACTTA/C/AJAATTTTAACTCTGTAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7926b	28 A T ---		CATTCCGCATCTGTCAACAGGACAGAA/JTGCATGGACAAGGATGAGCTTTACAAAGATGATGC ACTTTGGAGATCAGAAAATTCATATTTAAGCAAAGTGATACAAACACAGTGATTTGGGAATGCCTTC ATTTACAAATGCAATACTTACATTTTAACTCTGTAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7926	150 C A ---		CATTCCGCATCTGTCAACAGGACAGAAAGCATGGACAAGGATGAGCTTTACAAAGATGATGCAC TTGGAGATCAGAAAATTCATATTTAAGCAAAGTGATACAAACACAGTGATTTGGGAATGCCTTCATT TACAATGCAATACTTA/C/AJAATTTTAACTCTGTAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7947b	203 G T ---		AAGAGCCAGAGGTCAAAAAGGCCAACACACCATAAGCAGCCAGACCACAGGCCAGGTCCTGT GCTATCACAGGGTCACCTCTTTACAGTTAGAAAACACCAGCCGAGGCCACAGAAATCCCCTTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTGTCTCAATTCAAATCCATAGATTTGGAAGCCACA GA/GJTCTCTCCCTGGAGCAGCAGACTATGGGCGCCAGTGTGCCACCTG
WI-7947	203 G T ---		AAGAGCCAGAGGTCAAAAAGGCCAACACACCATAAGCAGCCAGACCACAGGCCAGGTCCTGT GCTATCACAGGGTCACCTCTTTACAGTTAGAAAACACCAGCCGAGGCCACAGAAATCCCCTTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTGTCTCAATTCAAATCCATAGATTTGGAAGCCACA GA/GJTCTCTCCCTGGAGCAGCAGACTATGGGCGCCAGTGTGCCACCTG
WI-7963b	145 T C ---		CATGTGCTGCATGAAGAGCTAATTTAAAAAGCAAAGTAAGACTAATATTTAAAAATAAAATGCC ACAAATTTCAATTTTCTCCTTCTAAGTATTACAATGGAGTTTATCTCTGCCTAAAAAGTGGAGAAT TGAGTGAATGA/J/AJAATTTTGTAAATTTAGGATAAGATCCAAGTTATTTTCCCCAACTCTTTGTTCCC CCATAAGGTTAGGCATGAGGAGGAGCACTATTAAAGGCAGAAAGACGGGAA

[illegible]

WI-8021b	57 C T ---	---	ACAACTCTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTGAATCTCATCTGGAAC/C/TJGATCCC ACGCTTTAGAACCTTCAACACAAGGAGTTTCTTGTAGTGATCTCAAAGTCTTGGTAGGCATTGGA ACTGGTCCCTTTACACTTTGAGATTTCTTTCTTTGCGCCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTGTAGGGGTGATTCGAATTCGGTGAATGGCA
WI-8021	57 C T ---	---	ACAACTCTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTGAATCTCATCTGGAAC/C/TJGATCCC ACGCTTTAGAACCTTCAACACAAGGAGTTTCTTGTAGTGATCTCAAAGTCTTGGTAGGCATTGGA ACTGGTCCCTTTACACTTTGAGATTTCTTTCTTTGCGCCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTGTAGGGGTGATTCGAATTCGGTGAATGGCA
WI-8024c	208 A G ---	---	CTGAAATTTACTATGCTCTCCACAACAAGAGCTCCCAATTTCCACAGACACAGTCAATGTCAAGTCA GCTTGATTCAGGAGGACAGGGCAGAGGATCCAGTGGCACTTCCCATGGGAAGACAGAGAGAGT GGGCCCCAGAGATGGAAGGACCCAGTGTCTATCACCACAACACCATTTTCAAGCGCTCTAGCCTCTAA TTCCCA/G/CTCTAGAACACAGCTGGCCCTGGTCTGTCAGTACACAAAGGAAAGAGC
WI-8024b	206 A G ---	---	CTGAAATTTACTATGCTCTCCACAACAAGAGCTCCCAATTTCCACAGACACAGTCAATGTCAAGTCA GCTTGATTCAGGAGGACAGGGCAGAGGATCCAGTGGCACTTCCCATGGGAAGACAGAGAGAGT GGGCCCCAGAGATGGAAGGACCCAGTGTCTATCACCACAACACCATTTTCAAGCGCTCTAGCCTCTAA TTCCCA/G/CTCTAGAACACAGCTGGCCCTGGTCTGTCAGTACACAAAGGAAAGAGC
WI-8077	167 A G ---	---	GAATGAGCCTTCTAGCGCCGAGGACCTGCTGCTGTTGTGGCTGCACATGCATTCTATGGAATGC TTTTTGCCAAAGCGGGGCACTGAGGACTAAGCTCTGANNNNNNNNATCGCCCAACCTCTTCT AAGGAGTCTGGGTGTCATGCCCTACAAACC/A/GJTAAATCTCATCAGATGGATTTTATTAAAGTT GTGATTGTGACTTACTTTCCAACTGACTCTGGCATAACAAGGGAAGAA
WI-8118f	114 GC ---	---	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGATGACCACCTCCCTTGGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACTGGCAATACAGAATGAGCTTGTG/GC/JTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCTCT AAAAATCAGACTCATTGTGACCAGTAGCTTGAGGACTCAAGCTGAATGA
WI-8118e	40 A G ---	---	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGATTTGGATGACCACCTCCCTTGGCTAAGGAAGC TATGTACTTCATGCTGTGGAACTGGCAATACAGAATGAGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCTCT AAAAATCAGACTCATTGTGACCAGTAGCTTGAGGACTCAAGCTGAATGA
WI-8118d	118 T G ---	---	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGATTTGGATGACCACCTCCCTTGGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACTGGCAATACAGAATGAGCTTGTGTTT/GJCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCTCT AAAAATCAGACTCATTGTGACCAGTAGCTTGAGGACTCAAGCTGAATGA

WI-8118c	44 C T	---	---	---	TCTAGGTTTAATCAAGCAATTTGCANTTTGGAATTTTGGAAATGA/C/TCACTCCCTTGCTAAGGAAGC TATGTACTTCATGCTGTGAAACTGGCAATACAGAAATGAGCTTGTTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118b	88 T C	---	---	---	TCTAGGTTTAATCAAGCAATTTGCANTTTGGAATTTTGGAAATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGAAACT/C/GGCAATACAGAAATGAGCTTGTTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8171d	299 C T	---	---	---	TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGGAGGGCTCGGGAAG AGGGGTAGGAGACCGAGCAGCATTCTCTGTAGAGGAAGACAGGAAAGGAGACCCCTCTTGGCACACA TTTATGGAGGTTGCCCTGAAGAGAAAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAAAGGC ACCAGTGGCAAGAGCACAAATGAAGAGGATGATATAAAACAATCACGGCA
WI-8171c	46 A G	---	---	---	TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAAC/A/GTGGCAGCAGGGCCTCGGG AAGAGGGGTAGGAGACCGAGCAGCATTCTCTGTAGAGGAAGACAGGAAAGGAGACCCCTCTTGGCAC ACATTTATGGAGGTTGCCCTGAAGAGAAAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACAGTGGGCAAGAGCACAAATGAAGAGGATGATATAAAACAATCAC
WI-8171a	46 A G	---	---	---	TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAAC/A/GTGGCAGCAGGGCCTCGGG AAGAGGGGTAGGAGACCGAGCAGCATTCTCTGTAGAGGAAGACAGGAAAGGAGACCCCTCTTGGCAC ACATTTATGGAGGTTGCCCTGAAGAGAAAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACAGTGGGCAAGAGCACAAATGAAGAGGATGATATAAAACAATCAC
WI-8171b	298 T C	---	---	---	TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGGAGGGCTCGGGAAG AGGGGTAGGAGACCGAGCAGCATTCTCTGTAGAGGAAGACAGGAAAGGAGACCCCTCTTGGCACACA TTTATGGAGGTTGCCCTGAAGAGAAAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAAAGGC ACCAGTGGGCAAGAGCACAAATGAAGAGGATGATATAAAACAATCACGGCA
WI-8314b	85 G C	---	---	---	GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTTGCAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCTCTAAGGG/C/GAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCAGCTGTCCAATAGAATTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAACCACT
WI-8314	78 C G	---	---	---	GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTTGCAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCTCTAAGGG/C/GTAAAGGGAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCAGCTGTCCAATAGAATTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAACCACT

WI-8321	178 G A	TTTTAAATATGCCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGATATACCCAGGNAATCCATTCTTGTTACTTTCAAGAGCTGCTGTATACTAGTCTCTGAGAAG TCCCTTAGATAAATAGCTGCCACTTTTCAGTATGGTTCCAGATG/AJAGTATCTTAGTATCTTTCTA TTTTGCTATGGTTCTAGTTATCAACCTACTTTATTAGCTGAACGTGTGGC
WI-8321	178 G A	TTTTAAATATGCCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGATATACCCAGGNAATCCATTCTTGTTACTTTCAAGAGCTGCTGTATACTAGTCTCTGAGAAG TCCCTTAGATAAATAGCTGCCACTTTTCAGTATGGTTCCAGATG/AJAGTATCTTAGTATCTTTCTA TTTTGCTATGGTTCTAGTTATCAACCTACTTTATTAGCTGAACGTGTGGC
WI-8332b	123 A C	TATGTACTCACTTTCAGTTACCCCGTGCCTCCAGATCGCATGTTGCTCCACCTGGGGGGGATATA AATTACCTCTAGATTGTCCAAAGCCAGTCTTTCCCTCCCTGTGC[A/C]GCCTTAGAACTAAGTAG CAGTACTGTTTGGTGTGTTGTTTCTTCCCAGCAATGCCTACTGCAGCTACTTAGTAACAACACTAG AGGTGGAGGGTNTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8332	114 A C	TATGTACTCACTTTCAGTTACCCCGTGCCTCCAGATCGCATGTTGCTCCACCTGGGGGGGATATA AATTACCTCTAGATTGTCCAAAGCCAGTCTTTCCCTCCCTGTGC[A/C]GCCTTAGAACTAAGTAG CAGTACTGTTTGGTGTGTTGTTTCTTCCCAGCAATGCCTACTGCAGCTACTTAGTAACAACACTAG AGGTGGAGGGTNTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8378b	311 T C	TGCGGGCTTAACAGGAAGCATGACTGGGAGGCTCAGGAAGCTTATAATCATGGCAGAAAGGCGAAGG GGAAGCAAGGACCTTCTCACATGGCAGGAGGAGAAAGAGAAAGGAGGAGTCTACACACTTTT AAACAACAGATCTCATGAGANTCCATCGGGAGACAGCACTAGGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCCAATCACTNTCACCAGGCCCCCTCCTCCAAACACGTGGGG
WI-8378	308 T C	TGCGGGCTTAACAGGAAGCATGACTGGGAGGCTCAGGAAGCTTATAATCATGGCAGAAAGGCGAAGG GGAAGCAAGGACCTTCTCACATGGCAGGAGGAGAAAGAGAAAGGAGGAGTCTACACACTTTT AAACAACAGATCTCATGAGANTCCATCGGGAGACAGCACTAGGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCCAATCACTNTCACCAGGCCCCCTCCTCCAAACACGTGGGG
WI-8426	184 T G	TTTAGCACATTTTAGCATTAAAGCCTCAAACGATACAGCAATATGTTACATTCTTGTGAAAACAG TTGTTGTAGACTGTTAANNNNNNNAATGTAACTCCGACTTGTGCCTAATAGGATTTGACCNNTAA GAGGNTCTTTTGTGTGGANGGGGTGCTTGTCTGAACTCCATTCTGT/GGCTTGTAGCTGGTG AGGCTGGGAGTATGGANGGNCOCGGGGCCCTTGGCNATGNATTAGTGAG
WI-8450h	61 C A	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACT[C/A]CA TCTTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATTATACCAATCCATTGTTATTTAAGA AAAAACCTCCAGTTATTGTGAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTATATGAGCAGTACAGAGICTTAATGCAATTCAT

WI-8450g	55 T C ...			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTC/JACACTCCAT CTTCTCTATCTTAGTCCAAAGTTTATGTTTCAATCCCAATTATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450f	108 T A ...			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTCCAAAGTTTATGTTTCAATCCCAATTATACCAATTCATTTGTTATTC/JTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450e	125 T C ...			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTCCAAAGTTTATGTTTCAATCCCAATTATACCAATTCATTTGTTATTC/JTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450d	125 T C ...			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTCCAAAGTTTATGTTTCAATCCCAATTATACCAATTCATTTGTTATTC/JTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450c	108 T A ...			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTCCAAAGTTTATGTTTCAATCCCAATTATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450b	61 C A ...			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTCCAAAGTTTATGTTTCAATCCCAATTATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450a	55 T C ...			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTC/JACACTCCAT CTTCTCTATCTTAGTCCAAAGTTTATGTTTCAATCCCAATTATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8458b	60 A G ...			CAAGGAAAGCTGTCAGTCTTCATAAACCTTCAAGAGTACAAAAATACGTATTTTAA/JGJCTA CAATTCAAGATTAGCATCCAAACCTACAAACATGATGATACATTCGTACACACCATACAACTTCAC ACCTGGCTACAGCAATGTTGACTTACATCACCATTGTTTATGTTTAACTTGTGAAAACTTTATTGTGCACAGT GACATCCATTCCGCCAGACTTAATGTTTAAAGCAGCTGAGCAGAGTGTCTCA

WI-8461c	105 A T ---	---	---	CTTCCTCTCCAAAATCTACATGAATACCTTGAAGACAATATACTACAACCTTACAATGCCAATTA GACAAAGAGANTAAATGATATAATAATAATCATTTTTT[A]NNNNNNNNNOCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAGAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461b	38 T C ---	---	---	CTTCCTCTCCAAAATCTACATGAATACCTTGAAGACAATATACTACAACCTTACAATGCCA TTAGACAAAGAGANTAAATGATATAATAATAATCATTTTTTNNNNNNNNNOCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAGAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	38 T C ---	---	---	CTTCCTCTCCAAAATCTACATGAATACCTTGAAGACAATATACTACAACCTTACAATGCCA TTAGACAAAGAGANTAAATGATATAATAATAATCATTTTTTNNNNNNNNNOCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAGAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	105 A T ---	---	---	CTTCCTCTCCAAAATCTACATGAATACCTTGAAGACAATATACTACAACCTTACAATGCCAATTA GACAAAGAGANTAAATGATATAATAATAATCATTTTTT[A]NNNNNNNNNOCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAGAAANTCAAGGATTTGCAAAAAGGGGG
WI-9438	77 A G ---	---	---	AATAACATGTTATGAACAAGCTGGTTACAAGTAGTAGTAGTACCTTAATTTTGATAAAAAAT TAAAAAGCAT[A]G/AACATGCATATAAAAAATTAGATTATGTACAAAATACCAACAGTATTTACTTC TGCTCAGTAATTAATAATCTCCCTTTGTTTTGCTTTTTAAAAACATTATTTCTGAAAAA ATCAGAAAAACATGATCGTGGAGAGAAATTATTA
WI-9439b	101 C T ---	---	---	ACAGAAATTGACCTTTATTTGTTGTAATAAGCCTGTTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAAAATCCCAGTCTGCAGCTCAGTACCTGT[C]TGTGCACACTGTACCATCTCAGTCCCACCT GCCTGTAACCTTAGAAAAACAGCCCTACCCACAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACTTGACCTGTAAAAACAAAG
WI-9439a	76 C T ---	---	---	ACAGAAATTGACCTTTATTTGTTGTAATAAGCCTGTTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAAAAT[C]TCCAGTCTGCAGCTCAGTACCTGTCTGTGCACACTGTACCATCTCAGTCCCACCT GCCTGTAACCTTAGAAAAACAGCCCTACCCACAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACTTGACCTGTAAAAACAAAG
WI-9446b	75 T C ---	---	---	GAAGGCTTGATTAAAGGGAGGNTTTATTTGATGTNAACCTTACCATTCCATAGACTATAAGANCATTA TAAAAAAAT[C]CCTCTAAAGNGACACATGCCCAAAATGACCAANGNCATAAGCAAAACCTTTTAAAT TACTCATCTTTCATATGTGTGTTTGTNCCCTACTNTTATCACTGTGCTCTGCTCTTGTCTACCTA TGNGAACTGCACACTATCTGTGGCAATATGT

WI-9446	75	T C	---			GAAGGCTTGATTAAAGGGAGGNTTTATTTGATGTNAACCTTACCAATCCATAGACTATAAAGANCATTA TAAAAAAAT/CJCCCTCTAAAGNGACACATGCCCCAAATGACCANGNCATAAGCAAACCTTTTAAAT TACTCATCTTTTCATATGTGTGTTGTCNCCCTAGCTNTATCACTGTGCTCTGCTCTTTTGCTACCTA TGNGAACTGCACACTATCTGGCAATATGT
WI-9497b	185	A	---			ATTAAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAATGGTATATATACTTTTTTT GAGATAATTATCTAGATCCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTTNCCTTAAATCAAGTATGTTAATGTCACCT GGAATCTACATGGAAAGCCCAACAAATAACTAAACTTGACTAATGAAG
WI-9497	185	A	---			ATTAAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAATGGTATATATACTTTTTTT GAGATAATTATCTAGATCCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTTNCCTTAAATCAAGTATGTTAATGTCACCT GGAATCTACATGGAAAGCCCAACAAATAACTAAACTTGACTAATGAAG
WI-9523b	193	C A	---			GTGAAAAAGTTTCTATTCCATCCATCATAACAATAGATTGTGCTAAGGATCAATTTTGGAAAGATGTG CAGCATTGAGAAAGTTGTATCTCATGTCAGTCACTCAGCAGCATTTTATCTAAAAGTACGTGCACA GACTCAGACAAATTACAAACTATTTCCAGCCATGATCTATGGTATTTCCACACATTTGTA/C/AJAGTG AAAGCTCTTCAGCTTGGAAACAATTGTCAAGGCAGACTGCATGCACATATAT
WI-9523a	47	G A	---			GTGAAAAAGTTTCTATTCCATCCATCATAACAATAGATTGTGCTAAGGATCAATTTTGGAAAGAT GTGAGCATTGAGAAAGTTGTATCTCATGTCAGTCACTCAGCAGCATTTTATCTAAAAGTACGTGCA CAGACTCAGACAAATTACAAACTATTTCCAGCCATGATCTATGGTATTTCCACACATTTGTACAGTGA AAGCTCTTCAGCTTGGAAACAATTGTCAAGGCAGACTGCATGCACATATAT
WI-9554	202	T C	---			AAAAACACAAGTTTTCATACATCACAAAAAACCTTCCATTATAACACAGAAAGTATTACCAGAC AAGCATCAGTGATGTATCTGCTTTCCTTCTAGTTTATTGTACAAATGCTGTAGATAATGCAGCCCATG CAATACACCCCAAGAACACTAGAGTCTACACCCCAAGTACAATATGATAAGCAGCCCTCTGCAAGTG GT/C/GCTGGATACCACTAAGAGTCTACTGCAGCCATGTTGGTATGATTTT
WI-9555	97	G A	---			CCAAAGCCAAACCATTCATATGTATGGATTTCATAAACATTTATTGATCCTTTTTTGAGGTAAGTAT AAATACCTTTACATGGCTAACCTTCTAAC/C/AJCTTGAATAATCAATTTCAAGGGACTCTTTAATCA GTTAAATAATCTGCTTTAGAAAGGCACAAATGATCATACTTCAGATTAAATACAGGTAAGTATTCAG GGNTAAATGTTACAAAAAAGGCTGTAACTCTTTTNCCTCAGATTGATCACA
WI-9625b	172	A T	---			TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCTCCTTGGGAAAAAATTTGGAAAAAATAACACGCACA TAAGTATCATAACTGAGGGTTGGGACAAGTTACTTCT/ATGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCAITTTAAAAAACACACTGACAAATCTTTTC

WI-9625	172 A T	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCTCTTGGAAAAACCTTGGAAAAAACAACACGCACA TAAGTATCATAACTGAGGGTTGTGGACAAGTTACTCTCTATGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCAATTTAAAAAACAACACTGACAAATCTTTTC
WI-9647	144 C T	TTTTCTGAGATCAAAGAGCTACATTTTGGTTAGTGTATGCTACTATACCTTTTTCATCCTTTCA ACATCTTTTGTACATTTTAGGTGATGCTCTTGTAAACAGTGTATTGCTAGACCTAAAAATCCAGCT TACAACTCTGTGCTTTTACCTGATACATTTATTCATTTACTTTCACTTTTGAATTTTAAAAATGTTA ACTTAATACGCTCTTTCAGATGTCCTGCTTTTGTAGTTAATGTGTTT
WI-9676n	114 A G	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAGATGAAGAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGCTTCTCTGCGCATGAAATAACTTGA CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676m	184 G T	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAGATGAAGAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCTGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676l	84 A C	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAGATGAAGAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCTGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676k	202 C T	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAGATGAAGAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCTGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676j	92 C T	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAGATGAAGAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCTGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676i	173 T C	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAGATGAAGAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCTGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT

WI-9676h	134	C A	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCTGCCCC C/A/ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTG AGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676g	202	C T	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCTGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGAGG C/T/CAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676f	184	G T	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCTGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCG[GT]CATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676e	173	T C	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCTGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTT/CJCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676d	134	C A	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCA[AG]GATGTGGCTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676c	114	A G	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCA[AG]GATGTGGCTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676b	92	C T	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676a	84	A C	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT

WI-9738b	40 C A ---	---	TGGACCAACACAGACAGATGATTCCTGGTGCCTGTGTAC[A]ATTACAACCTATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAACACACAGTAATGACTCCACATTTTCCCTTT GAGTCAACAAAGACTCTGCTGTACCTTGCTGGAGCGGGTGTTTTCACATATGTGAGTATCTA TCITTTATTCTGTCCCTATGTTGGTGGCACATGCTGTATTGCTGTCC
WI-9738	40 C A ---	---	TGGACCAACACAGACAGATGATTCCTGGTGCCTGTGTAC[A]ATTACAACCTATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAACACAGTAATGACTCCACATTTTCCCTTT GAGTCAACAAAGACTCTGCTGTACCTTGCTGGAGCGGGTGTTTTCACATATGTGAGTATCTA TCITTTATTCTGTCCCTATGTTGGTGGCACATGCTGTATTGCTGTCC
WI-9756	47 A ---	---	ACTGAAATGTAATGGCCAAAGGCCACCCAGGACCTTAAAAATCATAAGAAAGTTAATCTGTGGAAAA GAGTAACATCAAAAGCATCTAAACAAGAGCAGGATGTGATGTAATGTGTCCTTATCACATTTAGTC AGTAAAGATAAGAAAGCCCTGGTGGTATCCACTTCCACAAACACACAGAAATATACACTTTTGGGAG ATTCCACTTAACCACTTGATCTTCACTTTTTATGATTTAAACCTCTCCGTGG
WI-9758	135 A G ---	---	GATGTCCCTTAAGGATTTGCATTGGTTAATGGGCAGACTGGTGCAAAAGAGGCTGAATTGAATAAT TAGGAACTGGGAGAAATCAATTCAAAGAGAAATCTTGTTCGCAAGGTCAATTTTATACTATTTA A[A/G]TAAATAAAGTCTGTAGTTCTATAGCAAAATGCTAAGTAAAGTAACCGCTGGTTCTCTAAAT ATTACG
WI-9778	127 G A ---	---	ATTTAAATCCAGGCAGCGGGGAAATGGATACCTTTCATATGCTCTGTACCCAACTATAAACTTTTG GTTCTCATGCACCATTTTCATTTTGCTTCTCACTCCAGTACCACCTGATTTTACCAATTT[G/A]CTCTC ATAATTGACTTTGCTACTGGAAGAACTCTTAGAATGTTGGAATTTCTCTATTACACACTTTTGCCTCA AAGAAATGTCAGTCAGGACTAAAGGCAATAGTCTCAGGGCAGACAGCC
WI-9832	116 C A ---	---	TCCTCCCTTTGGCTCCTCATGCGCACTCCCTCAGCCTGCACAGAGCGTTTCTCCAGTGTAGTCTCTGGT CCATCTGCATCAAAATCACCTGCAGGACTTGTGACAATGCAGTTT[C/A]TGGATCCCACCCAGGA CTCAAAATACTAGGAATGGGAGAGAGGGACCTGGAATCGGTGTTGCTAGCAAGCCCCCAGGTGG TTTGTAAGTGGACTAAAGTTTGAGGACCAGACATGGAAGGTGGCTTTGGC
WI-9841	101 A G ---	---	TGGAAAAATAGCTTTTATCAATCTCTGATATGCTACATATGTCATGGAGAAATGCAGAAATGGCATGA TATGAAATTCATTTTGAATGAATAAAATATAC[A/G]TGTATGTATATATATATCTTATTAAACACTT AGGATTATATACACACAATAAAACGCTCTGTAAGGATAAACTAAGTTCTATCAGTGGGAAATGAGA TTGAAAGAGGGGGATGTTACTTGATATGCTGTTG
WI-9880c	222 G A ---	---	GAACTAACACCTTCTTGCAATGATTTTCTTGATATTGGCAGTTAACAATAAAATGTTATTAGATC ACTGGTCTTCTGTGGGTTGAGTTTTTATGATATCTCTGTTAGACCAATAAGGAGGCTGTGA GTTGTTTTCTACATCCTTGGACTATAGATCCTCTTTAAATTTATATTTTATAAGCACATGAA AATGGAATGAATAATGA[G/A]TTGACATAGGAATTACCTACATATTTTG

WI-9880b	157	C A	---			GAAC TAAC ACC TTT TCT GCAT GGAT TTT TCT GATT ATT GGC AGT TAA CAAT AAA AT GTT ATT AGAT C ACT GGT CTT CTG TGG GTT GAG TTT TTT ATG ATAT CTCT GCTT AG ACC CATA AGG GAG GCT GTGA GTT GTT TCT ACAT CCT TGA C/AJ TAT ATA AGAT CCT CTT TTA AAT TAT ATTT TAT ATA AGC ACAT GAAA T GGA AT GAA AT AAT GAG TT GAC AT AGGA ATT ACCT ACAT ATTTTG
WI-9880a	108	C T	---			GAAC TAAC ACC TTT TCT GCAT GGAT TTT TCT GATT ATT GGC AGT TAA CAAT AAA AT GTT ATT AGAT C ACT GGT CTT CTG TGG GTT GAG TTT TTT ATG ATAT CTCT GCTT AG ACC CATA AGG GAG GCTG TGAG TTG TTT TCT ACAT CCT TGG ACT ATATA AGAT CCT CTT TTA AAT TAT ATTT TAT ATA AGC ACAT GAAA T GGA AT GAA AT AAT GAG TT GAC AT AGGA ATT ACCT ACAT ATTTTG
WI-10183	127	C T	---			ACACT GAGG CACT CCAAT CCTNACAGACATATGCACCTCGGAATCAACTCAGGCATGCACAGCAT CCCTGTGCTGGAGTTTATTTTAAAAACAACGGCCAGTTATCACAGTTCTNTTTTGT[C/T]CACC ATTTTCCATAACAAAAGAGCTACACAAAATTTNGGGGGGAGANACTCTCTTTGGAGACTGACACATT TGCAGAGGGT CATGAATATGATCCAAA
FB25G10b	109	A G	---			TCCCTCAATGACAGATGAAC TAAATTTTCTCTGGGTAAGAAATAC TTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAAATGGA A/GJTGA TTTTAGATCCTCCCCAG TGACAAGTAAACTGAACTGACCATATTTATACATAAAATGGAATGTAAGAACCTATTTTGGATATCC CGGAC
FB25G10	109	A G	---			TCCCTCAATGACAGATGAAC TAAATTTTCTCTGGGTAAGAAATAC TTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAAATGGA A/GJTGA TTTTAGATCCTCCCCAG TGACAAGTAAACTGAACTGACCATATTTATACATAAAATGGAATGTAAGAACCTATTTTGGATATCC CGGAC
IB3071	102	C A	---			ACAACGCTGAAC TTTCCATAACAGTCAATGGTACAGTCAAAACATCACATGTACAGAACACACAATTTA GATGAAC TGAATTAAGNTAAATAAAATAAAAT[A/C]AATTTT CAGNAAAACAAAATCAAAAC ATTAAGGNTCCCTGNNATATCTTAAACCTAATGAGATTTCAC TGGNCTCAAGTCATTTTGTAGTGA GGCATTCAATATGACCCTATTTAACCCAGTCTAGGGATTCTG
NIB551	161	C T	---			CGTCTTTCTTTT GAGATTGCAATTAAGTAGATAATATGAGAGAGAACTGACAAATGGGTGTCCC TACTGAGCTTGGGGCCAGGTGTGTA CTTAGGAACCAATCCACCAGAGAGACTCATGTGTTA ACACTAAGGATGCCCTGGAGGAGGT[C/T]TGACCACATACATGCGGCCATTGGTTGATTTCAGCTTT GCAAGCAGCGTAGTGAGAAAACCAAGCTTGCC
S72904	51	G T	---			AGCATAGAAAGTGATTATATTTTAAATGGTTTCAAGTGAAGTTCCTTT[G/T]AATTTGT CAGTTC ATTCCTGGAATAATCTTTTGAGTTAAAATAAGGATCCTAGGACAGCACCTCGAACTACAGGCCCTAAA GAGAAAATGCCTCAAAACCAAGTGCTGTAAC TTTCTCCCTTTCTGTCAAATGGTTGCTTTAAATA TTGCAAAAGTCTGATGCTAAACAGTATTTGGAGTGTTCAGTGTCTGTA

UTR-00481	115	CT	---	---	TATCTTTTATCCTGGGGCCACAGTCTTGATTATTCCTCTTGTTGGTTAAAGACTGAATTTGTAACCC CATTGAGATAAATGGCAGTACTTTAGGACACACACACAAACACAGAGC/TJACACCTTTTGATATGTA AGCTTGACCTAAAGTCAAAGGGACCTGTGTAGCATTTTCAGATTGAGC
ESTC1	33	---	---	---	CCCTGTAGCAGTCTTCAGCCCTCCTCTACCCCTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37	---	---	---	GCTACTACCACGGCTGCTTCGTTTGGACAAAAATAACNAGGAGGCATCCACGGGATTAGTTA
ESTC103	21	---	---	---	GCCATCAAAATTTCCCTTCACANTCAATACTGTGGAACAACAAGATAACACATCTTCTTGCTCATCCC ACTTGAA
ESTC107	20	---	---	---	TGCTGGCTCACITTCCTCACANGCTGTATTACCTTTTCAGAGCTGAGTGAGGCTGTGCT
ESTC109	35	---	---	---	AAAACCGGAAGGCCCTGCCCGCAGAGGCACATGNACAGGGCAGTGCACAGTGACC
ESTC110	23	---	---	---	AAACCTCACACAGAAAAAGAGGANAACACTCAGAAATGTGATTACAGATTAGGCA
ESTC113	37	---	---	---	AAGGACACAGTGTGCTGACAAGGTGACACTGAACANAAACAGTTTCTCTTAATTGTAAGCGGG CATCG
ESTC117	24	---	---	---	AATTGGCTCTTCTCCACATGATACNTAAGTTCAAGTGCCAAAGTTCTCTATCACAAATTACAAAAAGC CTCCA
ESTC119	24	---	---	---	TGTCAAGCAGATCTTGAGGGTTATNGTTAAGCCTGATAACAGCCTCTTT
ESTC122	34	---	---	---	GACAATAAACAGCTAAGCTACTGACATAAAATATNCAATAAATTTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC123	21	---	---	---	GAAGCCAGTATGTTGTGGCAANATTCGAGAAAAACACACTGAAAAA
ESTC128	42	---	---	---	GCAGAGGCATCAGATAAGGCCCTCAGAAAGCCCGCCAGCCATCATNTCCATGGGACCAGGCTGGCTCAA TGTTGGAACCTGG
ESTC129	20	---	---	---	AGTCACCATGCCCCAGCCTAGNATGAGTTTAGTAAGATTGGTTATGCTGGGGAG
ESTC13	46	---	---	---	GTGTATCTGGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGTCTGGA TCAGAAAA
ESTC130	49	---	---	---	GCCTGCTCACAAGGTAGACAAAAACATAAATCTTCAGGAAAAATGAAACANGAGAAGCTGAAACAAAT CTACACCTGAATG

ESTC132	30	GGTAAAGTCTAAATTACTGCCCTTAGCAAACNCTATGTTGTCAGGTTTTTCTGCTGCA
ESTC137	21	CCAGTTTGGCTTCTGTCTCCANAGTCTCTCTCCATGTGGCAAACA
ESTC139	45	AGGAGCACAGCCTAAGGACATGAAGTTCAGAGTTTCTCAGAGAGNGGGCTGGTCCCTGAGCTAG GAGGAGG
ESTC14	20	CCCATTTGGTTCACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTCCCTTGTCATGGTTTAGAAAGC TTGCCCTGGTG
ESTC142	72	CCTAGGCTCATAACAATACAGTCTCAATACAAAAGACGTAATACTATTTTATTCAATTTTAAATC AAAGANACCATTCCATTTCCCTAACAAACA
ESTC143	29	GTTTACGAAAGTACTGAAATGCTATTANTAGCTGAATTTGTGATTTCCCTTTTG
ESTC144	26	AAATCCATATTTTCTTGACATGAGGTNGCTTTTATGACGCAATTTCCG
ESTC146	20	CATGTCAGGATAAGGAGCANACACAGGATTTATACACGGTGGCAGCG
ESTC148	42	TCCTTGGTTGTCTACACAGACACTTAAGTACTGTATCGCTGTNATGAGGGGCTGTGGAGGCCCTG GGGGTGGCTGGGCTGTGCTGAG
ESTC149	28	TCAGTTCAATTTATTTGCTTTAAGAGTTANATACCATGAGACACACAGTTCTGG
ESTC15	28	GGATTGTAATATTGCCAGCTTTGTAAGNCATTAAAGCAGAAAGTTCTTCAGTGATCTT
ESTC150	20	CCAGGAAAACAAGCACACANACTTATAGAATACCTTGGTTTAAAAAATTATTCATAATATCAATATT AAACCTGATGTTTAAAGAACCTAATGAGA
ESTC151	49	GAAGCTAAGGGCCCCATTTTTTTCTTTTAAATACAAATCTACTGGTGTNAAAACCTCAGAGCTTAGGA AACACAGCC
ESTC155	37	TTTTTAATTGACAACTCAATCTCTACATACATACAGTNTGCACGAATTATAAGTGGATCAACAAATT ATATTATTGATACAACTCATGAGCATTTACA
ESTC156	32	GCAGCATTTGTGACAGGAGAGCGCAAAACAAANCCCTGGCTGCCTCGGGATGGAGCGGGGGCGCCTCA CCACCACTGCAT
ESTC158	35	ACCAAGCCCTGGGATTTACTGTCTTGATGACTACANGGCTTTGCACAGTCTGAGATGCTTCAGTGTGC AA
ESTC159	31	AGCTGGCAAGAGACTTCTCTGAGGCACATCAGTACGTGGTCAATTTAGGGCACGGTCTGTTCTGCA GCTTTGAAAGG

ESTC16	23	---	---	---	CACTGAATGCTCTGCCATGAGCCNCAAGCAGCACAGTGATCATCAOCCACAAGGACAGGTT
ESTC160	38	---	---	---	TTTAGCATTGCTGGTGAGTGGGGCCCTGAGCTGGGNGCAGTCGGCAGTGTCACTGGGCCGTTTG GGACTGGGTTGA
ESTC162	36	---	---	---	CTCTCGTCCGTTTGAAGTTGCTGTTTGTTCAGNTACACCAGTCAGAGCTCCACAG
ESTC164	31	---	---	---	TCATTCTCCATAGAATATTGGTTTTGTAAACANGAATACAATCCAATATATAACATTAACAACAATCC GATACATACCA
ESTC169	22	---	---	---	GTCTCTGGTGTGCAGGGAATCANTTTGTGGATTAGAGGAAAGTGCCCGCTGTTTCCATGACTT
ESTC176	23	---	---	---	CACCTCTCCCTGAGCTACCCANGTAGTGTGGGAGCTGGCA
ESTC177	42	---	---	---	TGGGTGGCTCTTTAAATACCTTCCATTATATTTTCAAATTTTNCITTTATCTATTAAAAACCTTTTAT TCTCTTTATTCOCATAAAAGGCAACCAA
ESTC18	29	---	---	---	TCAGACACTGCCGACATCAGCAATTGCTCTCNTGTACAGTCCCTTCCCTGCAGGGGCCCCCTGGGAGAC AACTGGACAAGA
ESTC181	21	---	---	---	TAGGGATTCCAAGTTGCCTGGNTTAAATATAATACATATTCACAAAAATTTACACAGCTCATGCATAC CA
ESTC186	43	---	---	---	GCTTGACTAGCGAGGCTACATCACAATTTATAAAGTGCCAGATNAGTGCTAATTGTCAATCAGCTTG ATTTTCACTCA
ESTC187	24	---	---	---	ACCATGATTGCCTCACACAAGCATNATCAATGCCACGAGAGACTGGATGCCAAAAGAGTATGGCTGG TCTATTAAACAGGGTTATGTACACCCNTGTCAACCTCAAAACAGATGATACATCACTTGCTTCCCAT CTTGC
ESTC189	27	---	---	---	AAAGTACAATCCAGTATATGCAGAAAGNTACTCAGCATCAGACTCGTGATCA
ESTC196	42	---	---	---	TCCTCAAATACCACTTCCCTTAACCTTATCAGTCTAGTAAGCNTTCAAAGGAGGAAAATGGGTAC CTTTCAGGGG
ESTC197	26	---	---	---	ATCTCCAGTGTCTGCTGCCTCCTCCNGCAAAGTCTCCCAACAGACA
ESTC20	33	---	---	---	AAGATTAGGACAGACCGGTATAGTAAGCTCTGNGGAATCCAAAGATCTAGAGGGGCTGTGGGAA CGCTGCTTAGATC
ESTC200	44	---	---	---	TTTGGTGAAAATCCCAATATATGAGTTTAAAAAATCATTANCATCATTAACAGTACTTTAAAT CAATTACTCTTTTGCCTGCAACAG

ESTC201	35	TCCTACTTGGGTAGTTTAGCAAAACATTTTTAAAAACCACATCCACAGATTGGTT
ESTC202	22	CTGCTGGAGGAGGACAGACGGCAGGGCGCTGGGTGCCGCCAGAAAGGCTGGCGTGGATGTT CGAGATGAGCC
ESTC203	27	ACACTTAACAGGTTAAAAATATCCAAATNAAATTTACTGCAACTTTTGAGAAATTTATTGTGCTAC AAGACACGTTGCA
ESTC208	43	TATAGCCCCATCGCTCTCAGTTATTAGAATCTGAGAGGGATAANAGCAATAACTATTGTTTAAAAAGC CTAAGAGTGAAAA
ESTC210	29	GATGAAGTGGCTTCCTTTGGCGAAAGGATNAAGAAGTGAGTGACGGTGACCTGTG
ESTC212	27	GGTAACTGATGAGGAAGCTCTAGTNAGAAATTCAGGACGGGCTTCAGAGCAGAGGGCTTGGT TCAAGTC
ESTC214	21	CTCAGAGTCCTCTCTCANACCAGGGCAGGAGGTAGGGAAT
ESTC216	49	TGGCAAGAAATTTATTACACTAACAAATTAATTAATCACAGGTATNTTAGATTGGTCAGAAAA CAAAAGACCA
ESTC217	28	TTTTGTCAGTAAATGAGCAATACACTGANTGGAATCTGCATGATTAATAACATTAACAAGTTTCAT AAACACACCCCA
ESTC219	32	GTACACATCTGGGGTGAGCACACAGCAAAANGGGTGGGACGTGCAGAGAGGTATAGGGTAAAG GCAAAGGAAGC
ESTC22	41	TCATTGAAGAAAATTATGGGTTTTATTCTTATTCTAATTGNAGAAATGCTTAATGTCACAGGCTACA TAAGGGCC
ESTC223	27	CTTCTGAAGCCCAAGAGAGGGGCGAANGTAGTCTTGATTTAAAAAACAGAAAGGGAGGAGGA
ESTC224	37	CGAAGGTAGATTTCCCTCACATATTACAAAATACACANAACACACACACACACACACA
ESTC225	20	TGCACTGTTACTCCCCAGACNGAGAGCTTACATACCATATAGAAAAGAGCATAAGTGCTTCAGAAGGA ATGTGATGATCG
ESTC23	27	TTCTACTTTATTTTCATATCCACCACNATAACGACTCCTTTAATTTAACTAAAAACCATACAGGGT TCCTGAAAGGG
ESTC230	43	GCCTTCCTCCACGAATTTGAAAGACATATTGGCTGACCTGTATACNTAAGGAGCAGGCCAGAAATTAAGA
ESTC231	24	CAAAAGGGTAGTCATATTTCCCCANCAACAGCATGATAAAAATAATTCAC

ESTC28	23	GAAGAGCTGGGCACGCATCTGACNTTTCCTCTATTCTCTATAAAAAATAAAGGAAGCAGAAATCT GC
ESTC3	20	CAGACATGACCTACCGTCCCGGCCCTCAATTCATATTTTATTCTTGAGCCGCTTGGTCAGGTTTGAT TCGCACACTCC
ESTC31	32	ACAGCCCCACAGAACTATTGTAAACAATATTNTCAGTGGTGATCATTTGTAATATACAAATACAAAG CAATTTCTCAGA
ESTC33	25	AGCACTTCCAGCTCCTTGACGTTGTNGGACCAGGGAACITCCGGAA
ESTC39	26	AAGGAAAGGGAACCCACCTGGGCTTNGGTACAGAACTCAGAGCCTGGGCATTA
ESTC4	23	CCACTGAATCACACAACATGGACNAATCTCAAATCATTATGCTGATGGAAGAAACCAATT
ESTC40	22	GGCATGCTAGACAGAGGCATTANTTTGAAGATCTTTTAAAAATATTTTGACTTGTTCCTCCCTTCAC
ESTC45	37	TTTGGAGGTTTGTGCTGGAGTTTGTCTTTGTAACTCTCATCATCGAGGCTATATATAA
ESTC50	56	CTGTCCGTGGTGAGCCCTGCCGCTGTCCCATGGCCAGGGAGCCACTGGTGGGANCCGGGCAGATG TTTACCCTGT
ESTC56	45	GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGCAGGTTGGCAGGAAGNAGTGGAGGAAAGGACACCA AGT
ESTC57	20	AAGTGGGCCCTCCAGTCCCNCTCTCTGGGCACAGATCCACCACTCTGCTC
ESTC59	38	GAAACACAAAAGTGTGAGAAAAAACTCTCAAAATNGTCCAGACTTCAGGAAAAATGATTTCC ACATGGTAAGGCC
ESTC6	27	TCTGCAGCACTTCACTACCAATGAGCNTTAGCTACTTTTCAGAATTGAAGGAGAAAATGCATTATG TGGACTGAACCG
ESTC61	57	AGTGATTTGGCTAGGCGTGTCTCATCTGTGAAATTCACAGCGCAATGACAGCANCCTCTCTCCC ACCCACTCAAG
ESTC63	20	ACAGACACAGCATCACACCANAGGGCCACCGGGAGGGTCCGGGAGACGACACTTTTCCCTGGGAAA GGCAGCTCTAATC
ESTC69	20	GAGAGGCTAGTCAGGAGGGANACCCTCAAGTTAAATCCCCACACTTACTTACTGCTCATCCGT CACTTTCGCTAA
ESTC7	45	AGTTTCCCTAGAGCTGTGGGCCAGATAGCTGTTCTCCTGAGTTGCANGCACGATGGAGATTTGGACACT G

ESTC72	37	---	---	---	GGGCTTCCAAATGGGTATTGGGGCCAGGAGGCTGGCNTTTGGCGTGACGCCTAAAAAGTGTGACC AACAAATTCACAGCTACAGGAAATCTAGAACAAAATCAAAATATTCATCAGNTTGGGTTGAAAAAGTTG GAAGA
ESTC74	49	---	---	---	ATGACTTTCCTGTCCCATCGGAACACAGAGTTTCCCCAGGNGAGCCCTTCCTATCTGCGGTTA
ESTC77	40	---	---	---	GGCTCAGCACAGGGATAAGANCCCCACTCCGCATGTCCCCAGAGGGCAGCACTCCAG TTTCAGATGATGGGTCTGAGATGNTCCTCAGGCTGCATCAGCTGTCTTCAGTCTCCAGAACAGAAA GAGCCTGACCCA
ESTC81	20	---	---	---	CAAAATCAATACACAGATCCAGATATGTGAACCATATATACATATCTATACANCCATTATTTAGAC TTTCACAAACCT
ESTC82	25	---	---	---	TTTAGCTGCTATACCAAGTTTCCATAAANCTGTCTGCTGTTGGGAGGCTACAGCCTGACCACATTG TTTGC
ESTC83	53	---	---	---	ATTGCAAGGAAGTGAACGTGNTCAACACAGAAATGGTGACAATGA
ESTC85	28	---	---	---	CTGGTCTCTTCGTCCTGGCATTGGCTCCTCCTCNGGCCAGTGCTCCACCCAAAGTGCTCTCCCGATGAT
ESTC89	22	---	---	---	CTCCCTCCTCAGTTCACAGTGGAGACTANGGAGATTGAGGCGAGGATCC
ESTC90	33	---	---	---	GCACGTTCTTTGTTCTCCTCTCCAGAAGTTGNAGACGTCTATTTAGTTTGATTATCTGTCG
ESTC93	29	---	---	---	AAATGACTTGACGAAGCTCATAGAAGATTAGCAGGTAGTAGAATAATGACTGCTGACTCCTAAATCA GTGGATCTCCCTGGCCACCGTTTGTATTGAGCTGCAATGCTTCTTGACTGTTCTCCA[C/T]GCCAG ATTCTTATCAATGATCTTTCACCTAAGAAACAGCAAAAGATTCTGGCAAGCACACGATCTAGAGATAC ATCTTATTGCGATTTTTCACAAAAATCAAAAGAAAGAAAGGCTTAGCTG
DWU-100	127	C T	---	---	TTCCATCCTAGATATCTACTCAAAATAATTGAGACAAGTGTTCAAACAGAAAGACGCTTGTGCTGAA TGTTTCATGGC[A/G]GCCCTATTACAGTAGCCAAACGATGAAACACACCCCAAGCTATATATACCA GATGAAAGGATAAACAAAAATGTGTCCATCCATACAATGGAGTATTACACAGCCATAAAAAAGGAAT GAAGCAGTGATCCCTACTACACTGTGGAT
DWU-177	77	A G	---	---	CAATACCTGGACTATCAACCTTGTGCTTAATCCCTGCAGCATTCAGGTTAATCCATCTAAGTGAC ATTTTGAATTCAGCGGTGCCACCAATATCAGCCAGCTTCTGTGATATGATGAGATATACATTT ATGCTGACCTCCCTCAAGACTGATTTTTCATGTCTGGGACTTACAATATCTCAAGGAACAGCAATG TCAACAGGG[A/CT]GGGAAACCAAGCCCTATCTGAGTCTTGGCTCCCTCC
DWU-286	213	A C	---	---	

DWU-252	94 A G ---	---	---	AGTATACAAACATTTAAGCTGTGGTCAAGGCTACAGATGTGCTGACAAGGCACCTTCATGTAAAGTGT CAGAAGGAGCTACAAACCTACCTCA/A/GT/GAGCATGGTACTTGGCCCTTTGGAGAACAAATCGGC TGCATTGAAGATCCAGCTGCCTATTGATTTAAGCTTCTCTGTGAATGACAAAGTATGTGGTTTTGTA AT
DWU-330	85 C T ---	---	---	GAACATTCCTCTGCAGCACCTTCACTACCAATGAGCATTAGCTACTTTTCAGAAATTGAAGGAGAAAA TGCATTATGTGGACTGA/C/TGGACTTTTCTAAAGCTCTGAACAAAGCTTTCTTCTCTTTTGCAA CAAGACAAAGCAAGCCACATTTTGCATTAGACAGATGACGGCTGCTCGAAGAACAAATGTCAGAAA CTCGATGAATGTTGATTGAGAAATTTTACTGACAGAAATGCAATCTCCCT
DWU-370	231 A G ---	---	---	GAAATGTTAATTGGGAGGTGAAAGGGTACAGATGTGCTGTAGCAGACCTTTGGTTTTAAAGAG AAGCATCATTTTCCCAACAGGGCAACTGTAGAAGGCCAGCTGAAGAGTAAAGGAAAAGTCTGAGG ACTGAGCCTGTGGCTGGCTGGAAAGGTGAATGTTGAGGGCCCTTCACTCCATCACAAAGAAATC ATTAGACGGTACCAATTCAGTGTCTGTCTCTA/GJ/GCATCTATTCTCTCTGTGC
DWU-1537b	89 A G ---	---	---	CTCTTAACCTTCAAGTTCCCTCATCTATAAGAAATAAGGGATTCAAGTTGTGATCACATAGCTCAGGTAATC CAGGACCAAGAAACCCAGGAGC/A/GTGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTTCTGAACACACAAAGAAATCCAGTAAGCAGCACACACTGGCTGA
DWU-1537a	52 C T ---	---	---	CTCTTAACCTCAGTTCCCTCATCTATAAGAAATAAGGGATTCAAGTTGTGATCA/C/TATAGCTCAGGTA ATCCAGGACCAAGAAACCCAGGACATGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTTCTGAACACACAAAGAAATCCAGTAAGCAGCACACACTGGCTGA
ESTD-ADAb	196 C G ---	---	---	ACCATCTTACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCTGGGAAATCCAGGGTCACTGTTCCTTCTCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAGTGGGACTGTGAGGACATGGAGGCCCTCGGCACCTGAGCTG/C/GJAGA CCCGCAGACCAACTCCTGAGCTTTCTGGGCCCTCTGAGCTTTGTCTC
ESTD-ADAa	184 G A ---	---	---	ACCATCTTACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCTGGGAAATCCAGGGTCACTGTTCCTTCTCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAGTGGGACTGTGAGGACATGGAGGCCCTC[G/A]GCACTGAGCTGCAGA CCCGCAGACCAACTCCTGAGCTTTCTGGGCCCTCTGAGCTTTGTCTC
ESTD-ANT1	160 T C ---	---	---	TCTCCTGTCACTTCTACTCCATTAGTTCAAGGTCAAGTGAAGAACCTGGGGCAATTAAACCAAGTAATTCA TGGACTGCCCAACTCGGAACAAAGAGGGCGCAGTGGAGCAGGAGTATTATGCTACGGGTTACCTT TTTTTATGGAGGACCGAACTGAGGC/T/C/GAGCTCAGATGATCCTGT
EST10398 2b	168 A G ---	---	---	TGCCTGGGGTGGCAAGGCTGCAACCAAGGAGGCCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGTATGATGTTTCAACATTTGGGGCTTGACTTTCCAAACACGGAGAAG CATTGTTTTCTTCGGGCCAAGAAAGGTATCTACC[G/A]GATAGTGTCTATTAGGCATTG

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EST10398 2a	147 C T ...			TGCCTGGGTGGAAGGCTGCAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGTATGATGATGTTCAACATTTGGGGCTTGACITTTCCAAACACGGAGAAG CATTTGTTTCTTCTCTGGGCAAGAAGTATCTACCAATAGTGTCTATTAGGCATTTG
ESTD-C7	14 G C ...			ATATCGTGGCCTTAG/CJTACCTAGAGCTGGACAATCCTGCTGGA
ESTD- D4S95	90 T C ...			CTTTTCATGCACGATAGGCTTTCTCTACTAATCACAGAAATTTGAGAAGAGCAAAACAACCTTTCAAGG ATAATGGGCAATCACITTTCTTTT/CJCTTCTTAGAGTCTACCGG
ESTD- GPPK2L	38 G A ...			AGTCTTCATCTCGGGTGTCCAGGTAGATCCCTTTTACCIG/AJCCGAGAACTGCTCGATATC
ESTD- HRASb	82 A G ...			CTGGGCTCGCCGACGAGCTGCTGGACCTGGACGGCGGCCAGGCTCAOCTCTATAGTGGGTG TATTCGTCCACAA/AJGTGCATCTGGATCAGCT
ESTD- HRASa	37 C T ...			CTGGGCTCGCCGACGAGCTGCTGGCAOCTGGACGG/CJGGCGCCAGGCTCAOCTCTATAGTGGGG TCGTATTCGTCCACAAATGCATCTGGATCAGCT
ESTD- NRAMP	81 A G ...			GGAGCAGGAGGTGGGAGGGGTCTGTCTGCCAGTCCACAGACAGAGGAGCGGCTCAGTG TATCCCAACCCCA/AJGTGTGGCGCTGGAGATGAAGAGGATTTGATGCAGGT
ESTD-OTC	18 A G ...			GTGACCTTCTCCTTTAA/AJGAAACTTTACCGGAGAGAAATTAATATATGCTATGGCTATCAGC AGATCTGAAATTTAGGATAAAACAGAAAGGAGGATGTAACA
EST36751 7	36 C T ...			CCAAAGTGGTCAATTTAGCTTTGCAGGTTTAACT/CJGATTACTTTTCTATTCAAATCTCTGTA AAATTGAAATATGAACCTAGTTTCTGATCTATGGTTTCAAGTTAAACAG
EST40562 3	109 A G ...			CACGTGGAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAACTGTCCCAAACTTGTTGGCTGAC TTTATGGCTAAGAAATTTCACTGGATGCATTAATAACAAAT/AJGTTTTTACCTTTTGAACAAATAA ATGAAGGATTTGACCTGCTCGCTCTGGAAAGATATCCGTACCGTCTGACGTTTTGAAACAATACA GATGCCTTCCCTTGTAGCAGTTTTCAGCCTCTCTACCCCTA
EST18288 3	121 C T ...			GCCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA GATTGACAGGTTTCATGCAGGCTGTGACAGGATGGAAGACTGCTCCCTGA/CJGGGAGCCAGT GTGGACAGCACCCCTGGCTTCAACACCTACGTCCACTTCCAAGGTAAGGCAACCTCTCTGCTGGCTC TGGCCCTAGGACTTAGTATCC
ESTD-AK- 168	31 C T ...			GGGAGTGACAGCTAGAGCACCAAGGGGGGCT/CJTACAGCTGTGTTCTCATGGAGGACAGGCTTCT GCTCATTTCTGG
ESTD-ALB	180 A G ...			AATCCAGCACTTTAGGAGGCTAGGCAGGCATATCACAGAGGTCAGGAGTTTGAGACCAGTCTGA CCAACATGGTGAACCCCATCTCTACTAAAAATACAAAATAGCCAGGATGGTGGTGCATGCCTGT AATCCAGGAGGCTGAGGCAGGAGAAATCGCTTGAACCTGGGAGGCG/AJAGGTTGTGGTGAGCCGA GATGGCAACATTGCACCTCCAGCCTGGGCAACAGAGTAAACCTCTGCTCTC

EST70523 3	182 G T ...			TTCCGCCAGCCCCCATCTTGGCACCCCTGGTCCCTCAGGGGCCACCCCGCGGCACTCACCGCTCT CGCTCTGGTAACATCCGGCCGGCCGCTCTTGAACACATAGCCTGGACCGTTCCGTATAGGAGG ACCGTGTAGGCTTCTGTCCCGGGCTTCCAGGGGCCAGCCCTGTCAGAGAGAGGGGTCCCTGT GGTTGAGCTGAACACAGCTGTGGAGTGTCTCCACGCTG
ESTD- APOA2	101 C T ...			CCAGGTGTTGTGCACGTGCCTGTAATCCAGCTACTCGGGAGACTGAGGCATGAGAATCTTTTGAAC CGGGAGGGGGAGGTTGCAGTGAGCTGACATGCTGTCAGCTGCACTCCAGCCTAGGTGACAGAGC AAGACTCC
EST58707 7	112 C T ...			CAGTGTATCTGGAAGCCTACAGGACACCAAAATAACCTTAATCATCAATTGTTACAGGAGGCTTT AAGTTGAGCATCTTTGGCTCATGAAGGCCAAATCCGAGAGACCTCTAGAAAGATACACGAGAC CGAATGTATCAATGGACATTCAGCAGGAACCTCAACGATACCTGTCTGTGAGGCCAGGTTTATA GCACACTGTCACTACATTTCTGATTGGTGGACTCTTGCTGCTAAGAACCCTT
EST74167 6	137 C ...			AGACCATGAAGGAGTTGAAGGCTACAAATCGGAATCGAGGAACAACCTGACCCGGTGGCGGAGG AGACCGGGCACGGCTGTCCAAAGGAGCTGCAGGGGGCGAGGCCGGCTGGGCGGAGCATGGAGGA CGTGGCGGGCCGCTGTGTGAGTACCGGGCGAGGTGCAGGCCATGCTGGCCAGAGCAACCGAGGAGC TGCGGGTGGCTCGCTCCACCTCGCAAGCTGCGTAAGCGGCTCTC
EST43211 8	132 C ...			CGCTGTGTCAGTACCGCGCGAGGTGCAGGCCATGCTCGGCCAGAGACCGAGGAGCTGCGGGTGCG CCTCGCTCCACCTGCGCAAGCTGCGTAAGCGGCTCTCCGGATGCCGATGACCTGCAGAGCGCC TGGCAGTGTACAGCGCGGGCGCGGAGGGCGCGAGCGGCTCAGCGCCATCCGCGAGCGCTG GGGCGCTGTGTGAACAGGGCGCGCTGCGGGCGCGGCTGCTG
ESTD- AFSB	126 A ...			GGAGAAATGGAGCCTGTGGAGGAGGCGTCCGAGGGGTGGGCTTTGTGGCAAGCCCTTGCTGA AGCAGAGGGCGTGAAGAACCGGGAGCTCATCCACATCTCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTCGACGTGTGGAAACCATCAGTGAA GGAAGCCCATCCCCCAGAAATGAGCTGCTGCATAATATTGACCCAAAC
EST36770 4	144 C ...			TGTAGCCAAAGTCACTGCATCATCATTTGGCTGCTGGCAGGCTTGGCCAGTTTGCCAGCTATAATCC ATCGAAATGATTTTTCATTGAGAACACCAATATTACAGTTTGTGCTTCCATTATGAGTCCCAAAT TCAACCTCCCGATAGGCTGGGCTGACCCAAATATACTGGGTTTCCCTTTCTCTGATCAT TCTTACAAGTTATCTCTTATTGGAAAGGCCCTAAAGAGGCTTATG
EST26021 1	137 A ...			TAATGTAAGCTCATCCACCAAGAGCCTGCACCATGTTTGGAGTTGAGTGACATGTCGAAACCTGT CCATAAAGTAATTTGTGAAGAAGGAGCAAGAGAACATCTCTGACGACCTCACTACCAATGA GCATTAGCTACTTTTCAGAAATGAAGGAGAAAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTCTTCTTTTGCACAAGACAAAGCAAGGCC
ESTD- BA511	29 A G ...			GGGCAACATAGTGAACCCCATCTACA/G/AAATACAAAATAGCCAGGTGTGGTAGCAAG TGCCTGTAGTCCAGCTACTTGGAGGCTGAAGTGGGAGGATCCCTAAGCCTGGGAGGTGGAGGCTG CAGTGAGCCCAAGATGGTGCACTGCA

[illegible]

ESTD- CB22	119 C T	---	---	GGCAAGTTTTATTGATAGAGAGGAATCAAATAATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAATGGCAGTGCACACCCATAGGG[C/T]GGATACAAAAG ACAGCAAGGAAGGGTAGAACCATCAAAGAGGAATAGGCTGGTGACCCCAAAGCAAGGAGGACCT AGTAACATAATTGTGCTTCATTATGGTCCTTCCCGGCCCTCTCTCACACAC
ESTD- CB23	136 C	---	---	TAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCAITATGGTCTTTCCGGCTTCTCTCACACATACAGAGCCCTACCAAGGACCAGACAGCT CTCAGAGCAACCTAGCCCCATTACCTCTCCCTTCCAGAGGACCTGAAAACGTTGCCACCCGA GGTCGTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCCAAAA
ESTD- CB24	145 A	---	---	ACCAGGACCAGACAGCTCTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAA AAACGTGTTCCACCCGAGGTCGTGTTTGAGCCATCAGAAGCAGAGATCTCCACACCCCAAAAG GCCACACTGGTATGCCCTGGCCACAGGCTTCTACCCGACCACGCGGAGCTGAGCTGGTGGTGAATGG GAAGGAGGTGCACAGTGGGTGACACAGACCCGACGCCCTCAAGGAG
ESTD- CB25	146 A G	---	---	GTTTTCTTACAGCTGTGGCTTCACTCCGGTAAGTAGTCTCTCTCTTCTCTATCTTTCGCCGTC TCTGCTCTCGAACCAAGGCATGGAGATCCACGGACACAGGGCGTGAGGAGGCCAGAGCCACCTG TGCACAGGTJA/GJCTACATGCTCTGTTCTTGCAACAGAGCTTTACCAGCAAGGGGTCTGTCTGCC ACCATCTCTATGAGATCTTGCTAGGGAAGGCCACCTTGATGCCGTG
ESTD- CB27	125 C T	---	---	TTTTCTGTTTCCCTGAAAGATTGAGCTCCCAACCCCAAGTAGCAATAGGCTAAACCAATAAAAAAT TGTGTTTGGGCTGTTGCATTTCAGGAGTGCTGTGGAGTCTGCTCATCACTGAC[C/T]TATCTTC TGATTAGGGAAGCAGCATTCCTTGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCCAATGCT GCTTCTCCTGTTCACTCTGATGGAAGTCTCAACACCACTTCCATACC
ESTD- D4S338	59 A T	---	---	TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGA/TATGTGA TTTCTTAAACAATAAACTGAAAGTCCAAAATTACTCCTTGATCCATGGACTGCAGAAATAATGTTA TTTTAGCTGTCAGAAAAACAATACTAATCTTGACATATGTTTCATCAGAGCCCTTGGGTGACCAGGTGA TTGCCAATAAGCAGTAATAATTTGAGAGGAATCTTGTTTCAATGCAGTAG
ESTD- CYP2D6	61 A G	---	---	CAGGCCAGCGTGGTGAGGTGGTCACCATCCCGGCAGAGAACAGGTGAGCCACCCTATGCA/GCA GGTTCTCATATTGAAGCTGCTCTCAGGGTTCCTTGGCCTGAGCAGGGCCGAGAGCATACTCGG
ESTD- D11S1873	40 A C	---	---	AAAAAACATTTTAAACCTTTTCAATCATATACACCATAG/CATTTCCATTTTTCACATAAGTCA GTTTGAGCTGAGTTTTCOAATTACTTGCAATCTAAAATGTCACTAAGTGAATATGCAAGTTCAACAG ACAACTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATATGCCCA TATCTGCATGTC
ESTD- D17S33b	169 C T	---	---	CATCCCCAAGCCCATCCTCTTAGCCACTGGCATTTTTTCCGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGCCCTACCCCTTTGTAGTCCATGGAAAGGCTCCTCTGCGGCGGTG GGGTGTGTGGCTATGTGGTGGTCTTGTTGTAGA/C/TGGGGGCTTTGGTTTCAGTTGCATATTGCGTT ATTGCAGATTGCTTTGCTTTCCACCTGAGGAGCCCTC

ESTD- D17S33a	75 C T	CATCCCAAGCCCATCTCTAGCCACTGGCATTTTGGCCCTCTGACAGATACACTAGGGCCGT CATGCTGCTACACATCCAGGGGGCCCTACCCCTTTGAGTCCATGGAAAGGCTCCTCTGGGGCG GTGGGGTTGTGGCTATGTGGTCTTGTGTAGACGGGGCTTTGTTTCAGTTGCACATTGCGTT ATTGCAGATTGCTTTGCTTTCCACCTGAGCGAGCCTC
ESTD- D18S8	133 A G	TTTGAGACCACCTGGCCAACATGGCGAAATCACATCTACCAAAATACAAAATTAGCTGGGTGT GGTGTACATGCCATCGTAATCCAGCTACATCGGAGGCTGAGCGAGGAATTGCTTGAACCCJA /GJGAGGCGAGAGCTTGCAGTGAGCCAAAGATCACACCCTGACACTTACAGCCTGGGTGACACAGTGA GACTCTGCTCAA
ESTD- D3S11	44 G	AACTGATTAGAACCTGAAATACATATTTTATCTGAAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAATAAAATCCAAATAAAGTACACTGTAATAAGAAATTAACAGAAATATCATTTG TTATCAAACTATTATCACTTATTTTATTGGTAAGCCATACTAAATCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	37 A G	AGGTTCCACATTATGCTGATGTTTCTGATGTTTCCJA/GJGAGCCCTTGATGTCATCTGATCTCCT CAGGTATCCACCTTGAGACGTACTTTTCAAAAACCTCTACAGCCGTTGTTGTTATTAATCAAGGT TGAACATAAAGTA
ESTD- D3S2b	247 C T	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGTAGCAGAACATTTCCTGC TGAGTCTTATTCAAACCTGACAGCCATTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATCCC AGAAGTGAACATACCTGCTCCTAGAACCCAGAGTCATAGTGTCTGTTTGGTCTTCACGATGG CAGGTATGAAATATAATACTGTCTTATTGGAAGGATGCCGTTATGT
ESTD- D3S2a	248 G	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGTAGCAGAACATTTCCTGC TGAGTCTTATTCAAACCTGACAGCCATTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATCCC AGAAGTGAACATACCTGCTCCTAGAACCCAGAGTCATAGTGTCTGTTTGGTCTTCACGATGG CAGGTATGAAATATAATACTGTCTTATTGGAAGGATGCCGTTATGT
ESTD- D7S399	83 A G	TGAATCTTAATTGCTATCTACAAAATGTATAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCJA/GJGCTCCTACATCTCCTTTTCAAAACATTTTCATCCATGGACTCCATAG TAGAATATTGAAGAAACAACATGACAAACATTTTC
ESTD-DMb	146 A C	GTGGGACACCGAGGGCTCCAGGCTGGGGCTTGACGCTGTGGCTCAAGCAGCTGCTCGGCTCCACT TCCATGGGTGTGGGCTGGGACCTCACTGTCCCTGGGGAGAGGAGGGAGTGGGAGGGAGACA GAATGCTGATTAC/JCTGTGGTGAGAACCAAGAACTTCTGGCTGTGGGTAGGGCAGCTGCTTCCAAAG ACCTCCTGATTGAGGAAGGGGAGCAGAGCGAAGAGAACAGAGT
ESTD-DMa	66 C G	GTGGGACACCGAGGGCTCCAGGCTGGGGCTTGACGCTGTGGCTCAAGCAGCTGCTCGGCTCCAJC GTTCCATGGGTGTGGGCTGGGACCTCACTGTCCCTGGGAGAGGAGGAGGAGTGGGAGGGAGAGA CAGAACTGCTGATTATCTGTGTGAGAACCAAGAACTTCTGGCTGTGGGTAGGGCAGCTGCTTCCAAAGA CCTCCTGATTGAGGAAGGGGAGCAGAGCGAAGAGAACAGAGT

ESTD- DRD1	154 C T	TCCCAGCCCTATCGGTCAATATGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAACCCCATCAC ACAAACGGTTCAGCACCCCAACCTGAACCTGCAGATGAATCTCTGCACACATGCTCATCCCCAAAAGCT AGAGGAGATTGCTCTGGGGCCTTCGGCTATTAGAAACTAAGGTAC
ESTD- DRD2	144 C	TCTGCCCTTGGTGCAGGAGGCTGCCGGCGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGACCCGGTACAGCCCCATCCACCCAGCCACCACTGACTCTCCCCGACCCG TCCCACACGGTCTCCACAGCACTCCGACAGCCCGCCCAACCCAGAGAAGATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTGGATCCAGACCATGCCCAATG
ESTD- DRD3	109 C T	AAGACGATGCCAGGATGAGCGGCAGTAGGAGAGGGCATAGAGCATGGGGGGGCTGGCTGG CACCTGTGGAGTCTCTGCCCCACAGGTGATGTTCAAGTGGCCTCTACTCAGCTGGCTCAGAGATGCC ATAGCCCAGAGGAGGTGCGTATGCCAAGGGCTTCTGTGAGGAGA
ESTD- ERB82	93 C T	TCTTTCAGGATCCGCATCTGCGCTGGTTGGGCATGCGCTAGGTGTACGCGGCTCCACCAAGCTGG GGTGAGGGGGTGGTGGTCACTGCGCTGGGGGGCGGTGCAGACCCGCGGGCTGGGAGGACTTCA CCCGCTCACCTCCGTTCTCTGCAGCATCTCCGCTCGTACT
ESTD- ETS2	43 A G	ACTCACAGTGCTTTAAGTGAATGGTCGAGAAAGAGGACCCAGTGGAAAGCCGCTCTGGCGCCTG GCAGTCCGTGGACGGGATGGTCTGGCTGTTGAGATCTCAAGGAGCGAGCATGCTGTGGACACA CACAGACTATTTTAGATTTCTTTTGCCTTTTGCAACCAGAACAGCAATGCAAAAACCTCTTTGAG AGGGTAGGAGGGTGGGAAAGAAACCAACCATGTCTTTTTCAGAAAGTTAGTTG
ESTD-F9	111 A G	AGATCCTGATGATTTTCTCTATTTTCTAAATGTTTTACAGTTTGAAGTTTATGATTTATGCCCA TGCTCCATTTGAGTTAATTTGTAAAGTATGATGTTTAA/GTGCAAACTTCATTTTTTTTTTTC ATAGGTATGTCCAAATTTATCCAGCACAAATTTGTTAAACAAAAAAC
EST68787 5	144 A	CTTCTATGGGATTTGACTTTATTTCTCCATTGCTTACCTTTTACAGGTGTTAATATAGTGAAGAAG GAAGCTTCAGCTCATGACAAATTTGAAGCTGACAAATACACAAGAAAGGAAATAAATTCACAGTCAA AGAAATCAAGCACTTTTCGAAACATTTGAAGTTGTTTTTGAACTTGGTGTACACCTTTAATTACAACTAG CAGACGGAACTGAACCTCAGGGTAAGAAT
ESTD- G00H	200 C G	CGCAGACCGGTGAGTGGGGTGGGAGTGTGGAGGGAAGGAGGGGAACTGGGGGTTTAGGGACT TTCCGGGGTACTTTCCCGTCTGTGCTTGCAGAGAAAGGGGGGAGAACACAGAGCCAACTGGCTAA GTGAAGGGACCTCTGTGCGACCGTGTGTTCTGCTGCCCTGTTTACAGCTGTCTGTCTGCCGCACTC/ G/GACTCTGTCCCGAAATTCGAGAGCT
ESTD-GCK	88 A G	GTTTTATGCATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCTCTGGTCACCATGAC AACCACAGGCCCTCTCAGGAAGTACAGTAAGCCCTGGCAGGAGAAATCCCCACCCACACCTGGC TGGAGCAGGAATGCCGAGCGGGCTGAGCCCCCAGGGAAGCAGGCTAGGATGTGAGAGACACAGCTC ACCTGCAGCCTAATTACTCAAAAGCTGTCCCGAGGTCACAG

EST34088 2	62 A T	GTGGGGCAACAGTGGGAGAGAGGGGCCAGGGTATAAAGGGGCCACAAAGAGACCGGCTC(A/T) AGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCTGTGGACAGCTACCTAGCTGCAATGGCT ACAGGTAAG
ESTD- GNAT2	56 A G	GACCTGAGTACCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGGTCAAAACCCAC(A/G)GGCATCA TTGAAACCAAGTTTCCGTCAAAGACTTGAATTCAGGTAAGTGCATGGTTCCCTAGG
ESTD-HT2	154 G	GGCTAAATTTCCGAGCAACTTGCATAGACTGTTTATTGACTTGACAGGATTGCTAGAGATAGG CAGGAGAGGAAGATGTGTTACAGTTTGTACAGAGATAAAGGATAACCTGGGGTTTCTGTGC TTTGCTTTCACATCCCTGGGAGTTAATAGCTGCAATTTTCAAAGACGGTATACAGGGACAGCA AAGCGCAGTCTGAAGTTTCAAACAAGACACACCTT
ESTD-HT5	149 C	AACACAAAGCCCCAGCGAGAATTGAACCTCGGACCCCTGGTTTACAAGACCAAGTGTCTAACCCCT GAGCTATGGAGCCCTCGTCTGCTGTTGTTTTCTCTTTCATCTTATAGATTGATTATGCTCTTA GCATTCGGCTACCGAATAGGATGTTAGCTTGAGTAAATTCAGGATATTCCTCACAATAATGAAA ACATTTTCGTGCTCTGTAATCCCTCGAAAGGTTCT
EST37382 5	124 A G	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCCACCCCTCTTCTCTTCCCTTGA CTTTGAGTCAAAATTGGCTGGACTTGAGTCCCTGAACAGCAAGAGAGAAAGAG(A/G)CCCCAGA AATCACAGGTGGGACGTCGGCTACCGCCATCTCCCTCTCACGGGAATTTTCAGGGTAACT ACCCAGTGGAGCCCGCTCATTGCACGGTCTTGGCAGGAGTG(C/T)CTGGGAGAGAAGGAAGATG TTCAGGGCACACATAGCTTAGTGGAGACTC
ESTD- IGHV4-6	120 C	TTTACTATTTCAATGGATACAGAATTGTGGGAGTCACTATATTCCTATGAACAAAAAATTCAGATTT CAGTGTAAAGTAATGTTGCCCTACATTGTGAGTGACGGGCGAGTGGTGATCCGAGAGTGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGAAAGATGAGTATCTATGGATACGAACTGAAAGT ATGTAATACITTCACAAAATACTAATAACGGGAGTTGAATATAAAACCCA
ESTD-IL1A	110 A G	CAAAGTAAGCACCCCAATAAATGTTAGCTATTACTATCACTATTATTATTATTTATTTTTTG AGATGGAGTCTGGCTCTGTACCCAGGCTGGAGTGCAGTGGC(A/G)CAATCTCGGCTCACTGCAAGCT CTGCCCTCTGGTTTCATGCCATTCTCTGCTCAGCTCCGAGTAGCTGGGAATACAGGCACCCGCC ACTGTTCCCGGCTAATTTTGTATTTTAGTAGAGACGGAGTTCACCGT
ESTD-IL1B	99 A G	CCACTTACAGATGGATAAATGGGTACAATGAAGGGCCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGTCTCTACCTTGGTGTGCTTCTCTGCTC(A/G)GGAGCTCTCTGTCAATTGCAGG
EST74082	134 A T	TCCAGGTGGCTGGACCCAGGCCACGCTCTGCAGCAGGGAGGACGTGGCTGGCTGTGAAGCATG TGGGGTGAGCCAGGGGCCCAAGGACGGGACCTGGCTTACGCTGCTCAGCCCTGCTGTG(A/T) TCCAGATCACTGTCTCTGCAATGGCCCTGTGGATGGGCTCTGCCCTGCTGGGGCTGCTGGCC CTCTGGGGACCTGACCCAGCCGAGCCTTTGTGAACCAACACCTGTGCG

EST45311 0	151 C T	GGCCTCCTCTCTCCAATTCGTCCCTATAGTTTCTCTCTATTAAAGTGAACATACATGCATCTTTTAGT GGATAGATGCACACAAACACACAGCCATTATGGGAAGGATCCACGTGTGGCCATATTGTAAACA CATTTTCTGCAAAATC/TACCTCTTTCATTTAACAGCCCTATTCAATGGCCCTTTTCTTTTTCAGTA GTACATACACATCTGTGTCATTGTGAAT
EST65258 8	80 A G	TGCCCCATACGCGCGGAGACATGGCTTGCCACAGCTCTTGAGGATGTCACCAATTAACCAGAAAT CCAGTTATTTTCG/G/GCCCTCAAATGACAGCCATGGCCGCGGGTCTCTGGGGCTCGTCGGG GGGACAGCTCCACTCTGACTGGCAGAGCTTTGCATGGAGACTTGAGGAGGAGGGCTTGAGGTTGGT GAGTTAGGTGCGTGTCTCTGTGCAAGTCAGGACATCAGTCTGATTAA
EST38216 3	26 A T	ATGCAGATGAAGGTGGACAGGGAGGAT/GAGGGCCAACTGTCTATCCAGGCGCTGCAGATGTCG CTGGACTATGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGG
EST62782 149 G T	ATACTAGTACAAGTGGTAAATTTTGTACATTACACTAAATTTAGCATTTGTTTAGCATTAACCTAA TTTTTCTCTGCTCCATGCAGACTGTTAGCTTTTACCTTAAATGCTTATTTTAAATGACAGTGAAG TTTTTTTCTCTC/G/TJAAGTCCAGTATCCAGAGTTTGGTTTTTGAACGTAGCAATGCCTGTGAA AAAGAACTGAATACCTAAGATTCTGCTTGGGGTTTTGGTGCATGCA
ESTD- KRT10b	183 C T	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTAAAGTAACTGCTAAGTTTTTCCATTAAACCACCTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGT CTCTGCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT10a	133 A G	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTAAAGTAACTGCTAAGTTTTTCCATTAAACCACCTATTACTTCTAIA/ G/GAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTC TCTGCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT8b	231 C T	ACCTCACCCCTCCCTTAGCCCGTGGGAGGAGGAAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGCTTTAACAGCAGGGCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCCGTCTCAGGTTTACCA/C/TGTCAACATTGACACA
ESTD- KRT8a	21 C T	ACCCTCACCCCTCCCTTAGCC/C/TGTGGGAGCAGGAAATCTCTCCAAATCCATGAATACACATC GGATTGGACACCTTGAGAGCTTTAACAGCAGGGCTGACATGAGACCTCAGACAGAACTTTCTAGAG TTTGCTAGAGGTCAAGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCAT GGCTGCCTATCTCTCCCGTCTCAGGTTTACCACGTCACATTGACACA
EST75099 6	82 C T	CACCTTGCTGTAGATCTCCTCAGTGGCCGCTCTACTGGGTTGACTCCAACTTCACTCCATCTCA AGCATCGATGTCAA/C/TGGGGGCAACCGGAAGACCATCTTGAGGATGAAAAGAGGCTGGCCCCACC CCTTCTCCTTGGCCGCTTTGAGGTGG

ESTD- LF79	142 A G	GGGTGATTTGAGGCTCAGTTAATATTTCAAAATGTAAACCGTAGCAAAACTGCATTGGTATTAGA AAAAATAAAATTTCCAATATGTAGTGTGTATACCTGCCTCTGCCATGCAGCATCATAGCCTGT GGGAACCAG/GGGAGGGCTTCCCTTACCACCCAGA
EST35879 9	142 A C	GAGATCGGTGTGTGAGTTATTAGGCATGTTACCTGTGATTCTCCCAATCTTGTGCGTCCACCGATG GAACTGCCGGCAAATCCTGACACGTGTGACCCAGGTGTACCCAAATTAGGTGAACATGGCTTCGAG AGAGTTG[A/C]ACAGATTCTCTGGAAGACAGCAGCGGGATGGGGCAGGAGAGAGCTGCCTGGATGA A
ESTD- LMP2	35 C G	TACACACTTTCCCTTACCCATTCACTGAAACGACTC/GIGCAAACTGGAGCCTTGAGGAATGGAGT TGACCTTCCCCAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	113 C T	TGTCAGTGTCCCTAGGGCACCTCACCCTCCAGCTTCTCAGCTCTGGCCTGTCTGCTGCCTGCA AGGTTTGTCTTAATCTCAATCAATGCTCTTCATCTTTAG[C/T]AGCTGTGGGTTTGTGTTG TTCTCTGTTTGTCTAGTATCTGACTACTTTTAAATAAAAGAGATGTATCTAAACAAAATAG AGATTGTTATCAGAAGTTCACACATTTATTTAAATTTTTCACCTG
ESTD-MCC	45 C T	TTGTCAGGAGTGTGCTGATGCTGCCTCCCGCTCTGCTCCCTAGC[C/T]GAACTTCAGGACAACGTGC AG
ESTD- METH	118 C T	CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTCTGTCTTCCAAAGGTTTGGTCTAAGTGTGATTACC[C/T]GGATTTTCTGACG ATCTTCAACTGCTAGAGCATCTGGTCTCTGTTTAGCATGG
ESTD-NF1	25 A G	ATTATCCAGATGAATTTACAAAAC[TAG]TACCAGATCCACAGACTGATATGGCTGGT
ESTD- NFKB1	107 A G	AAATGGACTTGATATTTGTACAAAAAAGTTTTATTTTCTAAAAAAGAAAAAAGAAAGAAA AAATTTAAAGGGTGTACTTATATCCACACTGCACACTGCCT[A/G]GCCCCAAACGCTTATTGTGT AGGATCAGCCCTCATTTTGTGCTTTGTGAACCTTTTGTAGGGGACGAGAAAGATCATTGAAATTTCT GAGAAAACCTCTTTTAAACCTCACCTTTGTGGGGTTTTTGGAGAAGGTTATCA
ESTD- NPPA	45 A G	TGTCCTTAGCCCCAGCCCTGCTTGTCTCCCTGGCTGTTATCTT[C/A]GTACTGCAAAAGAGAACACA GACAT
ESTD- NRAS	202 C T	GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATAATTTCTTCTGCAGGCATATAGAAATTTGGT GGGTTTCTTTTATGTAGGGTGATATTGGATACITTTTGTGTTGTGATTATATAGCAATTTGAGGG ACAAACAGATAGGCAGAAATGGCTTGAATAGTAGATGCTTATTTAACCTTGGCAATAGCATTG[C C/T]ATCCCTGTGGTTTTTAATAAAAAAT
ESTD-PAI1	100 A G	GCCACACACACCCACCCAGCACACCTCCAACTCAGCCAGACAAAGGTTGTGACACAGAGAGCCCC TCAGGGGCACAGAGAGAGTCTGGACACGTGGGG[A/G]GTGAGCCGTGTATCATCGGAGGCGCCGGG CACATGGCAGGGATGAGGGAAGACCAAGAGTCTCTGTGGGCCCAAGTCTTAGACAGACAAAAACC TAGACAATCACGTGGCTGGCT

ESTD-PAR	120 A	CTCTCAGGAACCAACAGTCTTCTTACCAACACGACTTATTGCTGTCCGAGAGGTACAACCCGTAGA ACTTCTTCTAACTGTAATTTAGTTAAAGGAATCGAACTGGCTCTGAAGACATGGAGATACTGCCT AATCGACTGGCTTTCATTAGCTCTGTAGTGTTTCTTCACTTCTGTTCTAGAACGTTTTTCTAG GACTGGCAGTTTAAGCTTTCACCTTACCTTGGCTTCTGTATACCCATGCCC
ESTD- Per/RDS	74 A G	ACCTACAGACGTCGCTGGATGGTGTCTCAACCCGAGGAATCTGAGAGCAGAGCAGGGCTGGCTG CTGGAGA/G/GAGCGTGGCGGAGACCTGGAAGGCCT
EST68308	29 C T	GGAAGAGATTAAAGAGCTTGATTGGA/C/TAATTCGGTCTTGTAGTGTGGAAGAGTTCATGTC TCTGCCTGAGTTACAACAGATCCTTTAGTACAGCGAGTAATAGATATATCGACACAGATGGGAAT GGAGAAGTAGACTTTAAAGTAAGAAAGTAGTATTTTTTA
EST54045	39 A G	GGAATATTAATAATTTTAAATACCTCCATTTTGTTC/GTTCCTTTTGTGAAGATGATACCTGC AAAGACATGGCTAAAGTTATGATTTGTCATGTTGGCAATTTGTTTCTTACAAAATCGGATGGGAAA TCTGTTAAGTAAGTACTGTTTGCCTTGGAAATGGATTTTAAATGTTGACTTTATCAT
ESTD- PXMP1	88 A G	ATGAAACATGGTCTTAAATTTATGATATGTTTGTATAGTATCTTAAAGGGCTCTCTTTTTTTA ATGCAGAAAGAGGGGAAAAA/A/G/GAGCGAGCTGTGGTGAAGGTGTTTTCTCAAGGCTCATAC AGATTCTGAAATCATGGTCCCTAGAACATTTGTAAAGAGGTAAAGTCTTATGAAATTTAATCTT
ESTD-RDS	127 A	CCCGAGGAATCTGAGAGCGAGCGAGGGCTGGCTGTGGAAGAAGCGTCCCGGAGACCTGGAAGG CCTTCTGAGAGTGTGAAGAGCTGGGCAAGGGCAACAGGTGGAAGCCGCGCAGACCGAGG CCAGGCCCCAGAGGCTGGCTGAGGGCCCTGGGGCCCCCTCCCTCCCGAACACTGAGAAATAGTGCAT CCAGAAACGTGGATCTCCCCCTCATCCAACCTCCGAAAGTCTGAA
ESTD- s14544	94 G T	TTGGGAAGTTAGAGCCTATATTAATTAACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAAGTTGAAATGTCAGTTC/GT/CTGTGTGGTTAGATGCAGGATTTATATGATCCGTTA ACCTCT
EST52908	45 A C	ATCACAGGTCTCTGGTCTCTGGCCATCATTTCTCTGGGAGAGATGG/A/C/JTGGTGGTCTGCAAGCCCTT TGGCAATGTGAGATTTGATG
EST19590	55 C T	AGGAGAAGCTGAGGAGGGGAAGAGAGACAAGAATGACATTGATGAGTGAAGATGT/C/JTGGCTCAG GATGCCGGAAAATGAC
EST76136	39 C T	TGAAGCTTCTGCCAGCTTGCAATTGTTCTAGGAGAAC/C/JTGGCTCATACCTTTATCTATAGCCTT CCCTAGGTCCT
ESTD- SPTB	176 C T	TGAACACCCCTGTGGTCCGGAGCCAGGTGTGTTCTCTCCGGAGCCTGAGGAGTTTGTGTCTGTGTG CAGTCCCCCGGCCACCTGCTGTGTGAGCCTGGACATACACCTTCACTTCTTGGCCCGGAGAAAGAC ATTTACCCACCTGGCCATGTCCTGGCCTGTTGTGCACAC/JTCCCTCTGTGAAGACCCCAACCCCTGC CTCCCCACCCCAAGCCAGTTCTCTAGCAAGGGCAGGAC

ESTD-TAT	224 C	---	---	AAATGGTCCAGGACCCCTGATCCACAAGAGTGGTACCAATTCATCAGGCCATCAGTTCATTACGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCATTATCTTAAATGACTTGTGGACAGGATCA ATTCTCTCACCTAGAACGTTGTTTACAACITTTCTCCAGTATGGATGGATTATGATGGGGGG GAGAAGCAAAATTTAAATAGGACCCATGAGACACATCA
ESTD- THPB	125 A C	---	---	TGGGCCITTTCTCCGGCAGGGTAGACTTCTTACTTGGCTGTTGATTCCAAAGAGAAAGAGTCCCAAG CACACGAAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAAATCACACAGGATC[A/C]TCTCAT CCACTGGATTGGCCAAACAAGTCTGAGTGCAGCCAGGACTCAACGGTCCCTGTAGATGGG TAGTGAAGTTTTTCATCTCTGTCAGCTTCTGGATTCTTGTCCACCCGCAAGAAGAGTCTATGC CAAGCAGAAAAGCTGGTGCTTCATGGGCAAAATCAATGCTCTCCAGATTTCAGTATCCCCAA GCAGTGCATCCATTGACACATAAATATGCATCCAGACAAAGAGGTCAATAAATTGATGTCGTATAA CATGGGTGTGATCCATTTTTCATTTGGCCATAGGTCCTATGGGATGACA
ESTD-TYR	122 G T	---	---	AGTAGTGGATGAAGCTAACCCAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGGTCTAACAAATGCCCTACTCTCTATGCATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTAATCACTGATTCTTCTTCACTTTATTACCTTCTTCT AATACAAGCATATGTTAG[A/C]ATTAAAGTTCTAGGCATACTT
ESTD- TYRP1	222 A C	---	---	AGTAGTGGATGAAGCTAACCCAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGGTCTAACAAATGCCCTACTCTCTATGCATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTAATCACTGATTCTTCTTCACTTTATTACCTTCTTCT AATACAAGCATATGTTAG[A/C]ATTAAAGTTCTAGGCATACTT
ESTD- TYRP1	222 A C	---	---	TTCOAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGCTGTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAGTCAAGAGACAGGACAGACACCCAGTG ACTCTGAGATGTCA[C/T]CAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCCGGGG ATGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12	148 C T	---	---	TTCOAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGCTGTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAGTCAAGAGACAGGACAGACACCCAGTG ACTCTGAGATGTCA[C/T]CAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCCGGGG ATGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12b	148 C T	---	---	TTCOAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGCTGTGTTTCTATTACA GGACAC[A/G]TGGATGCTGGAAATCACCCAGAGCCCAAGACACAAGTCAAGAGACAGGACAGACCA GTGACTCTGAGATGTCAACAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCCGGGG ATGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12a	74 A G	---	---	TTCOAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGCTGTGTTTCTATTACA GGACAC[A/G]TGGATGCTGGAAATCACCCAGAGCCCAAGACACAAGTCAAGAGACAGGACAGACCA GTGACTCTGAGATGTCAACAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCCGGGG ATGGCTGAGGCTGATCCATTACTCATAT

EST58607 0	105 A G ---	---	CTCTGGATGGGTTACAGGTGGCAGGCACAAAGCCAGTCCATCCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCCTCACTGGAGAACAAAGGACAGCCACAG/GJTGCGCGGGATGGCCGCGGGAGTTC TGGTTGCGGCCACGGCTGTGCCCTGTTGTGAACGGTAGCCCTTTCGCGTTGCGATGCCTAAACCTTTGT TTCTTGGCCAAAGGAGGGCGGGGTGCCATGCCTGAGATGTAGATGCGGCG
ESTD-VWF	36 G ---	---	AGGTAGGAAAAGCAAAGAGTTGATTAGTGAAGGAGAGAATGGACCTACCTCCACACTGTCTTTGG TCCCTAGAGTCTG
EST71770 6	189 C G ---	---	AGCACCACTCTCACGTCAGGCTCAGCACCAGATGCTGTTCTATAAGGATGACGTGCTGTTTACAA CATCTCCTCCATGAAGAGCAGAGAGTATTTATTCCTGAAGTCGGATCTATGACTCAGGGACAT ATAAATGTACTGTGATTGTGAACAACAAGAGAAAACCACTGCAGAGTACCAG/CJGJGTTGGTGGA AGGAGTCCCAGTCCCAGGGTGACACTGGACAAGAAAGAGGCCATCCAAGG
ESTD- TNFα	152 A G ---	---	TTCTGCATCCTGTCTGGAAGTTAGAAAGAAACAGACACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGTTTTGAGGGGATGAGGACGGGTTACGCTCCAGGGTCTACACACAAATCAGTCAGTG GCCAGAAGACCCCTCJAGJGAATCGAGCAGGAGGATGGGAGTGTGAGGGTATCCTTTGATG CTGTGTGTCGCCAACTTTCCAAATCCCCGCCCGCGGATGG
ESTD- TNFα	88 A ---	---	TTCTGCATCCTGTCTGGAAGTTAGAAAGAAACAGACACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGTTTTGAGGGGATGAGGACGGGTTACGCTCCAGGGTCTACACACAAATCAGTCAGTG GCCAGAAGACCCCTCAGAAATCGAGCAGGAGGATGGGAGTGTGAGGGTATCCTTTGATGCTT GTGTGTCGCCAACTTTCCAAATCCCCGCCCGCGGATGG
EST52418 6	113 A G ---	---	CAAAATACAGGGTCAACTGCTATGATGTTTGGAGCCAGTCACCTTTGGTGGCTACAAGATGTCG GGGAGTGGCCGGAGTTGGCGAGTACGGGCTGCAGGCATACACTAGJAGTGAAACTGTGAGTG TGG
EST13586 3	89 A G ---	---	CCCACTCTATTTGCCAGCCCCAGGGACAGAGCTGATCCTTGAACCTTTAAGTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCCJAGJGGGCTGGCTTATCAGCCTCCAGCCAGACCCCTGGCTGCAGA CATAAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGGTGCGTCTGCTGCTGCC CCGGTCACTC
EST51976 7	123 A T ---	---	AGGCAGAACTGGCCCCCATGGGGGACGTGAAGGCCACTTGAGCTTCTGGAGAAGGACCTGA GGGACAAAGGTCAACTCTTCTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAGJATCTCTCTC CCTCCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGGAGGAGCAGCAGGAGGATGCTG GCCCTTTGGAGAGCTGAGCTGCCCTGGTGC
EST11458 6	140 A G ---	---	CCACTTTGGTAGTGCAGTGTGACTCATCCACAATGATTTCTCCAGTGTCTATCTTGTCTCGAGTTTT CTCTGCCATGTTGCTATTGCAGGACGGACCTGTCCCAAGCCAGATGATTTACCATTTTCCACAGTGGT CCCJAGJTTAAAACATTTCTATGAGCCAGGAGAAGAGATTACGTATTCTCTGAAGCCGGGCTATGTG TCCCGAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCG

ESTD- AT3aa	60 C T ...	---	AGACCTCAGTTCTCTCTGTAAGGGAAGTTTGTCTTGATCTCCATGGGCCCCAGC/C/TJAGCA CTGGTGCCCTGTGAGTCTGTATCAGGTAGAGGAGATGGACAGGTGGAGAGGAATTTGAAAGGGCA TTGGAATTCAGAGCAAGAGACAGATATTAGAGCTGGGAAATGTGG
EST39852 8	108 C G ...	---	CGGTCTTCTCCAGGTATTGTCAGAAAGCCGAGATGACCTCTATGTCAGATGCATCCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCACCTCTTAC/C/GJGTACAGAAAGGAGATGCATGAACA GCAGGAACACGTGGAAGGCCTGTTCCAGTGTAAAGGCATGCAAAAGGCCTCCACAGGCTGCTAT AATACAGCCCT
EST62448 0	112 A G ...	---	ACCTGGTGTGCTGTGGTGAACCTGGTCTCTTGCCATTGCGGCCCTCTCTGGGCCCGCGTGG TCCTCTGGTGTGCTGGGTAGTCTGGAGTCAACGGTCTCTTAC/GJGTGAAGCTGGTCTGATGGCA ACCTGGGAACGATGTGCCCGAGGTCCGATGTCAACCGGACACAAGGGAGAGCGCGGTACCC TGGCAATAT
EST36027 2	120 A C ...	---	AGTGACTCCAAGGAATGGCTACCCAACTTGCCTTCATGCGCCTGCTGGCCAACTATGCCTCTCAGA ACATCACCTACCCTGCAAGAACAGCATTCATACATGATGAGGAGACTGG/C/A/CJAACTGAAAA AGGCTGTCAATCTACAGGGCTCTAATGATGTTGAACCTGTTGCTGAGGGCAACAGAGGTTCACTTAC ACTGTTCTGTAGATGGCTGCTCTAAAAGACAAAATGAATGGGGAAGACAA
ESTD- COL2A1cc	112 A G ...	---	AGAATGTATATAGTCTCAACTGGCCATCTCCATTTTCAAGTCCAAAAGTTATACAGTAGACAACA GTGGTACATACGTTGCTATTTATGCTCTCTTTCTGTCACTTTC/CJ/GJGGGTTCGAAGTGGAAAA GGTGAACAGGTCCCGCTGCTCCAGGCTTCCAGTCAAGTCAACTCAAGCATATACAATACTGCCT TTGTCAGCCTATTGAGCTGTAAATCACCATACCGTACCT
ESTD- COL2A1dd	97 C T ...	---	TGAGAGAACACCTAGTCTCCATCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTGCTGGGACCTGGAACA/C/JTGGACTTCTTCTACTGCAGCAGACAAGACTTA CCCAAGAGAGATTAAATGGCAAGATATACAATACAATTTTATTTGACCAAACTATCATGGAACA GCATT
ESTD- CPT2	150 A G ...	---	GCCGAATGCCCGGAGTTCTCCAATGTGTGGAGAAGCCCTTAGAAGACATGTTTGATGCCCTAGAA GGCAATCCATCAAAAGTTAACTTCTGGGAGATGAAAGCTACCATCACTTCTCATCATGAAAC TGGAGGCCGGGCAT/C/GJGTGCTCATGCTGTAAATCCAGCATTTGAGAGGCTGAGGCGGGTGGAT CACTTGAGGTCAGGAGTTTGAGACCAACCTGGCCAACAT
EST12274 0	135 A G ...	---	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTGCTTCCAAATAGAGCCTTACCAAGTGAT TACATAAAGAAGTCAAGTGGTTTACTCTCATGACCAATATCTTTCCCTCCTTAGGATGAGGTG A/GJTAGTAAATGACCGATGGGTGAGAACTGTTCTGTCAACCATGGAGGATACTATACTGTGAAGA TAAATCAAGCCACAGAGCTTGCCAGATC
EST76807	91 G ...	---	ATGCTAAGGGGATCGGACATGAAGGACCTGTGAGCCGATTTGCTCTATCTCAGCGGCCCTGTCTATC CAGCTCACTCATCAATGGGCCAGTCAGGCCAGGCACTGGGCTCCGAGGACTCACCACTGCCCT GCTGCCATGTGGACTGGTGCAAGTTGAGGACTTCTTG

ESTD-SSA1	111 C T	TTCACTTTGTGGATTGTTCTTTTGTGTGCAGCACCTTTTCAACATGATGTGATCCCATTTGTCCAAG TTTGGCTTTGGCTGCCTGCTGTGGGATATTTGAAAGAGATC/TTTGCCAGTCCAAATGCTCCTAGA GAGTTTCCCAATGTTTCTTGTAAATAGTTTCATAGTTTGAGGCCCTAGATTTAAGTCTTTAATCCATT TTGATTGATTCCTGTA
ESTD-RVRI	109 A G	CTTCGTGACGGGAGGTACAGTCCTCGCCCTCTTCATGGACATATGGATGAGTGTCTGACCATTTCC CTGCTGACAGTATGATGACCGCAGACTTGTCTACTATGAG/GJGGGAGCTGTGTGCACTCATGCC CGTCCCTCTGGAGGCTGGAGCACTGAGAAATCAGCTGGAGTGGAGCCACTGCGCTGGGGCCAGCC ACTCGAGTCGGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD-WT1	70 A G	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCTCCCTTCTCTTACTCTCTGCTGCAGGATGTG CG/A/GJCGTGTGCTGGAGTAGCCCGCACTCTTGACGGTGGCATCTGAGACCAGTGAGAAACGCC CTTCATGTGTGCTTACCGAGGCTGCAA
ESTD-F2 EST44438 7	100 C ... 62 C T	GATAAGTACACTGAGGCCCGCAGGAGTTATTGCCTAGTAGCCCAACTGTGCATGCACGCTTAACCTCT GCACCAATGGCTCCAAAGGCCGTAGGGAACTGGGGGATCTAGGGGATGGTGAGGAATGGCCC AGCCAGTCCGGCCGTGCTGGTCCCAACAGAGGAGGCCGTGGAGGAGACAGGAGATGGGC TGGATGAG
ESTD-PBDA	103 A G	GCAGCCAGGAGCCGCTGCACCATGCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGA/C/TG TCCTGCTCCGACCTAAGCGGAGCAGCCTCAAGAGCCGAGCGAGGTGGG
EST12839 3	122 A G	CCTTCATGCCAGATGGAATTCAGTCCCTTCAGGATCTGCCTAACCTGTGCAGAGTCTAAAGAGT CTGAGCCGTGGCTGGGAAGGCGAGGACTAATCCAA/GJTCCTACCCGCGAGCTTGCTGCGCATACAG ACGGACAGTGTGGTGCAACATTGAAAGCCTCGTACC
ESTD-CTLA-4	48 A G	TGCAAAACACACAAAATCTTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCCTCTTTGCT CCTAACATCTATGACTGGATTATCTAAATGAACACAGCAGCTTACTCCAGAG/GJTCAAAGTCCA AGGCCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGGAACTTGAATGTTATTCAAC TGGATTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACCTTAGCTTAG
ESTD-ACE	96 C T	ATGGCTTGCTTGGATTTCAGCGGCACAGGCTCAGCTGAACCTGGCT/GJCCAGGACCTGGCCCTG CACTCTCCTGTTTTCTCTCTTCATCCCTGCTCTGCAAGCAATGCACGTGGCCAGCCTGCTGT GGTACTGGCCAGCAGCGGAGGCATCGCCAGCTTTGTGTGAGTATGCATCTCCAGGCAAGCCAC
EST54419 8	88 A G	GATCAAGGAGTGCACACGGTCAAGTGGACAGCTCTCCACAGTGCACCATGAGATGGGCCATATA CAGTACTACCTGCAGTACAAGATCTGCC/C/TGCTCCCTGCTGGGGGGCCAAACCCCGCTTCCA TGAGGCCATTGGGACGTGCTGGCGCTCGGCTCTCCACTCTGAACATCTGCACAAAATCGGCCCTGC CTTCTGCCTAATTTGAATGATATTGCTGTGGGACCTGAGCACCTTTATGGCACAAATGATCACTA TTTTCTTGACCCCTACTTAC/GJATCCTGGGAGATGATTTGGGTTAGCGTGGTGCATGTTGTGCTA CTATAGTCCAAGTGAA

ESTD-PS-1	99 A G	GGGGAGTAAACCTGGATTGGAGATTCAATTTCTACAGTGTCTGGTTGGTAAAGCCCTCAGCAACA GCCAGTGGAGACTGGAACACACCAATAGCCTT/GJTTCGTAGCCATAATTAATGGTTTGTGCTTAC ATTATTACTCCTTGCCATTTTCAAGAAAGCATTGGCAGCTCTCCAATCCATCCATCACCCTTTGGGCTTGT TTTCTACTTTGCCACAGATTATCTTGTA
ESTD- B3AR	104 C T	GGCTGCCAGGGTTCCGTGGAGGCGCCCTAGCCGGGCGCCTGCTGGCGCTGGCGTGGGTGGCCACOC GTGGAGGCAACCTGCTGCTCATCGTGCCCATGCC/CJTGAGACTCCGAGACTCCAGACCATGACCAA CGTTCGTGACTTCGCTGGCCGACGCCGACCTGTGTGATGGACTCTCGTGGTGGCCGCCGCGCGGCCA CCTGGGCGC
WI-567b	48 A G	TCTCACACTGACCCCTTACCTTCATCCTCACCTCTGCTGCCCTGGTTC/GJAGCCCTCATCTCTTTA CAGGGATCCGCCACAGCATCCCAACTGATCTGGCCTTAGGTCTTCTCTCCAATCCATCTTCAAAG GCTGCCACTGTGATCTTCCCAAAGGTGATCTGTGATGCTACCATCTTGCTTCAAGCC
WI-801c	58 G T	ATGGAACATTTCTCCATAATGAATGAGGTCTCAATCCATTACACATCCCTTTCTG/TJAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTTCAGGGGTGGGGCTGTGC ATCTGTGATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCACCAGAGAGTTAA CATTTCTGCCACCCCTC
WI-801b	58 G T	ATGGAACATTTCTCCATAATGAATGAGGTCTCAATCCATTACACATCCCTTTCTG/TJAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTTCAGGGGTGGGGCTGTGC ATCTGTGATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCACCAGAGAGTTAA CATTTCTGCCACCCCTC
WI-1099b	76 A G	GAAATTCACCTATACAAGAACTATTTCTCTAATTAATTACATTAGTCTCATTCTGAAATATTAT TTTTTACA/GJTACCCCTTTGATTATTTTGATTCAATTTGTAAAGAGAGATTACAATATCAGTAACGC TGTTCAATGATAGTGCTATCACAAATGTCTAAATACTTTTGGTCAACATCAAAATTAGAAAGAA CTTACAAAGTTTATTTGCTTTATGGTTTA
WI-2529	71 C T	AGGAATGGCTGATCTCCTGGTGGCTTCATTATAGTAAAGGAGATGTAATGCTTGATGAGCCTCT CAA/CJTCTTAAGTCTGCTGCCCTCAGTCAGTGAACATTTAATGAAGTCTACACAAATTAATTAGTGT AAGTTGTAATGCTGAATAAGCTTGAATAAAGTGAAGAGGTAAAGAAAGGAGACAACTGTGCTTT TTAAGAAATAGAAGAGTCACITTCATTAGAAATGGCTTTGGGGATGACAAGTA
WI-10088	205 C G	TAAGGGCCTGTCTTCCCGAGAGGCCCCACGGGACAGAGAAAGCATCTTGATACCCAGGGCCACAAA TGAGCAATCCATAGATACTACATATAAGAGAGACCTGTACCCCTATGAGGTAACTGAGGATGAAGGA GTGAGTCATATTGGGTGGCAATTAATGACCCAGCCTCCTCTCTCAAGAAGACTTTTACATTTTAGAC AGG/CJGJAGCAGAAGCAGCAAGGAGGAAAGGAAGT

WI-2625	98 G A ...	---	---	GGG CAG T C C T G G C T G A G T A G A C A G C A C T G A A G G A T G A G A G A G A A G A A C A G G C A G A A G C A C T G T G G T A G T A A C A A G G C T T A T T A G G A G A C A A A T T G A T A C T C C C T G A G G A C T C G C A G A A A T T A C C A G C A G T G G A C A G G G T A T C T G T G G T A A T C A G T T A T C C A C T T G C A G G A G G A A A G C C A G C C A G C A A A G
WI-2924	54 G A T A G G	T G A C C T T C C T A G T C T T C T C T T A	G C C T A A G T G T A A T C A C A G G G	T C T G T T G T C A T A T T T C C C T C T T T G A C T C T G A C C T T C C T A G T C T T C T C T T A T A G G G A C C C T G T G A T T A C A C T A G G C C T A C C T G G A T T A T T A G A A C A A T C
WI-2939	72 G T G T C C T T T	G G C T T G T C T C A G T G C C T T T	C T T G T G A G G G A A G G T C T T G	C C A T T G T G A G G T G G G T G C A C T T G T C A T T C C C T G C A C T C A C A A A G T G G C T T G T C A G T G C C T T T G T C A A G A C C T C C C T C A C A A G A A T G T C T T C C A T G C T C C G T G T C T T T G A A A A T T C G A C T T T A T C C T G A A A A C T C A G C T G C A G T G T A T C T C C G G T A T A A G C C A C T C C T G
WI-3203	99 G A A G A G	G G T A T G C C G C A G A C G A G	T C A A G T A T T G C C T T G T G T G G	C T T G C T A C C A T T T C A G A C A T A C A C C C T C A G T G A A T G C C G T A A C C C C A T T A T A A A C A T C T T G C A T C G A A G G G T A T G C C G C A G A C G A G G A C C A C A A G G C A A T A C T T G A A G T G A C T T G G A G A A T A A G A T T T G G A T G G A T G A A A G C A G A G A G A G A T G C T A A A A G T G A
WI-3473	101 A G C C C T A G G G A	A A G C A T T T T A G C C C T A G G G A	C C T G A T G T C A C C A A C A T T T T C T	G G A A A A G A A A C C T G A A G G A T G A G T A G A A T T A A T T G G G A G A T A G T T G G T A G G C C C T G T T T G G A G A T T G C A G A G A A G A A G C A T T T A G C C C T A G G G A G A G T A G A A A T G T T G T G A C A T C A G G G C T
WI-1796b	29 A G ...	---	---	A C A C A C T T T C T G T A T G C T C T T C A T C A A A G A G T G C A G G C G T C A T T T C T G C A C A T G G T G A T A T T T A A G C A G G A G A G C A T T G C T T G G C T C C C
WI-1796	29 A G ...	---	---	A C A C A C T T T C T G T A T G C T C T T C A T C A A A G A G T G C A G G C G T C A T T T C T G C A C A T G G T G A T A T T T A A G C A G G A G A G C A T T G C T T G G C T C C C
WI-4360	93 C T A A A T A A	G T A G T C A C A T T A G G T A T T T C C	G A G A G A T A T T T T T C A G A G G C A T T T T	A G T C G T C C A T C T T C A G G G T C T A A C T C T G G A T C G G C C T G C A G A G T A G G A A A G A A G A T G G G G T G A G T A G T C A C A T T A G G T A T T T C C A A A T A A C T T A A A A T G C C T C T G A A A A A T A T C T C T C C C A T G T C C C T G T C T A A T A T A C A T T T T C C
WI-1959b	87 C T ...	---	---	G C T G A C T T T G T G C A G A G C C A G G G A C A A T T C A G C T G C C G G A T T T A T A G A T T C T G C A G C A C T G C A A C A G G A A C C A A A A T C A G T C T C T T G G G T A A C T G A G A G T G G T T T T C A C A C C C A A A
WI-1973b	28 A G ...	---	---	G T T G C C C T G T A G C A G A C A C A G A A G G C A G A G A G A G G A A A A G C C T T T T G T C C A G G G G C T T A C A C T G A A T C C C C T C A A A C A A T G C A A G A T G A G C T A A T G G T C T T A G A G G T A T A A T C T A A G T G T G A G A A A A C A A A G G T A T A G G G T T G
WI-1980b	140 C T ...	---	---	C T T G A G T A T G C G T G G A T T T T G G T A T A C A G A A A A T G G G A G A G C T G G A A C T A A T C C C C C A T A T A C C A A G G G A C A A A T T G A T C T G T T T C A C A A T T A C A G T A G G A G A C A T T A T G T C C A T G A C A A T G G T A A T T T T A A C T T G A C A G T T T T A A T T G A G T G A A A T T A C C A T A A A A A A T A A T A A T A G T A G C A G C T A A T A T T T A C T G A G C T G T A C T A G G T G C C T A T A A A T A G C

WI-2015b	190 A G	TGTCAGATAGTCGGTCTCTACCTAGGTGCAGTAGGATGCTAGGAGCTATTTAAAGTACACAATTATGCT ATATATTTATACAATATACAATTACTTGCAGATAGCATGACCATGCTAGTGAACCCCAAGACTAT GTGTGAATCGTCTATTAGGGTTTGTCTATAAACTCTACATGGTGTCTTTTCCAACTA/GJCATATACCTT CTAATACCATAGAG
WI-754b	49 C T	GAAGGCACAGGGGAGAGATGGCTGTCTACCTACAGCCAGGGAGAGAGG[C/T]ACATTTATTGGTAA TCCTATAAAGTGCACTTCTTTAAATTTTGTTACTTTTAGA
WI-754	22 T C	GAAGGCACAGGGGAGAGATGGCT/CJGTCTATCTACAGCAGGGAGAGAGCCACATTTATTGGTAA TCCTATAAAGTGCACTTCTTTAAATTTTGTTACTTTTAGA
WIR-1b	56 A G	AGGCAATCAGACCTACAGAAGGAAACCCCAATAAAACTCTGATGATCGTACATCC[G/N]JTGCGCTG GAGGGTGATGCCCTCTGAGGACATGGGAGCTTCATGTTTGAGCCCTCCCTG
WIR-1	56 A G	AGGCAATCAGACCTACAGAAGGAAACCCCAATAAAACTCTGATGATCGTACATCC[G/N]JTGCGCTG GAGGGTGATGCCCTCTGAGGACATGGGAGCTTCATGTTTGAGCCCTCCCTG
WIR-3b	72 A G	TAAATTTAAATGGGGCCAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GAAGT[G/N]JCTAAAGTTATTAGCTCAGAGCCTCACACATCTCAGTGAATGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-3a	69 A T	TAAATTTAAATGGGGCCAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GAATGTATCTAAAGTTATTAGCTCAGAGCCTCACACATCTCAGTGAATGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-4	47 T	GAGCCTTTCTAAATTAAGGATTGTGACTAGCAACCTCCTGTACAGATTCCTGTCTCACACATGTGCA AGGCAGCAGCAATTTGCCAGCTGCC
WIR-5g	209 C	CGGGACAGAGACAGAGAGAGAGATTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG
WIR-5f	196 C	CGGGACAGAGACAGAGAGAGATTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG
WIR-5e	194 C	CGGGACAGAGACAGAGAGAGATTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG

WIR-5d	191 A	---	---	CGGGACAGAGACAGAGAGAGAGAGTTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG
WIR-5c	177 C	---	---	CGGGACAGAGACAGAGAGAGTTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG
WIR-5b	159 A	---	---	CGGGACAGAGACAGAGAGAGTTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG
WIR-5a	37 A	G	---	CGGGACAGAGACAGAGAGAGTTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG CTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCGTGGTCCCACTGTT AGGTTTGAAGGGAAGGCAAGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACACAC AGGTTTACGTCCAG
WIR-6	63 A	C	---	TAACCTGAAACITTTGCTCTCCTCATCTCAGGGAGAAACACAGACTTCATGTTAAGACCCAGAA[A/C] CGCAGTCTGGGTTGGGCGAG
WIR-7	12 C	T	---	TTGCTGACTATTCTAAGCATCTGTAGAATATTGAATACATAGTCTTGAGATTGATC
WIR-8	46 C	T	---	GGCGTCTATGACTATCCTGGTCATTGATTTGACTAATGATTCCTG[C/T]GCCCTTG
WIR-2	56 C	G	---	AAACAGAAAAATAGAGGTTATAAGGATGGAAGTAAAGTTGTCAAGAGAGGTATGA[C/G]CTGAAG AAAGAACTACTCTCTTTGACCAATAATAACAATTGGGAACACTGGAAACCATGGCTTGATTACT GACAAC
WI-7069	93 G	A	---	TGCTCTGCTTATGCCTCCTCTTTCGCTTGGCAGGATGATGCTGTCATTAGTATTTCACAAGAAGTA GCTTCAGAGGGTAACCTTAACAGAGT[G/A]TCAGATCTATCTTGCAATCCCAACGTTTACATAAAA TAAGAGATCCTTTAGTGCACCCAGTGAATGACATTAGCAGCATCTTTAACACAGCCGTGTTCAAAAT GTACAGTGGTCTTTTCAGAGTTGGACTTCTAGACTCACCTGTTCTCACTC
WI-18694	41 A	T	---	GGTCATTTCCCTTTTATCTGTGAGCAGCAGCTGTGACTT[A/T]CTCTCTGTTTCTGTCATCTCTCCC CCACATACCAACTTCTTCCACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18612	37 A	G	TGC	CACACTGTTACACCTATATTTCAAGTTTGGAAATGC[A/G]ATTTCGAAGCAGCAATACAAAAGTA TTCATGAAGAATGCATAATCTCTGAAATTAATGAAAAACATCCCT

WI-18517	87	C T	CAGGAATCAG CAGCCTGA	TGTTGGACAA GTGCAACA	TTAAAAATCAACTAGGGCTACCCCTCAACACCCCTCCATTGTGCAACCTCTACAGCCTGCATGCC ACAGGAATCAGCAGCCTGA/C/TGTTGCACTTGTCACAAACACAACTGACTGC
WI-18868	76	C T	GGCGAAAAAC TAGGCAAAA GCTGTCACTCT AGCATCTGGA	GCTAAATTAAA CTGCACCTTTT GC	CGATTGACAAACCTTTATTTTCAACTTAGGTAAACAGTCCAAAATCAGTGTAGATTGGCGAAAACT AGGCAAAA/C/JAGCAAAAAGTGCAGTTTAAATTTAGCAAGGCTCAAGACAGTATGTGGAAAGGAA GGTGAGATTCCCTCCTACT
WI-18680	75	T C	A	CCTCCTGAATA TACAACGGAGC	TAAACATACGAGTACTGTACACGCAAGCATGCATCCCTGAGTCTGAGTGAGGCTGTCACTCTAGC ATCTGGAAT/C/JGCTCCGTTGTATATTCAGGAGGGGA
WI-18704	99	A C	GGGTTCTCCGA GGGTAC	TGAAGGCCCTG CTGG	CACCCAGGCTGTACCCAGGCTTTCTGTGCGAGCACCAACACCAAGGGCAGGTTGGGCTTGAAGGAGCC CTTGAGGAAACACGGGTTCTCCGAGGGGTAC/C/JCCAGCAGGGCCTTCAGCTTAAAGTCG
WI-18673	29	A G	TGTGGCAACCTTGTTTTAATTGCAAC/C/JIACCTAATTACAGCACATTCAATAATGAACCAAC AGGAGAGTTGCTGACTTTGTAAACATATGAATATATAAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAGCGCATACAAAGGAAG
WI-18640	121	T C	GTCGGGTG G3GG	GCAATACCAC TGAAGAGGAC A	ACCAGTCATGTTTTATTGGAGGTTAATTCCTATTAGGATATGAAGGATTCAGCAACGATTGAGATT GTGTTCTCAGCGAGGGCTCGGGCAAGGTCGTGGGGTGCAGAG/C/JGTGTCCTCTTC AGTGGTATTGGGAC
WI-18533b	91	T C	GGGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTAACTCCCGAGATTTCTTCTTTATTT TATATTTTCACTTTTTCATCCTAAT/C/JTTACTGAAGCCATTTCTTTGGTTAACTTTAGA
WI-18533a	59	T G	GGGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTAACTCCCGAGATTTCTT/GJCTTTA TTTTATATTTTCACTTTTTCATCCTAATTTAC/GAAGCCATTTCTTTGGTTAACTTTAGA
D11734	83	A C	TTC	AACCAGGATA AGGCTACAACT ATTT	GAGCATATGCTGCATGAGGACCTTTCTATCTTACATTTAGGCTGGGAATCTTACTCTTTCATCTGATA CCTTGTTCAAGATTT/C/JAAATAGTTGTAGCCTTATCCTGGTTTTACAGATGTGAAACTTT
D49493	159	A T	TCTGGGAATT	ACTTTCAGGCC AGGC	CAGGACTTGTGGTGACGCTGCAGACACAGACAGCAGCTCATGGGCAACATCACTGGGGCCAGAGAG AGCTGTCCGCCAGTGCATCATTAGGGGTCTTTTCTTCTAGTACTAGCCCTTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAAT/C/JGCCCTGGCCTGAAAGTGCCCCATCATTCATACCCACTGTT CT
EST10030	98	T C	TCTCAAGTCCC	GCAGTGTGGT ATGGATGA	TATTTATAGAGGAGACCTAGGAGGAGTTGACACAGCACACTGCTCAGCAGATGACTTAAATTTT CCCTTAGCCATTTTGTCTCTCAAGTCCCTT/C/JTATCCATACCACACTGCTGATTG
EST10052	24	G A	GAGGCTG	TGTGGAACCTC AATCTTAGACT TC	TATTTGGCTCACTTCTGGAGGCTG/C/JA/GAAGTCTAAGATTGAGGTTCCACATCTTGTGAGGGCCTTC CTGTTGAGTGCATAACCTGGTGGGAAGTCATCATGTGGCAAGAGAGAGGGCTACAGAGCAAGAGGAA A

EST10605 2	118 C G ...				CTTGGTAAATCACAGTTCTGTATTATCATACAAAACITTTGTTTTCTCTGACAAAACGTACACATAGA AACAAATTTCCAAATGGACAGGAACCTTAAATTTGTGGAGATGCCCATGT[C/G]TTGTGAGACTTAA AAAAAGAGAAAGATCCC
EST11048 0	61 T G ...	CTCTCAAGTAG ATAAGAGGCA TAATCT	GCTAAATTTTC AGAAAGAATT TTGTTT		CATGTGTAATCCCATGATTGAAAAGACATGTTGCTCTCAAGTAGATAAGAGGCATAATCTT[G/JAA ACAAAATCTTTCTGAAAATTTAGCTTATGAACCTATTACACTGCAAAACAGAGAAGGAGCAC
EST11260 8	101 G T ...				TATGGAGGCCAGAGGAAGTGACACTATATGTGGAAAGTCTGAAAGAAATGAAGTGTCACACAAAA TTCTATATCCAGCTAAATATCATTTAAGAAATGAAG[G/T]GGAAATGAAGGCAATATCAGATAAA
EST11349 9	109 C T ...				TTTGATGGAGAAATCCGAGGCTGCCAGCATCCCCACCAGTAGATTTCTTTGGACGAAGAAATCCT TCTGTGGATTACGCTTTTACCGCTTTCTCTCATCTGCTGGTG[C/T]TTCTCAGAGCTTTAATGTCCGT CCTGCTCTCCGAGTCAG
WI- 16632a	71 A G ...	CCAACCTACTT TGGAGCCCT	TOCAGCTTTCT CTAAAACTCC T		GAATTCGGGTATTAAATAGCGGGTCCACAGGAGCACATAGGAAGAGCATCCAACTACTTTGGAG CCCT[G/J]AGGAGTTTTAGAGAAAGCTGGAGCCCGAAGACCAGTAGTAGGAGGTAGCCAGACCAA AAGGAGGAAGGAGTGGGA
EST11772 6	74 A G ...				CCAGGAATAAAGAAAAAGAGTCAGAGGAACAGTCTTTGATGTTATGAGGCTGAGACACTACTC TTCTTCA[G/J]GAGTATTTCACTTCTGACTATAAGTGAATAAATACATTTGAAGACTTCAGGAGCTCA
EST11795 3	82 G A ...				CTTGCCATTTATTTGTGCATGTTGTTCTTAAAGGCTTGAAAGATAAAGTGGAAATGTTGGAAAC ACATAGATCCAG[G/J]ATTAAAGGGGCTGGAAAGTAGCCCTTAAGAC
WI-16644	42 G A ...	CAATAAGCAG CTCATTTTGAT TAC	ACTTCATGAAT TTTACTTCATG TATACC		AGAGCAATGGTGGCATCTCAATAAGCAGCTCATTTTGATTAC[G/J]GGTATACATGAAGTAAAAATTC ATGAAGTAAAAATTCATTATACCAAAAAGCCTCCACAGAACTTTTCATGCACCTGAGCTATGTGAAC TGAAAAGTAACAGTGGGAT
EST12005 9	56 A G ...	TTGTATAATA ACACTCAGTA CAAAGTCTGT	GGCTGGTCACT TCTGGAT		GCCTAGTAATCCAAAAGGAACATGTTGTATAATAACACTCAGTACAAAAGTCTGT[G/J]ATCCAGG AAGTGACAGCCCGACGTGTGCTATGACCCCTCTGAACCTCCCATTTCCATAGTTTTTGAAATC
EST12055 9	32 T C ...				GTGGAAAATTTTTTATCTGTACGTCTTTCC[C/T]ATTATATTTATCTTGTCCTTGATTTTCAGCAACC CACCCGATTTGCAGGCAGTGTCTTTCTAAACTGTGCCCTGTGAGCTGTAAAAAGTCTTCT
EST12492 1b	95 A G ...				CCCTAGCAAAATGACTGGAGTTGTGCCAATACCAAGTTACATACTGTGCCAAAATTAAGCTCTC TTCCCCAGAGGCATTAACTGAGATTAT[G/J]GGAAACGCACAGCAAAATTTGACGATGCAGCTTTTA CCTTTTTA
EST12492 4	25 A G ...				ATCTTGAGGTTCTGGCCTGTCAG[G/J]AAGTGACATCTTTTACTACCAGGTCAGGAACCCCTAT AAAGAACTGTGTAGAAAAGATATCAGGTCAGACTTTTAAAGGGCTTCTTATCAGCTCAATAAA

EST12502 2	52 C G	...	ATACTAGGGAGAAACCAAAGTGGAGGCAAGTCCACAGGTACACTGTGCA[C/G]CAGCAAGTAT AAACAAAGTGGTTTCGATGAAGAGAAATGCTACGGGGGAAATGACCAATTTTAAGGGCCATGTG GTCGTGAGGCGTAGAGG
EST12619 8	105 T C	...	CCAGAGAAAAATTAGAATGTATCGGTAAAGAAATAGGAATGCATATTTCAACTCACTGTACAAA CAGGTGTTTATTATCCCAAATGACAGTGTGCCTGAGAT[C/G]GATGCATGTGGCAGACGAG
EST12620 0	67 A G	...	TTTTCTCTCTCATTATTCATTGTTCAAAACACTGTCTAGTACCAACATTGTCCACCGGC[A /G]TTGAGAATACAATTTGAAGAAGAGTCACTGCCTCTGGAAAAATCAGAGTATTGA
EST12817 9a	22 C A	...	TTGGGTTCTCAGGATCCAG[C/A]CTCGTAGCTGATGTCATGAGGTTCTCATCCATGCTCCACGG GTTCTTGGGAGTGACCGGATGGGAATCCATGTTGCTTGGTACTCCATCAGTCATTGCG
EST12941 8	23 T A	...	TCTCAGCTTCCACCTGACCTGCA[T/A]CAACAGCCAGTTATTCACCAGAATTTTGTTCGGTTTCA ATGTAGTGTTAGCTTTAATACACTGCACCTTGTTTTG
EST12949 2a	52 A G	GGCTTTAATCA TAACCTAATA ATACTGTT	AGGATTTTCATGAGGCTTTAATCATAACCTAATAACTGTAAAAACAACAC[A/G]TCTGTCACTTG CAGAGACCCACAGGGACACACATCTCTCTCACATAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST13067 4	104 C T	...	ATTTTGTGTTTCTTAATGAAGCATAATAACAGTTAAAAATTCAGAAAAATCATCTATAGTTGA GTGTAAACCTCCCTAAATCAGTCTTCTAGGGCCACAC[C/T]GGAGCAGAGAAGCAGCTTCCCAACCAAG CACCTCTGAAC
EST13117 6	68 A G	...	TGCTGTCTGCATCAGTCTTTAAAAATTTAATCGCTTTATACAATTGACACCAATAAAATGCAC[A /G]TATTTAAAGTTTACAATTTGAGAAGCTGACACGTGTCCATACAGACACACCTCATTTTACTGTGC TTTACTG
EST13121 6	44 C T	...	TCTGCTTTAAAGATTCCTCATAGCTGCTTAGGTTTGTCTTC[C/T]AGCATATTCAGCTATAATCA CCTACATTCCTCCACAAATATTCCTGTGTGTGCCAGGCCAGTCTCCTCACTGTCCCATGAATAGCC AGTCTTATTCCACTCT
EST13226 6	74 T G	...	AACTGTTTACTAACAAAGGTGCTTTAATTTGAAAAGCATTGAGGAAATAAATTAATGAATAGTCT GGCATT[T/G]GACTAACCAAGTCTACAAAATTCACATATCCGTCACCTCAGATGAGCATATACCAAG TCAGAGGAACAAAACATG
EST13230 6	72 G A	GCTCAGATGTG AGAGACGC	GCATCATCAGCGGCTTTTACTGAACCTTACAACCAACTTGCCGCTCAATATGCAGCTCAGATGTGAGAG ACGC[G/A]TCTCTGTACAGGAGCGGTACTGTCTTCAATCCTTTGCATGCGAGGTTTACCACAGGCA AACAGTTTACTCCACAT
EST13236 9a	70 T C	ACAAGAGGGTT TGACAAAAGA TCTCAGGCT G	AAAGATATAAAAACAACTCCCATCAGTAGCAATACAAGGTTATACATTTTAACCAAGATTTTCTCAGG CCTTTCTTTGGATACCTTAGTAGTTAACTCTCTTTTGCAAAACCCTCTTGATATAACCA

EST13278 2a	51 A G G	CATTACCGAA CAATATTTAG	CATATCTTGG GTGGTGAGAA	TTCCGAGAACGTTTACAAGCTCCAAACCTTTACCCGAACAATATTTTAGGAGAG/ATTTTGAATAT TTCTGTAGTTCTACCAACCAAGAAATATGACAGCTTG
EST13282 0	98 A T	CCACACATTTC AGTCCAAGA	GATGGAAAAAT TGAGGAAGGT	GCTCACTAGATGAGCATTGACCAATATTTAGATAACCTGTTGGGAAAGTGCTGAATTAAGCC TGCCTGAGAAATCCACACATTTGAGTCCAAAG/ATTAACCTTCTCAAAATTTTCCATCTCCCATCAGA
EST13290 9	39 A G CTT	CAATTTTAGA AGTTGGGTTT	AAATCAGTTCA TGGAATTTCA	AGCTCATCTGCAAGCAATTTTGAAGTTTGGGTTTCTT/AG/CTGAAATTTCCATGAAGTGAATTTT TTTTCTGTGCTTAACCTTCACTTAAAGACCTAAAGACAAGTGGTATCACATCACATATTTTGT ATGTGGGGCTTTTGG
EST13518 2	45 C G	GAAACATCTCCAGTAGTATTGAGGTTAAATGATTGAGCATT/AG/CTGAAATTTAAAAATTTACCTCA ATGTTCTCGGAGTCGTCATAGTTTAAATGACTCTGCACCTTCTTATAACCTTGATTG
EST13522 8a	68 A G	CAGGTTGGTGATTCTCAACTAGGAGCTATTTGCCCCCATCCCCACCGGAGTGCTGGAGAC/AV GIGTTTGTATTGTCACAACTGCGAGAGGTGGTGCTACTGGAATCACTGGGTAGAGGCCA
EST13568 6	69 T C	CTTTAAGGAAGTGAGCCAGATGAATCCAATGACCAACCTGGTTGAGAGCCATTGGTCTAGGAGTAGA AAT/CJGCACACAAGGAATAAGGGAGAAGGAGTTCCGTTAGTTGAGGGAGAGAAAGTTGGAAGCA TTTCAAGCTAAGTAAATGGT
EST13785 0	101 C G	AAGATTACGGACCATAAGAACTGCCCCCGACCCATACACACACAATTTTATAGCAGGTAAACCAA CTGAAAGGAACAAGTAATGACTTTCTTGAACAAA/C/GT/GATTACGAAAGTGAAAGGCTACAGGG TGATTACTA
EST14038 1	25 A G	CCTCAACCATCTGTAAACCCGAGCCCA/AG/CAGTGACCGGAGCTTGCTGCTTCCCCATCCCAGCCCTCT CCTATCAGCATCCGCTAAGCGTCAGTCAGCAGGTG
EST14083 7	23 A G	CAATGGTGTCCTATGTGAACATAT/AG/JACCTATTTCATAAAGTTAAAAATAATCCCTTCTTGCAATCA CAGTGCAAAAGGCATGAGGGTGAAAGTCACTCTGCTAAATGACCGAACACAGGAGGTAGGAGG
EST14221 5	42 T C	GCATGCTAGA CAGAGGCATT	GGAACAAGTC AAAATATTTT AAAAGA	AATATCAATGCATCTTGTGGCATGCTAGACAGAGGCATTAT/CTTTTGAAGATCTTTTAAAAAT ATTTTGACTTGTTCCTCCCTTCACACTCATTTTAAATGT
EST14812 2	50 A G ATA	CAAGTCAGCTT CTACATTCTGA	TAAAGATTTAG TTAAATCCCAT TATGTACT	TTCACTTAGTACCAAGGATGCCCTTTCAAGTCAGCTTCTACATTTCTGAATA/AGIAGTACATAATGGG ATTTAAGTAAATCTTTAGAAGTCCCGAGTTGGCTTTTCTAACATTTTTCATATCAGGTGAAACAAT TTTTTCATATGGGTGATT
EST14815 3	128 A T A T A C T G G T	CATCACCAACC GTACCGGAA	CGGGAAAAACA GTACCGGAA	TTTGCTTCGGCAATACATAGTGGCAATGCAGCGTGAGTTCGGCCGCTCTCCCCACTGAACCAAGTAAT TCACCAGACAATGGCGCACCACTAAATAAATCTGCGGTCATCACCCACCATACTGGTT/ATTTCC GGTACTGTTTCCCGTA

EST15420 6	109 C A	TTTAAACCCAAAGACTTGTAGATGTCAGGACTCCGATCATTTTCTCTGCCTATAGCTTGGATATCTTA ATCTCTCCCTTTTGTATCATATAATCATATAGCCAAAGGACT[C/A]GGAATTTTGGCTGCTTCAAGTCA TTCCAAAACCTCTCAGG
EST15700 6	48 G C GGA	GAAGAAGACAA AGACAACAGA	GAATAGCTGA AACAGAGATA TTATTCTC		GTCACCAGCACATTTTAAAGACGTGAAGAAGACAAAGACACAGAGGA[G/C]AGCAGAGAAATAA TCTCTGTTTCAGCTATCCAGGATGTTATGCCAATTATCCAGAGTCTTGTATGATGTAGTA
WI-16739	57 G A	GGTTTGGCAT CACAAAGC	GATAGTTGATG TTCATTATTCC CTATAA		AAGGATTGAAAACATACCTAGATCATATAAATTTGTGAAGTTTTGCCATCACAAAGC[G/A]TTATAG GGAATAATGAACATCAACTATCCTACAGCTAAACCTAATGAAGACCAAAATGGCTCCAAAGT
WI-16782	96 C T	GGTGGGAGTCT CACTGTAAGG	CTTCTATCTTT CTGTTCTCTCA TC		CTTCTCTCTCTAGACGTGGAATACACACGGATACAGTATCTGGAGATGTAGCAGCTGGCTCTTGAC CATAATGGTGGGAGTCTCACTGTAAAGGA[C/T]GATGGAGAACAGAAAGATAGAAGAGTTTGGGGT GCTGATGAAATTGTGGGG
WI-16783	64 A G G	TOCTGAGATGT CTTTACCTGA	CTGCTTGGTTC AATCCTTATTA G		AAAAATGTAAAACTTAGAGGTTGCCTCTTTTGTGTGCATTTTCTCTGAGATGTCTTTACCTGAG[A/G] CTAATAAGGATTGAACCAAGCAGTATTTTAAATGGCAAAAGTCCAGATGTAACTCGAGT
EST15948 2	58 T C	CAGGACTTAAGTCAATTTGCCTGGAAGACTTTAACTAAAGGTGAGGCAACATAGGA[T/C]GTGA CAGCACCACTCGGACCAGGAAGTGTCTGAAATCGTCACTAGCTGCCAGGCCCTTTTCTCTGGC TGCTCTGCCTCCAGAGC
EST16088 8	89 G C	GGTTTGAAGACGAGCTTATCTCCACCTGCCACTGGGATTCATTTTGAGAGCTGTTTGTGACGCC TTTTCCAGAAAAGGCCGCT[C/G]GGGTTTTCTGAACCTCTATGGGCATTTTGAAT
EST16089 9	96 C T	CGTCTGAAGTTTTCTTTATCACAAGTCACATCAATCCCTCGGGCCCTGCTCAATGCCACCTCTTC CTGAAAGCCATCCCTAAGTAGTCTCT[C/T]AAAGAGCCATCCCTGCCCTTTCTTTGCT
EST16100 1	24 C G	ATCCAGCTGTGAAGGGACAGGAG[C/G]GTAAACACAGTCCCATTTATAAGGGGTGTCACATTCCCA GGGCTCCAAATAATGCAACATTGTTTCACTCGTCCATGCTGTATAGTTTCATAGTAAAAAAGTC ACTCCAGACAGGTTGGCTC
EST16104 9a	83 A G	TTCTTTTAAATAACCCACAGACACCCATGACACTTCCAAATTTACAGAGCAAAAAGTGATTTGCAG CTGGTCTCTCCAGGA[A/G]TTGGCCCCGAAGCTGGCTCAGTTCACCTCCAGGACCTCAGTC
EST16118 0b	119 T C	ATGGTATAACAAAATCAGTCCAGGTTTTTTCTGAACAAATGATCCTTTGGTCTTTCCCGTGGCATG CTCCTAAACAACTAAACAAACCCCTCTAGTCTAATCAGTCACCTAAGATA[T/C]CGAGTGGCAAGT CTTTCACA
EST16118 0a	32 C G	ATGGTATAACAAAATCAGTCCAGGTTTTTTT[C/G]TGAACAAATGATCCTTTGGTCTTTCCCGTGGC ATGCTCCTAAACAACTAAACAAACCCCTCTACGTCTAATCAGTCACCTAAGATATCGAGTGGCAAGT CTTTCACA

EST16151	53	CT	---	AGCCAAITCAACGAACTCTATCAAAACACACAAAAGGCCTAGAGGAGAGATTACCTAATGAACGCT AAATAATTCAAGGCAATTTTGATCTAAAGCATTTTCTTAGCTCTACAAAGGCATGAATGAGGTGT GGTCACGTTTTGTATAGGA
EST16182	54	GA	---	CATTGGTTGGTAGGGAAGATAGTAGTGTGCAAAATAAAATGGTAAACACAGCAG[G/A]AAATGGAA TTATAGCTTTCTTTTCATATAGGGAATTGAAATTTATTTACTGAGGTGATAGGCAGAAAGTAGTA
EST16183	59	AG	---	GCAGGTAACACTGTGGTTCAACACGTAATTGTTCTTTTCATAAAGAAAGAAATATCTAGTTG[A/G]GTAG AGGAAGGCACGTGCTTCCCTGGCCCTCTTCGTTTCATATTTTATGTCACTGTCTCAACGTGGGCCGTGT GCAAGAGAGATCTTTGAGA
EST16198	28	GA	---	AATCTTAGGCTCTTGGCTTTCAAATCA[G/A]TACAGACAGATAAGAGCTTTTAAGTATTTCGCATTT CCCCAGAGGAAAAAGTCAGCATATAAACCCACATGGGTACATGCTCAGGCACATGGTGTC
EST16229	52	TC	---	TGTGAATCGAAATTCGTTGTCCAAAGTCCTGAGTCACAGTTTCATTTGGGAGT[C]CCCTGTGCAGCC CTTGCAGTTTCCACGAGCAGGATACTCCACTAGCTGATTCAGACAGGCAGAGGCTGCA
EST16229	45	TC	---	TGTGAATCGAAATTCGTTGTCCAAAGTCCTGAGTCACAGTTTCATTTGGGAGTCCCTGTGCAGCC CTTGCAGTTTCCACGAGCAGGATACTCCACTAGCTGATTCAGACAGGCAGAGGCTGCA
WI-16816	124	AG	TGGGGTTA	CAGACTTTTCCCTACACCTCATTTGGCTGGAACTGGGTGCACATGCACATCCTTGAACATATCATTTGGCAA AGGGAATGGGTGCATCAAAAATTCGTTAAGGCCAAGCAGGAGCCATTGTTGGGGTTA[A/G]ACTGTCC TGAACAAAATCTAGGCTC
EST16269	49	GA	---	GCCACTCTCTGTGGCTTGCTCTGCTCCAGCTGCTGCCAGTGCCACA[G/A]TGGTCTAGCCTCATGG CAGAAAGCATTTAGCCAACTCCTGGTCTGCTCCACTCTCTCTTCTCCGCCGCTGGGCTCACCACC TCTTCTCTCTCAATC
WI-16824b	83	GA	---	GTCACCCAGCCAAATGCTTCAGGAATAAATGATGGTGTGCAGCTGTTGTTCTTATGAAGAAGTCAG AAGCTGATAAACGTGG[G/A]CTTACACCTTTAGCACGGATAGTTTCTGTGCCAAGTGGGTGTGGA GCCTTCCATTATGGGAATA
WI-16824a	47	TC	CAGCTGT	GTCACCCAGCCAAATGCTTCAGGAATAAATGATGGTGTGCAGCTGTT[C/G]TTCTTATGAAGAAGTC AGAAGCTGATAAACGTGGGCTTACACCTTTAGCACGGATAGTTTCTGTGCCAAGTGGGTGTGGAGC CTTCCATTATGGGAATA
EST16445	96	TC	---	TTGCTTTTATTATCCAGAACGGCATGCTACAGATACTGTACAGCATGAACATTTTATTCATTACAAA AATGGCTTCCAAACCATTAAAAATGAACTT[C]GGAATAAGAGCATAAAAACGGAAACAGTAACATCA
WI-16857	47	GA	A	TATAATCCATCTCTCCAAACACACACAAAATAAGCAGCTAATGGCAAT[G/A]CTAGTGGTCTTCCCAA TTCACAAAGACTGTGCTTCAAATTTGTTTCTGATAATGTGGAGAAATCTGCTCTTTATGTA

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WI-16879	79 C T	GATACAGGC ATATTCCCA	CAAGGCTTCT AGAACTAGAGT CC	AGACAGGTCAAACTCCTAGGGATAAAGATATAATCCAGCACAGCATTATTTCCAGATACAG GCCATATTTCCCACTATAGGACTCTAGTTCTAGAAAGCCCTGGGGAGAACAGGCCACCCAG
WI-16882	99 A G	GAAATGCCA CGTCTCTGAC	GACACATGTCA GGTAAATCGC	ACATGAATGGCAACCTCTAGGTGGGAGAGACAAATTTCTCCCTTTACCCCAAGGTTACTCTGAC AAGGCTATGAATGAAATGCCACGCTCTCTGACAGGCGATTTACCTGACATGTGTCACTCCCT
WI-16888	70 G A	GCTAACTTTGG GCAGGTC	AATGTTCTGAA TTGACCACAAATT TAA	GTAGTAAATGTTTCATCACTACCCGGGGAGAGCAAGAACCATGGAACGGTAGCTAACTTTGGGCAGG TTCTGAGATTAATTTGGTCAATTCAGAACATTCCAAAT
WI-16905	75 C T	ACTGGCCTGT GTGTTCA	GTCTATACTCT TCTAGGCAGTG GG	TTTGTGTTTGTATTTCCTCCCAACATCAGAACATAAGTTCCATGAAAAACAGGAACCTTGGCCTGTG TTGTTCACTGCCACTGCCCTAGAAAGATATAGACA
WI-16910	74 G A A	AAGAGTAAAG ATGGCGCTAG	CAAAATGAAG TATCGTTTCTA TAACAGA	AGTTTTCAGTATGTGCTTAAGGAGGTTATATTCGCTATGACTTTCATCTCAGAAAGTAAAGATGGCG CTAGAAAGATGATCTGTTATAGAAACGATACCTTCATTTGGCCTGAACCGTGAAGGT
WI-16918	93 C T	CAGCCATTAA CACCAGCAC	TCCTGATACAG AAGTGGCATC	GGAAAGAAAAAATAAACTACCACCATCTCTCTGCTACCACAGAGCACTAAAATCTAGGAATTTGAC TTTACTGCAGCCATTAAACAGCAGCACCTCTCTGATGCCACTTCTGTATCAGGAACCTTAACGCTGACAACC ATGAAAGGTCCTCTGAAAG
WI-16947b	127 A C	GGAAGCAGA CCTGGG	ATGTGATTGCC CGTGG	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAATAGGCCTGGAGCACAGGATT TGGCTGAGGCTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAGCAGACCTGGGGAC/CJCCA CGGCAATCACATGAGATG
WI-16947a	58 C G	CATGGAATA GGCTGGAG	GOCTCAGCCAA ATCCTGT	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAATAGGCCTGGAG/CJGACAGG ATTTGGCTGAGGCTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAGCAGACCTGGGGACCA CGGCAATCACATGAGATG
WI-16966	43 T C	AAATGCACAG TACATAACAA CCTAA	TGCAAGTTATC AGTATAAAA CTCATATT	CATTTGTTTACTTTAAATGCACACTACATAACAACCTAATA/T/CJCTTAACCTTGGTCCAACCTATT AGTATAACTAATATGAGTTTTTATACTGATAACTTGAATGCCATTAAA
WI-16995	55 T C	GAGCAGTAGA GACTGAGGTA	CATGTTGATTT CCAGCGGT	TTGAGTGCCAGACATCAAGCATAGAAGAGCAGTAGAGACTGAGGTAAATAGTATTT/CJACGGCTGG AAATCAACATGCGCTCTCTCTGTGAAGTTGTACGATGGAGCTGAGAGGCTGAGTCAATCT
WI-16992b	60 T G	---	---	AAATACATGGTGTCAACCTCAGCTAAGCACCCAGAGTACACTGTGCGCCCTCATCTGAGAT/TGJGTG TAGGACTGTAAGGGAATGTGTTTGGGGTTTAGGAA
WI-16992a	46 G A TC	AAGCACCAG AAGTACACTG	CACATTCCCTT ACAGTCCTACA C	AAATACATGGTGTCAACCTCAGCTAAGCACCCAGAGTACACTGTG/CJGJCCCTCATCTGAGATGTG TAGGACTGTAAGGGAATGTGTTTGGGGTTTAGGAA

WI-17010	23 T C	T T C A C A G G A	A A T A A T A C G G T	A T G T T T C A A C A G G A A A G C C A T G [T/C] A T G A C A T T C A A A A C A C C G T A T T A T T A G A A G C T C A T T T A A T
EST 17127			G T T T T G A A T G T	T G T T T A A T G C A G A C A A A A A T C A A G G C T A A C T A A A A G C A G A T C C A A T G A C C C A G T A C A C C T A G A
9b	74 C T	C A C T C G G C A C	C A	G G T T C C A C G
		A A T T C T C T T A T	G G G A G G C A G G	A T T C G T C T C C A A C A G C A T C C C A G G C G G G C A T C C C C C A C G A T T T T A T A A T A C A C T C G G C A C A G A
WI-17040	94 T C A	C A T C T C A A G C C	G G T G	C A G A G [T/C] T T G G G A G C C A T G G G C A C C C C T G C C C T C C C C A G G C T T C C T A A G T A A C A A C T
			G	C A C G C G T T C A T T A A A T T G T A C A A A G C A T G A A C A C T C A G G A C A G A T T G G C A C A A T A C A T G C A G T T C
				G A G A A T T C T C T T A T C A T C T C A A G C C A G [T/C] A T C A C T G A A T A A G C C A T A G T C C C A G T C T G T T T T C C
				A A A T C T T T C T C A T A T T G T
				T T G T T T G T T T T G T T T T C T C C T G C C A A G G G A T T A A C G T A T A G G [G/T] C T T A A C A A G G G G A T C
WI-17044	47 G T G	T A A C G T A T A G	G G G G A T C C C C T	C C C C A C T T A T A G C T G A C A G C A G C T G C A A C C A C T G A C T C T C C T G C A G A A T G C A G G A A T C G A A T
			T G T T T A A G A	C A A A A G A A A A G C A A G T G
				G C A T G T T G G A G C A G A T C C C A T G G T A A G C C A A A A G T G G A C T T G T C A G C C T A T A A C T A C T C [T/A] G
WI-17021	62 T A A C T C	G C C T A T A A C T	T G T A G A G T T A G	C A G C T G C C A C T A A C T C T A C A G G C A C A G T A A C T A C A C T T T A T A C A G G A C A C A T G C C A A A G T G C C T G G
			T G C C A G C T G C	G A G G T G C C A A T A A A A T C A A
WI-17065	90 T C T T	C C A G A A A G G A	C C C A A G A G A C	T G T A A A A A T G T A G A C A T G G G G A A A A A C A T T C G T A A T C A A C A T G T G C T G T T T T C T A C T T C C G G T A
			A A T G A A A T C C T	C C A G A A A G G A A A A G C A T A A A C T T T C A G A G A T T C A T T G T C T C T T G G G T
WI-17068	32 A C T	T G T A C A G C C A	G A G A T G T T G A A	T T C A T A A G G T T G T A C A G C C A C A C A T C A C T G T T [A/C] A T T C C A G A A C A T T T T C A A C A T C T C A A A A A G A
			A A T G T T C T G G A	A A C T C T G C A C C C A T T A G C A G T C A T T C C C T G T A G C T T C C C T C A T A G G C A A T G G C A A C T G C T G A T C
			A	
WI-17074	86 T G			T G C T A C T G T C A T G A C T T A G T A A G G C C A T C A C A G G T T G C C A G A A C A T C T A C T C A A C T G T T C C A A G C A T
WI-17104b	108 T C		---	A A C C T C C T A C A C A G G C C T T [G/C] T A C A T A G G A G T A T A T T T G G C C A A G A C T C A C C A C T A G A A G T A T T
				C A G A T G A G A A C T C A T G C T G G C T C A T C T G C A A G C T T C C T G A T G C T T T G C G A G C T T T C C C A T T C A T T C C A
				A A T C A G A A G C A G T C A G T G G C C C C G T G G T T C C A G A C G G C T T [C] T C T C T T T G T T A A G A A A T T A
WI-17114a	37 T C	T T C C A T C A A G	T T G T A T T A A	A G C G T C C A A C A G A T G T T C C A T C A A G G A C T T T G T T T T [C] G T C T C T T C A C T C T G C T A T T T A T A A T A C
			A T A G C A G A T G	A A G C T A C C T C C C A A G C C A G A T G C T A A G T G C T A A A A A G A A G A G A C T G C A G C C A A T C A G A G T T A C A T
			A A G A G A C	G G G A
WI-17150	76 T G C T C T T	G A T G A A A T T C	T T C T C A G A A T C	C G T G C T G G A C T A A G T G C T C T T T C C A T G T G G A C A C A T C C C A C T G A A C A G G A T G A A A T T C A G A T A G T C
			C T G G A A G A T A T	T T C C T C T T T [G/C] A T A T C T T C C A G G A T T C T G A A A G G C C C T C C T T T G T C T G C T C T A A T T T
			G	
				G A A A T C G A A T A C G T C C A T T T C T T T G T A A A A T A C A A T A A C G T T [A/G] A A G G C A A A A G C A A G A T T C T G
				T A A C C A C A C A T T G G A A A G G G G C A C A G G G G C A G A G G G A A G G G C C A G A T T T T C A A C G G T T
WI-17163	43 A G T A A C G T T		C A G A A T C T T G C	C C T C C A C A T C T G C A G A C A A A
			T T T G C C T T	

WI-17178	127 T	C	GGACTCCCTCA	CCCTCAATTT	AGCAAATGTCCTCCCAATTCATTAGCTATGAGGTTATCAGTTTCATTTACAGAGCGAATTACTGG GGCGAGGGGTTTAATATCTGATGGTTAATTCAGTGAGGACTCCCTCATGAGGAGCTTC/JAGAA GCAGTTGAAATTTGAGGG
WI-17180b	81 C	G	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAATCCTGCACCTTCCCAAGTCTCGTCGCACAG GCTTCAACAATTAC/C/JAACATCTTGCCCAATTTGTTTTCATTATCCGACCCACACTGACAGATGAG GGAGTC
WI-17180a	47 T	C	TGCA	TGCGACGAGAC TTGGG	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAATCCTGCACCTTC/C/CCCAAGTCTCGTCGCA CAGGCTTCAACAATTACCAACATCTTGCCCAATTTGTTTTCATTATCCGACCCACACTGACAGATGAG GGAGTC
WI-17158	54 G	C	TCCCA	CAAGAAATAT ATATTTGATTG	TGAGGTAGCAGGGCATCTTAAGAAATGTTCTCTAACTTTAGATATCTCCCATTC/C/JTTCACAGA ATCAAAATATATATTTCTTGTTGGAAATTTAAATGTTCTTAACATATCTGCCTACCATCCACCTCAAT TAATATTCCTG
WI-17149b	79 T	C	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAACATCTCATGCACGTGCGTGGAA ACCCAATTGTCATTC/C/JGIGTATGAACACAAAGGATGGGAAAGAACACATTTCTCTACA
WI-17149a	48 C	G	AGGAGGAACA	CCACGCACGTG CATGA	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAACATTC/JTTCATGCACGTGCGTG GAAACCCAAATTGTCATGTGTATGAACACTACAAAGGATGGGAAAGAACACATTTCTCTACA
WI-17197	67 G	A	CTGGGGCTAC	GGTGAGGTGGT GCATACC	ATTTGCTATGTTGCCCTGGGCTGGACTCCAGCAATCCTCCTGCCTCAGCAGAAAGTAGCTGGGCTAC/C /AJGGTATGCACCACCTCACCTGCTTATCAGTTTCGTTAATAGAATAATTTGACTTTTAGATGCGCA TGATTTTCAGTACTTTCTCCCTGCTGCTAGTTTC/JTAAATTTCTCAGTGGACAAATGGACAA ACCATCTCTGTTGAATTTGAATACACAGATACATGCAAGATATCTTACAAGAAACAATGCACATCC TTC
WI-17198	38 A	C	CCTAGTTT	TCCATTTGTCC ACTGAGAAAT	TCGCTATGCTACCCAGGCTGGTCTCATTC/JTCAGGCTCATGCGATCCTCCTGCTGCAGTGGCTGG GATAAGACACAACCTGCCACCAGGCTGCCCTAGGAGTAGTCTTAATGCCGTGATGGTGGG
EST18753 8	27 C	T	GGTCTCAT	GGATCGCATGA GCTGA	TTATTTTAAACATAACCAGATGCACCTTGGTTTTTACATTTCTGTTGCCATTCAAGTCTCAAAGT AAACAC/C/JTGGGAGCATATGATAAATCGTAGTTTAAAGGAAGCCATAGCACCTTACAGAGT
WI-17108b	74 C	T	CA	CC	ACACAAAATTTACCATCGTGACCAATTTAAGGGTATAGTTCA/JG/JGTGGCATTAAAGTACATTCAACT TTTTGAGCAACCCGCCCATCACCATTTCATCATCCATCTCCGTT
EST19067 2b	41 A	G	TTTTGAGCAACCCGCCCATCACCATTTCATCATCCATCTCCGTT
EST19067 2a	40 A	C	TTC	AAAAGTTGAA TGTAATTAATG CCA	ACACAAAATTTACCATCGTGACCAATTTAAGGGTATAGTTTC/JC/JAGTGGCATTAAAGTACATTCAACT TTTTGAGCAACCCGCCCATCACCATTTCATCATCCATCTCCGTT
EST19125 8	28 A	G	CTGTTTCTCAGAGATGACACTGCCAACA/JG/JTACAGATTTGCATACAATACAGTTATGTATTGGC TATTCACAAATTTACAGTAGTGTGTTTTTCTCTCGAAAAA

EST20824 8	115 T	AGTCGGGAGT GCTGATG	AAGATTTTATC TTGGACCCGA	GTGTGGAAGCCGGAGTTTATTATTATTCAAATCAGTCTCTCTGAAAACTCAGGGATTGAGGTTTTTA AGGATAACTTGGTAGAGAGGGCCAGTAAGTCGGGAGTGCTGATTGTTGTCGGGTCCAAGATAAA ATCTTAGG
WI-17347	50 A	ATCCTCAGAA CTTCTCAGCCT	TCAAGCATCCA CTTGTGCTA	TTGGTTAAATGATGCCAGATGGGGTCACATCCTCAGAACTTCTCAGCCTAGGCTAGCACAAGTGG ATGCTTGAAGAACTCAGTCTTGGAACTCAGACAGCAATGGAGCGGATGTGAGTGGGACCA
EST21904 b	128 G	TTCATATGGCC ATTTTAATAA GTG	GGCAGGTGTTT AGAAAGCAT	TGATTGTGGTCTGGGAGCAGGTGGGAGTTCAGTGAGGAGCAGAGGAAAGTAGACGCAGTAGAAAT GAGACTGGAATCAATAGAACAGAAAAATGTACTAGGCTTTTCAATATGGCCATTTTAATAAGTG(G/A)TA TGCTTTCTGAACACCTGCC
EST22111 3	82 T	GAAGATCTGT CTGGCATCTT	TGGAAAAACA GCCCCAC	CAAAACAATGTAGACATAAGGGAACAAATTCAGAGAGCTCAAGTCACCATGTTTGTCTAAGAGAAGAT CTGTCTGGCATCTTTTTCGTGGGGCTGTTTTTCCAAAGGCACA
EST22197 2	78 T	AATTATTCTGC TATTCCTGCCA	ACCATGAAGG ATGGGT	GTTTAAATGATCACTCACCAAAATCCACAGGAGAACTCTTAAATGTTTACAAGCACCAATTAATTCTGCT ATTCCTGCCATT/CJACCGCATCCTTCATGGTAGAGTATCACAAAGTAAAAAGTTTCTGGTTGTTTCATC TACTTAAACCA
EST22311 9c	92 T	---	---	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAAAATCCACCACCTGTAAACAG TAGCATTCATGTTTACTCTAT/CJGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACITTCATCATTCAG
EST22311 9b	54 A	---	---	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAAAATCCAGTGTAA CAGTAGCATTCATGTTTACTCTATTCGCAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACITTCATCATTCAG
EST22311 9a	41 T	GGATTAGATC ATCTTTTATT	TTGAATGCTAC TGTTTACAGTG	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATTCJACATAAAAAATCCACCACCTGTAA CAGTAGCATTCATGTTTACTCTATTCGCAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACITTCATCATTCAG
EST22319	19 A	---	---	TCGAGGAGCTCTGAGGAGC/CJACCAAGGGAGCTGTGTCCAGGGCCACCGTGCAGGCAAGTGTG GTCCAACTCCTCCTCCCTTTACAAAACTCCAGCCTCACCCACACAAACACTGGCTGACAGGCCCTCT TAAGCCTTTTAACTGT
EST22433 c	103 A	AAGACATGTT CACCAAGTGA	CAGCTTCAGCT TAACTGACAGA	GATGTTAATGACTTTCCTTTGAGATATGATGGAAAAATATTCAGGTACACATGGAAAAAGACATGTT CACCAAGTGAACCAATCTAACCGAAAGCTTTACC/CJGTCTGTCAAGTTAAGCTGAAGCTGAAAT CTGGGAGCTTGACATGCTG
EST22657 9	71 A	AAATGGATCC TTATCTGCACA	AGTTTCAGTTT GCATGAATTTT	TATCCATTTCAAGAAAAAAATGACITTAATAAATACTATCCAGAAATGGATCCTTATCTG CACA/CJCCATTGAAGAAAAAAATTCATGCAAACTGAAACTATGCTTT

EST22993 5b	71	T C	ATCCTTTTGT TCTACCCC	TTGCGTGTAA TTTGACTGTAA TG	GCCTTTTATTGCTCCTTTTAAACATCAAAATGTTTTATAACACACACTTGATCCTCTTTTGTCTACCCCCA ATTTCATTACAGTCAAAATTACAGGCAATATAATAGGCTAACAGAAATGCTTGCAATT
EST23021 0	108	T A	TTATTTCTCAGCTTACCATTGTGTACTTATCTCTGTACAAGGTGTTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTAAATTTTATTAATCTTTGCCTTTTATGTTTGTGACAGTTTGTGCTCTTTCT T
WI-17387	55	C G	CCTTTCAGAT TGAAGAAAA	GCCTTTGCCTA AGATTAATAGT AACTACT	ACAGAAATTTAACATGCAAGTTTCATTTACATTACCTTTGCAGATTGAAGAAAAA[C/G]AATATTAG TAGTTACTATTAACTTAGGCAAAAGCCATTTCTTG
EST23689 1	101	A C	AATGTAAGCT CCAGAGGCAG	CCTTCCCTCC TGTAAGC	TTTTTGGCTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACTTTGCTCACTCTCCCA AGTGACACTAGGCAATGTAACTCCAGAGGCAG[C/G]CTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTCTGGCTCACTG
EST23733 9	31	T G	GGCTGTAGTT TTGTTTTGTTT	TGCACCTTTAA TCCCATCAAT	AAAGCTGTTAGTTTTGTTTTGTTTTCTCTT[G]TATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAAGCCTAGAGAAAGATATAGGCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGATACCCACCTAA
WI-17470	83	A G	GTCCCGTCCG CCAG	CCAGTGACGAG GCGA	CTGACACGTCCTGTGTGCGGGGTGCTCATGTGCGGTGTGTGAGTGAGACATTTTTACTGCGTCC GTCCGCGCAGCC[T/A]GTGCGCCTCGTCACTGGCCTTGGTCACTTTGTATTCTGCTTGGTTGGAA TACCATCAGCCTTC
WI-17519	55	T C	GTGCTCAGC TAATGAATGC	AATTATTATT TGCAGGCAATA CTC	TTTTAACGAAATCTCACTACTGCAAAATGCATTTGTTGCTAGCTAATGAATGCA[T/C]JAGAGTATTG CCTGCAAAATAAATTAGATTCTATTTTTAAGAAGCTTAGAACAGTACATGGTGCATAG
EST25356 3b	95	C G	TCITTGATACAGGTAAACCAGTTTGTAACTATTACAGAACTTCACTGTATCTTCAAGTTTTGATAT CAGCATCTGTGGAGAAAGCAGTGTG[C/G]TATAATGTCAACATCAGGATTTCTTTTT
EST25356 3a	26	A C	TCITTGATACAGGTAAACCAGTTTGT[T/A]JACATTATTACAGAACTTCACTGTATCTTCAAGTTTTGA TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTTCTTTTT
WI-17581c	99	C T	GGGTGACGCTCCAGAAATGGAGACAAGCCAAATTTGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAGTTATTGATAATGATAGAACC[C/T]TAGGCGCAATTTACATTGACGCGTCATGC
WI-17581b	86	T C	ATTCAACATT ACTACCAGTT	CGTCAATGTAA ATTGCGCT	GGGTGACGCTCCAGAAATGGAGACAAGCCAAATTTGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAGTTATTGATAAT[C/G]ATAGAACCCAACTAGGCGCAATTTACATTGACGCGTCATGC
WI-17596	86	A G	ACTTCTTTGTG TAAACACTCC	CATTCTTATAG CTAGAAATCGA CAATAT	GTGTGCTGGTAAATGGATAATAGCAGTCTCTCATCTCTGAAGGGTGGGAAGTAGGAGAAAGGCCTACT TCCTTGTGTAACACTCC[C/A]GIATATTGTGATTTCTAGCTATAAGAAATGGGCCACTAAGTGGGTC

WI-17623	46 T C	TGTGGTTTAAATTTAAATTTCCCATATAAATTAATGGTGGGCACATTTC/GCATGTGCTTACTGGGTC ATTCATATATCTTTGTGAAGCATCTGCTCCAATCTTTTGCTGACITTTGGAGTTTTTGGT
EST26419 11b	46 T C	ATTTACACAGAGATACAAAGGCAACTATGTGCAGCAACAATCTGATTC/GJGGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGTTAAATGTCATGATGGCTGGTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26419 1a	35 C A AG	CAAGAAGTTTG GACTGCCC	ATTTACACAGAGATACAAAGGCAACTATGTGCAGC/AJAAACAATCTGATGGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGTTAAATGTCATGATGCTGGTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26780 5	69 G C	TCAGCTTTAATTTAAGGGACATGTAATAAAAAAGATGCATTTGACAGGCAGCAGACTAGTTCAAGC AG/GC/JAGGTTAGACCAGTAACAACAACCAAGAAAGCAAAGTGCTCGTTTCCATCTTGGCTTTACCA CACTTACAACTGATACCC
EST26800 7	39 A G	TACTCAGTTTAAGGCAAAATCCACACAGAGACTGTC/A/GJGAGACGGGCACAGAACCCAGACACC GTAGAACACCACCACCACCATGCATGACGGGAAGCAGAG
EST27152 1	101 C T	CAAAGGATTTATTTTGTTCCTAAAAAGTAAATCTAGAAAAATAGCAACCCACTGCAAGAAGAGATT CTATACTAAAAACATTTTCAATCATCTCTCTCTC/TCTTACATGGTGTACTCTTTCATGTACACAT CATCGGAAAAACAGACTGA
EST27504 0a	33 G A ATTT	GCTGGTGTGAT GCTACTGTAAAT G	TTTTGCACTTTGCACAACATTTAATAATTTATC/GJAJCATACAGTAGCATCACACCAGCAGTCAAT AATGCCACTTTAGGCAAAAGTCTTCAGTATTTCTGTTACACATCTGTTAACAAAGAACCCATACATT GGTAAATTCATTCT
EST27662 4	51 C T CTCCAGTCTG C	TTATGGAATG GCTTATGTAAC	ATCTTAAAGGACCATTAGAAAAAGGCCAGTCACATCTGTTCTCCAGTCTTG/C/JAGGTTACATAAG CCATTTCCATAAATCTATAGCCTTCTCTTAGAGTAACACACACTCTTGTTTAGGAATGTTT
EST27788 3	100 A G	ATTTATTAGCGGTACAATTTCCAAGTGGTAAGGGTGAAGGAAGGCGAAGGCAGGCAATACAT TATTGAGCTGAAAAACAACCTTTACATTTCAAGGAC/A/GJGCTTCCAGACAAGCCATGTAGAACCCAGCAT GCCTTGGGACTGTGTGGAT
EST27828 4	58 G A AGAACCCAC C	GTCAGAGAGG TACTCCAAGTA	TCCTTAAACCTTTCTCTGTTGGATCCCAGTGACGTGGAAAGTCATCAGAACCCAC/GJAJGTACTT GGAGTACCTCTCTGCACCAAGATAGCTGGCTGATTTTCTGCTCAGTCACAATTTTACTTGAA
WI-18369	58 G A ACAATC	AATAAATTC AATCTGTAC	TAAAAATTTGAGATACATTTCCCCAATGTAAACAATAAATTTCAATCTGTACACAATC/GJAJAATG GATAAGGCCTCTTGACAAATTTCTGCCACCTCCGTTTAACGCATCAGAACTCAATCTTATCTC
EST28036	37 T C	TCCCGCTTCCAAAAGCTTTATTGGCAATATGCTCTA/TCTJAAAAGAATGATCAATCCTGTTCCTCT AAGTCAATGGAATGAAGAGCTGTGTCCAGGGACACACACGCGTGTGAAGGAGACTGCTGTGTG TCCACCTCTTATTCATAG

EST28483 7	31 T A	GGAGTAAAG GTGTTCTTCT TTAAA	TTTCTGCAAT TATTTTATAC CA	CATTTGGAGTAAAGGTGTTCTTCTTTAAATTAATGATGGTATAAAATAAATGCGAGAAACATTAAAC GGAGAATGTACAGACAACAGACGAGACATGAGTTGTTTCTGACTGTGACACATTGGTGAAA
WI-17724	50 T C	TGGGCTCTCC TGTC	TGGGTTGGCAG TGTC	AGAAATTGGTCTAGTAATCGTTCAGGATTTCGGTGATGGCCCTCCCTGTC/CJGGACACTGCCAACCC CACAGCTGGAGGGGCACCTTAAGGCACGTCATTTTGATTAGA
WI-17730b	68 T C	TGAGCCTGGGAGAAAGACCACAGAAAGTGAAGTGCTATTAGTTACATCATACCAAGTGATACATACTG TT/CJACATGATTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGATGATGTGCA
WI-17730a	39 A C	GACCACAGAA GTGAAGTGCT ATT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGAGAAAGACCACAGAAAGTGAAGTGCTATT/CJGTTACATCATACCAAGTGATACATA CTGTTACATGATTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGATGATGTGCA
EST29041 5b	53 G A	GGAACAACA CATTAAAGCAT CA	GGTATTGTTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTCATGAGGAACAACACACATTAAAGCATCATTTGTCACCT[G/A]GCTAACTCCT CAAATCAACAATACCCCTTATTTTAGCCATGAAAAC
EST29128 4	58 A G	CTTTAGAGGACACACAGCTCTGTTGGACTTAGGGCTACCCCTATCCAGCAGGTGCC[A/G]TTATTT TCACTTGGTTACGTCGTGAAGACCGTTTCCAAATGAGGTTACAGTCACAGGTTCTGAGCAGACATGA GTTTGTCTGGGACACT
EST29912 3	103 C T	TCTGCCAGCTT ACAGGCT	GCGTAAGTGTC TCATTCTTCTG T	ATTATTAGGTATCTGCTGTTGGGGTGGGGAGATTGTTGAGATACTGCAACAGACACAAA AGCAAAGAAAGAAACATTTCTGCCAGCTTACAGGCT[C/T]ACAGAAGAATGAGACACTTACGCGATG GCCATGATACACAGCAGTGA
EST29936 8	121 G C	TATTGGTATGCTTAGGGAAGATTCTGATTAGAGATATTAAATCTTAAAGTTAACTCACCATGAAA TTTAACTTCTGTAAGTGGCTTCACTGATGAGGCAGTAACTACATAGGATAAA[G/C]AGCTCAGTA TCTGGAATCATGCTTCTG
EST30223 2	99 A G	AAATAAATACATCATGGGGAATGGGATATCCATCCCTCAAGCATTTATTCTTTGAGTTACAAGCAA TCCAATTACACTCTAAGTTATTTTAAATATTC[C/A]GGAATTAATTTCTTCTAGTTCAATCTTGGGA GG
WI-16260b	86 G A	CTTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAAGACCCAGA GTTTCAACAATATAGGTAGC[G/A]ATAACCAGGTCCTACTTCCCTTCCGTGAGAACTTCGTGGGAC
WI-16260a	59 G T A	TGAGGTGGATT CAAGAAGAAA A	CTACCTATATT GTGAACTCTG GGT	CTTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAA[G/T]ACCC AGAGTTTCAACAATATAGGTAGCAGTAAACCAGGTCCTACTTCCCTTCCGTGAGAACTTCGTGGGAC
WI-17835	30 G A TG	ACAGGAATA TTGTGCTTTCT	TGGGGTATAGG AAACAGGC	AAGAGAAACAGGAAATATTGTGCTTCTTG[A/G]CCTGTTTCTTATACCCCAATATCATAAGAAAT GTTGTTGCTTCTATATGTTGAGCTTCAAAATCTTTTGTCTTAATCAATCCAAATGAATTAACCTGAAT TTCTCCTCTGTTCAAAA

EST31951 4	87 C T	GGGTTGTCAG CCAACA	CCACCAAAAT CACCTCC	ACAGCCATTATTATGTTACTTGGTAATATCAGAGACTGAACACATTTTCACTCTTTTAGCAATGACA TCGGGTTGTCCAGCAACAAC/C/JGGAGGTGATTTTGGTGGGAAATCTTATCACAATTATTCT
EST31968 8b	95 T G	CGAATTTGCTCTCTATTATTTGTGATCTAGTAATCCTAAAGATTTGGGGGGGGTACTATAAGT GCATTTTATAATGGGGATTTTCTGCTT/GJAACTGCCCACTGATTTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTCC
EST31968 8a	75 T C T	GCGGGTTACTA TAAGTGCATTT T	TGTAAGAATCA GTGGCAGTT	CGAATTTGCTCTCTATTATTTGTGATCTAGTAATCCTAAAGATTTGGGGGGGGTACTATAAGT GCATTTT/CJATAATGGGATTTTCTGCTTAAGTCCCACTGATTTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTCC
EST32063 2	103 C T	TCCATGGATGAACAGACGCTACCATGCCACATCCCACATCCCCTCCGACCAGATGTCGTGGCCAGAGC TGGCTTCCCCTCCAGACCTAGCTGGCTTTGTAGT/C/JGTTCCAGGCCCATTTGAAATAGCAAAACGCAC AGTCATGTAGCACTCGG
WI-16303	65 A G	AAGGCTTCCAAAGCATTCAAAAGGCACCTGGGTGTGCTCTAAGTTTCTGGTCACTGCAGCCCCQ/AG JTCGTGATTAGGGAGCACCCCAAGCCAGTAACAATATGGTTCTTGCAG
WI-17800	29 C G	GGGAGCACAA GAGAACTCA TT	TTTCTACAAT TAATCCCAGTC TT	TGGACATGGGAGCACAAAGAGAACTCACTC/GJAGACTGGGATTAATTGTAGGAAATATTTACACAG TTTCCACAAGTCAGAGAGCTAATCCCAACCCCTGTATCTGGAACATACACTGCTGCCATTTCTGCG CCATGAAGGGAAATACCC
WI-17857	34 T G C	CCTAAAGTCTG GGATGACTTTC T	TTGGCTTAGGT TCTACTTGATG T	AACTGTCAATTCCTAAAGTCTGGGATGACTTTCCTT/GJATCTACATCAAGTAGAACCTAAGCCAAAT TCAGAATCAGAATCCCTTTTGTCCATCAAAATCCAGCTAACTCCAAAGCTGAATTAATGTTCATTCT GTATCTGATGTAGTTAACCATGGCCTGTCATGATTATATTGCTATAAGGAAGGGAACAAATCTTTA TAGTGTCCAAAAGATAATTAATCTTGGTTTAAATCTTTGCCAGCAAAAGCAAATTT/AJCCGACTGAC TGCTCCTTAGTCTGATC
WI-17860	121 T A	TTTGCCAGCAA AGCAAATA	ACTAAGGAGC AGTCAGTCGG	GTATCTGATGTAGTTAACCATGGCCTGTCATGATTATATTGCTATAAGGAAGGGAACAAATCTTTA TAGTGTCCAAAAGATAATTAATCTTGGTTTAAATCTTTGCCAGCAAAAGCAAATTT/AJCCGACTGAC TGCTCCTTAGTCTGATC
WI-17866	43 A T	TTTATAGCCT ACTTCTCAA ATTGTT	CCGTTGTCAC AATCACACAA A	CAGCAACCTTTTGTGTTTATAGCCTACTTCTCAAAATTTGTI/AJTTTGTGTGATTAGTGACAACG GGGGAATCTACAATGCTCACATCACAGTAACTACCA
EST33301 4c	80 G A	GAAAAAAAAGTCAAAATGTTCCTTTATGGGTGATGCCACCATGATTGCCCTCACACAAGCATGATC AATCGCCACGAGA/GJAACTGGATGCCAAAAGATATGG
EST33301 4b	63 G A	GAAAAAAAAGTCAAAATGTTCCTTTATGGGTGATGCCACCATGATTGCCCTCACACAAGCAT/GJAA ATCAATGCCACGAGAGACTGGATGCCAAAAGATATGG
EST33460 1	44 G A CA	AGCGTGGTTT CAATACTAAA CA	CTGTATTTATT GTTAAATATTT GCATTGTT	CTATCCAAAAGATATTTATTCAGCGGTGTTTTCATATACTAAACA/GJAAJGTAAACAATGCAANTATT TAACATAAATACAGTGATTAAATAAGCCATGCCATATCCAGTTGATGTAATACTTTTGCAA

WI-17904	50 A G	AAAGCATGAC AATAAAATGA ACAC	CGCTTATGTTA ATAGTAATTCC CG	CAAGTGAATATTGATACATGGCTGACAAAGCATGACAATAAAATGAACAC[A/G]TACGGGAATTAC TATTAACATAAGCGGATAACATCAAAACATCTGGTAAATGCAGTTAAACACAAACACAAATGA
EST34149 5	69 A G	TGCCAAATAC TCAAGTGTGA GAT	AACACTAGCG AGAACAACTA ATAAAATC	GTITTTCTTTGAGTGACACAGCTGTTCAITTTTGAGAAAATGTGCCCCAAATCTCAAGTGTGAA T[A/G]GATTTTATTAGTTGTTCTCGCTAGTAGTTTGGTATTCTATGAAAAAAGCAGCTAGTTTCAGC TTACAAATCACACAAGT
EST34343 8	95 C A	TGGGAAAACATAAGTTAACTCAAGAATATATTCCAGTCTTTATGTTACTAAACATTTGTAATAGTGT TTTATCAATGATGCCGAGGTCACTGCT[C/A]TACAAAGATTAAAGAACTTACCATCAAAACACTTC CAGTGCATCAA
WI-17982	98 C T	GGACCATATG ATATATAACT CCTAAAGC	CAGAAATTATG TGATAATACT CCTTCC	GGTACACAATTTTAAATGGAAGGACCACAGGTATGTTGAAAGAACATCAGTACAGCTGGAGACAGG GAGGGACCATATGATATATAACTCTCTAAAGC[C/T]GGAAGGAGTTATTATCACATAATTTCTGGGC GCTACAGAAGTTTTTCATCA
WI-17993	118 A C	CTCAGTAACTCCGGTGTTAATCTGCCATTTATTGATTTATTATGATAAAACACCTCTCATTTGTGA AAACAGCTAAGGGTGACATCTCCAGACCCAAACCCTGTCCTGTAATG[A/C]CTGCTGAGAGTCC ACATTTTGGAAATCCAAT
WI-17996	84 A G	GTAGAGCGGA AGGGAACAG	AGGCACATGGG CAGC	CCCATCCAGAAACCCAGTGTGATGGTGGAGCAGCATGAAACAAACATCTCCCCAGGCCCTCGCAGT AGAGGCGAAGGGAAACAG[A/G]GCTGCCATGTGCTCTCTAAAGACGCCACCCTCAGGTTGATGT CACCTGTGGGAGACCGGGT
WI-17136	33 C G	ATCTTTATAAAACACCATGTCCCTAAAATGT[C/G]ATTCAACATATATGCACACCTTCGATGTAT AGGACACTGATCAAAAAGACAGAGAAATGTGTCCT
WI-18041	24 A C	GCCACTGAAAAAGGTGCTCTCC[A/C]GTTTCTAACTCCCTGGACTCCCTCATTTGGAACCTGAAGCTC ACAGATGTTTCAGCTGGACTAGTTAGACTTTGCTGTATTTTAAAGGCAGTGTGATGCTCCAGGAT TCAAATACITTAATCA
EST35164 8a	57 A G	CACAGCCCTGC OCCC	CCCTCTGGATT CTGAATCTCAA	TTGAACCAAGGCCCTAACAGATGACTCAGCAGGGCCCTCAAGCACAGCCCTGCCCC[C/A/G]TCTTGA GATTCAGAAATCCAGAGGGTGCTCAGTCCCTGGTTTAGGTGCTCTGTGACATTTCTCTTTG
WI-18052b	67 A G	AGCGAATGAAAATGCTACATAGGCTCCCTGAGTTCTTTATGTACGAATC[T/C]TGGTTACACATCTT A/GACAGCAGAGCTGCCTGAGGGAGGGTTGTGTTAATGTGTATGCTATGCATGCTCAGCAGAGTGTGGC ATGGCCCATCCATGCTTT
WI-18052a	50 T C	CCTGAGTTCTT TCATGTACGA ATC	CTCAGGCAGCT CTGCTGT	AGCGAATGAAAATGCTACATAGGCTCCCTGAGTTCTTTATGTACGAATC[T/C]TGGTTACACATCTT AGAACAGCAGAGCTGCCTGAGGGAGGGTTGTGTTAATGTGTATGCTATGCATGCTCAGCAGAGTGTGGC ATGGCCCATCCATGCTTT
WI-18054	46 G A	GGGAGTGGGG GAGTAAAA	CGTCACCTGC TTCCA	CTGTTGTGCTGAGAACAGAGGGGTCAAGGGAGTGGGGAGTAAAA[A/G]TGAAGCAGGGGTGACG CATGCAGGAGTCCAGACAAAGACGGGIGATTTTGTCTCAGGTTGGTAGCAACAGAGGTAATG

WI-18064	54 G A	GTAGCTGCTA AGCTGTATTTC	CCAGTGGTATG ATTGTGACATT C	CAGCTGCCAATCATCTCTCAAAACCCCTGTGGGTAGCTGCTAAGCTGTATTTTCAGATG/GA/GA/GAATGTCA AATCATACCACTGGGGAGAGAGTAAGCACAGTGTCTATTAGGTGCCAACTGGGTACCTGGGAG GCAGAAA
EST35347 2	97 T C A A	GCATAAAATT TTCCAGTTGGT	COCTCGGCACC TGCT	TTTAGCACCATCTTAGTGGAGCAGGATCTTGATCATGGGGTGAATTTTGTGTATCTGGGCTTCAT GGGATGCATAAAATTTCCAGTTGGTAAGT/C/JAGCAGGTGCCGAGGCTCTGGATCAGAAAAAAGG CAGGCA
WI-18070	28 A C	AACCCACTAC TTACTCAGAGT GTGTAT	AAAACATAA AGAACTGGA GGTTTT	AAACCCACTACTTACTCAGAGTGTGTAT/C/JATATTACACATGAAAGATATAATCTTAGAAAAA ACCTCCAGTTCTATTAGTTTGATATTTCTGTACTCAGAACATTTTAGGTTGCAAGGATATAA
WI-18080c	80 C T	TGGCATAAAGTTTGCAAAATCAATATCAAACTAGTCTCTCTTTGTAAATTAATCTACTATGCCGTG TTTGACTTTTATC/TJTC/TATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCTTTGGTGAT
WI-18080b	65 G A	TGGCATAAAGTTTGCAAAATCAATATCAAACTAGTCTCTCTTTGTAAATTAATCTACTATGCC/G/ AJTGTGGACTTTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCTTTGGTGAT
WI-18080a	41 T C	GCAATATCA ATATCAAACT AGTCTCTC	CAATTTACATA AGAGATAAAA GTCAAACA	TGGCATAAAGTTTGCAAAATCAATATCAAACTAGTCTCTCT/C/JTTGTAATTAATCTACTATGC CGTGTGGACTTTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCTTTGGTGAT
WI-18086	63 G A	GTGGCATCCTATAAAAGCAGCCATGTGTTGAACAAATGATATGCACAGAAAGCATCTT(G/A) TGGCTTTGTACACGGGTTTCTTCAAGAGGAAGATGACTCAGCCCTCCAGCTTCTGCAGTCTAGC TTAGGAGAGGTGTTGAA
WI-18115b	71 C T	AACTACATAGTAGTGGCTGGCTTAGAATCAATGGGTAAGCCCTTTAGTGACCTTTGGTATTCCT TTC/C/JTTTGGTATGAAGACAGACACCTCTGCTGGAGGACTCATTACAATGTAAAGAAAGGGTGAG TCAGT
WI-18115a	70 C T	TTAGTGACCT TTGGTATTCCC TT	AGAGGTCTGTC TTTCATACCAA A	AACTACATAGTAGTGGCTGGCTTAGAATCAATGGGTAAGCCCTTTAGTGACCTTTGGTATTCCT TTC/C/JCTTTGGTATGAAGACAGACACCTCTGCTGGAGGACTCATTACAATGTAAAGAAAGGGTGAG TCAGT
WI-18136	78 A G	TTTTGAGAAGCACTCTGTAAAGGCAAGGATGCATTCAAAAATGGCTTTGAGGATTAATCTTCTCTTTA GGTAATTTGC/JA/GTAAGAACATAAAAGCATTTTAAAGTCCACTGCCGCTTAGAACT
WI-18169	115 A G	CCATCTTCCG GAAGCTC	GAGTCTGCTT GTGCTCCA	GGCAAAATATTTTACATCACACCTGGAATCTGCCAAGTCTTCCACTATGAAGCAATCGTAGAG TGTGCAGGAGGAAGGTGTATCCAAAGCAGCCATCTTTCCGGAAGCTC/JA/GTGGAGCACAAAGCAGA ACTCGGTGGGTAGAGTGA
WI-18190b	26 G A	TGAAAGAAGTCGACACAGCGGACACT/GA/JTCATAAGTGGAAACAAAGGATGAAGCTAATCATGGAG GCAAGCTCCCTGGAGAGACAGGGACAAATCAAGAAATGAGCTGGAGACATTAATCCTGGCGA

WI-18190	62 G A	TGAAAGAAGTCGACACAGCGGACACTGTCTATAAGTGGAACAAAGGATGAAGCTAATCATGGA[G/A] GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGAAATGAGCTGGAGACATTAATCTCTGGCGA
WI-18181	100 A C	CAGATC	CGTTTACCAT TTGTTAAGCTT TTG	GACAGTGAAACATTGAAACACAAAATACAACAAACATTAGGAACAAGAAATGTGTAATCCAA TGTTGTGAAAAATATATACAACACTCCCTTCAGATC[A/C]CAAAAGCTTAACAAATGGTAAACGTA TGTTGTTCTTGAAC
WI-18215	78 G A	CTGCCCTC	AGCAGAGTTC CCTCCCTCTCT CCCCC	ATTGATACAAGCATTTCTCTGAGTACAAACTAGGGGACAGGTATTTTACAAAAACAATAGAGCAGA GTTCTGCCCCTC[A/G]GTGCGGGGGGAGAGAGGGGATTTCAGCATTTGGTGAGTATGTTAATT CCCTCAAGTTAATCTTC
WI-18232	60 T A A A	TGGTGTGATT GTGATACACTT	AAATAAAGGT TTTCAGGGGTT C	CATTTCCGAAAATCTGATAGTTAAATATCCCGTCTGGTGTGATTGTGATACACTTAAGTT[A/GAA CCCCTGAAAACCTTTATTTTGAATTTGAAGTTTTGCTCAGAACTGGGCAGAACTTTTCACATTCTG AC
WI-17892	76 T C A C A	GGAAAACCTG AGTTTGAGATC	CACAGAAGTG AATAGACTAGT GAGACA	TTTAAAAATGCTTAGATTTCCTCAGTATTTTATCAATAGTGTAAAGCTGGAAAACCTTGAGTTTGAG ATCACATAT/CCTGTCTCACTAGTCTATTCACTTCTGTGGCATTTTCGGCAGAAAGTGGC
WI-18242	30 G A AATCGTAACA	CCCCAAATGTT CCTTC	GCTAACACTTC TACTGTAACAG CCTTC	AATATCCCCAAATGTTAATCGTAACATACT[G/A]GAAAGCTGTTACAGTAGAAGTGTAGCAAAAAT TGGATGCCACAACTTATCTCACCATTCTTTCAAGCAAGTGAGGTCAGAAATGTTTCTTGCCCTATATC TGCAAAAAGATCGAACAAG
WI-18266c	119 C T	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATGAAAAGTGTTCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACATTT/C]TGAGAC CCGCAACTCCGAGGTACCT
WI-18266b	124 T C	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATGAAAAGTGTTCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACATTT/C]TGAGAC CCGCAACTCCGAGGTACCT
WI-18266a	97 C T	AAATAGGAAA TATGGACTATC TTCAAA	TTTCATGCATCA TTTGTGCA	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATGAAAAGTGTTCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]TGCAAAATGATGCATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18312	73 A G A A	GCTGTCAGCTA TTGTTATTTCA	GGAGAAAAGG GAGCAGAAGA	CTGAGCCTCTTGATATGTGGTTAGTGTCTATCATTAATTTTGGAAAGCTGCAGCTATTGTTATTTTC AAAT[A/G]TATCTCTGCTCCCTTTTCTCCCTTTTCTGGGATTCTCATTTCTGCATGTTTATA
WI-18330b	68 A G	AAACATCTACAGCTGTCTTAGGCCATCCTGTAAAGAAATCAGGGATAAGAGCTGAGGAACAAGAGGGI A/G]TATGTAGGCGAGTGAGTCAGGACTATGCAAAACCATAAAAATAAAGAACATAATTTTTTTTGTGAT TCACA

WI-18330a	49	GA	AAGA	TCCTGTAAGA AATCAGGGAT	AGTCTGACTC ACTGCCTACA	AAACATCTACAGCTGCTTAGGCCATCCTGTAGAAATCAGGGATAAGA[G/A]CTGAGGAACAAGA GGGATATGTAGGCAGTGAGTCAGGACTATGCAAAACCATATAAAATAAGAACATAAATTTTTTTTGTGAT TCACA
EST37564 5	85	T	CIAGA	AAATTCAAAGC CATCTACAAA	CTATGGAGGCC TCAATGAGA	AAATTAGTTAGCCATAACAGGCTGGAATTGCTGGTTAGAACTACTGCATGTTATTTAAGCTAAAATTC AAGCCATCTACAAAAGATT[C/T]CTCATTTAGGGCCTCCATAGGCTGCAAAACACATCAAAAGGCATTAC TGTAAGGAGAGGACTGAG
WI-18327	104	G	ATT	AAACAGCTTT CGTTAGGCTAG	CGCATACAATG GCTCAGC	CAAAGGGATTTTATTACCTACACAAGTAAGGAGGACAGCTGGGGCAGTTTCCCAAGCAGTACCTC CCAAACAATGGTGAACACAGCTTCGTTAGGCTAGTT[G/A]GCTGAGCCATTGTATGCGGAGGCAGA GT
EST37624 6b	102	GA	---	---	---	GTGGCAAGAGCAGCTAAACACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGCACGCTGATGG CCTGCAGTCTCTGCGGTGCTTGGCTCTCTGGACG[G/A]TTCAATCTACATGGCTGCTTTCGGTCC TCTGACCTCCCCATTCC
EST37624 6a	58	CT	---	---	---	GTGGCAAGAGCAGCTAAACACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGCACGCTGATGA TGGCCTGCAGTCTCTGCGGTGCTTGGCTCTCTGGACGGTTCAATCTACATGGCTGCTGCTTTCGGTCC TCTGACCTCCCCATTCC
WI-18357	89	C	G	GCATCAA	AAGGACTCAA AGACTGAAGAT GA	AATGTTTTAAAAAGTCTACCGTGTGAGGTGGCCATGAAGCCAAAGCCCATGGAGAGACATTTTCAGA TAATCCCAGCCCTTAGCATCAA[C/G]TCATCTTCAGTCTTTGAGTCCCTCCAGCCAGGTCCTCAAGCTT GTGGACACAGAGACAAAGCC
WI-18012g	117	A	G	---	---	TTTTATCTGGTCAAGTCTCTTCTTAATGGCCTGAAGGTCACTCTCTTCAACTTTCCAGACTTGGAAAG ATCCCCGCTGTCCACTCTTAGAAATTGAAGCCACTTTTGCCCTTCGTGA[G/G]GTGTTTCTTGATACA CGCTGACGTTTCGAGGG
WI-18012f	113	G	A	---	---	TTTTATCTGGTCAAGTCTCTTCTTAATGGCCTGAAGGTCACTCTCTTCAACTTTCCAGACTTGGAAAG ATCCCCGCTGTCCACTCTTAGAAATTGAAGCCACTTTTGCCCTTC[G/A]TGAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012e	112	CT	CCCTT	GCCACTTTTGC CCCTT	TCAGCGTGTAT CAGGAAACA	TTTTATCTGGTCAAGTCTCTTCTTAATGGCCTGAAGGTCACTCTCTTCAACTTTCCAGACTTGGAAAG ATCCCCGCTGTCCACTCTTAGAAATTGAAGCCACTTTTGCCCTTC[G/T]GTGAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012b	46	T	C	---	---	TTTTATCTGGTCAAGTCTCTTCTTAATGGCCTGAAGGTCACTCTCTTCAACTTTCCAGACTTGGAAAG AGATCCCCGCTGTCCACTCTTAGAAATTGAAGCCACTTTTGCCCTTCGTGAAGTGTTCCTGATACAC GCTGACGTTTCGAGGG
EST38390 4	75	A	G	CTCTGCATTG	GCTAAAGTCAG CTGATTAATAA ACTTAA	CATATCATAGCCAGATCTACAACCCAGAGTAATCCCATGGTTATGTTACATGGCAAAAAGGACTC TGCAATTGT[G/A]GTTAAGTTTATTAAATCAGCTGACTTTAGCATTTGGAGATTATCTGGAT

[illegible]

EST38878 9	47 T	AAACATCATT ACTAGCCTAG C ATCCTAA	CCTTCAATAAA TCTCATGTCTT CA	CCAATGAGAACCAAGTAATTAACATCATTACTAGCCTAGATCCTAAAT/CJTGAGGACATGAGATTT ATTGAAGGGAATCCTCAATTAATATGAACATTTCTTGAGAAATGGGAAATTTGAAACATTTCCC TTATCAATGTCTATCTCACACATTTCTTTATTTTATTTTATTTTACCTTTTCAAAATATCGGATTTGTC TCATGAGAATAATGGCTGAGGGAGCTGGCAGCGCAGTCTTCTCA/GC/GCTCCCTGGATAGCTAAAT TTA
EST38882 6b	113 G C	TTATCAATGTCTATCTCACACATTTCTTTATTTTATTTTAT/CJTGTGTTTTCACCTTTCTCAAAATATCGGATTT TGCTCATGAGAATAATGGCTGAGGGAGCTGGCAGCGCAGTCTTCTCAGGCTCCCTGGATAGCTAAAT TA
EST38882 6a	35 T C	TGTCATCTCAC ACATTTCTTTAT TTTT	CGATATTTGAG AAAGTGAAAA CAA	
EST38899 5	47 A	GCACAGCATG GCTAAAACG	GGTATTTGTG ATCCCATCTT T	GCACTAACTAACTTTTCATTTGTGGATTGACACAGCATGGCTAAAACG/A/GJTAAGATGGGAATCAA CAAATACCATTTGAAGATATGGAGCAAGAGAACTCTCACATACTGCTGGAGGGAATATAAAT
EST38911 9	85 A G	GTTGAGGGAA ACTTATAACCT CAC	TGTTGTTTGT GAAACAAGCG	AACTGAATGGCAGTGAAACACTACACATCAAAACTTAGGGAATGTGGTTAGTGTGGTACGTTGAG GGAAACTTATAACCTCAC/A/GJCGCTTTGTTTACAAAACACAGCAGACACAGAGATTTCCAACCTC CAGCAATGACAGGCTAGGG
EST38955 5	30 G C	TGAATCCCTT GGTGGG	CACGTGCAATCT CAOCCOC	TAAACATTTCCCATTAATTTCCCTTGGTGGG/GC/GGGGGGGGGTGGAGATTGCAGTGTCAAGATAAA TATCACAAATATATCAAAACCTTCAAAATGTCTATGCAATTCACACACTGACATGAGCCACAAACATT CCTTTCACAGGACTGTAC
EST39002 0	42 G A	GGACCCCTCGG TGACC	CTGGCAGGGAG CCTG	CCTGCTATGATGCTTGGCAGATCCCGAGCCCTTCGGTGACQ/G/A/CAGGCTCCCTGCCAGGCTTGG CCCTGACCGGGCTCCACAGCTCGGCCCTGACTGTGGAGGAGCTGAAATACGCTGACATCCGCAACCT C
EST39004 8	79 T G	GGTGGTAAGG CCTAAGGAAT	ATCTCGGCTGG CGGC	CACGTGGCCCTAAGTTCCGGGTCTTCTCAGTCTGGATGGCTGTGGAAAAAGCTTGGTGGTAAG GCCTAAGGAATTT/GJAGGGGACAGGGGGCGATGCCGCCAGCGAGATGGTCCCTGTAAGCCTGTGGTC AAGACCTAACTTCTGGA
WI-16398	90 T C	TCCCTATTATT CCATGATATTT TCA	GAATGGTTTGT GAAAAATATA TTGATAT	AAAGATAATGTCTATCACACGCAACATATAGAAACATAAAAGAAAAATAAGTATCCACCCTAAAAAT CCCTATTATTCATGATATTTTCA/T/CJAGCAACTAGTATATATATCAATATATTTTTCACAAAACCAT TCAGTTACAC
WI-16403	69 T C	CCTTGTCTC AATTTTAAAC C ACT	TAAGGGCTAAT TCCCTATATAA AAAG	GGTTGTCTTTCATGTATTTTCTCATTTCTCATCAGGTTTCTGGTCTTTTGTCTCAATTTTAAACACTT T/CJTTTTATATAGGGAATTAGCCCTTAAACTGTGGTACATGCTGCCAAAATTTCTCCAGTT
WI-16406	24 C T	GCTTAAATGGC TACAGAAAGA AGG	CCAGAACCAG ATGTGTTTAA AA	GCTTAAATGGCTACAGAAAGG/CJ/TGGTTTTATTTTCTTTTAAACACATCTGGTTCTGGCAGC AAGTTATATTATGCAATTTAGAGCAATAGGTGCCCTGAA

EST39236 0b	57 C G	TCATCTGAGA ATAAACTTCCT GTC	CATTATAGGTA CTGAGTCATAC ATTAAACA	TCCTTTTATTCATGTTTTCATCTGAGAATAAACCTCCTGTCTAATTTCCAA[C/G]ACTATGTT TAATGTATGACTCAGTACCTATAATGAGACTGGAATAATATTACCTGGCAAATGAATGAGGTGCTC TTT
EST39294 4	63 G T	CCTGAAACAG GGATGCC	GCACAATTAA ACATAGTACCG AGAA	CAACAGACCTTTGGTTGAGCTCACCTGGTGACAGGAGACTCCTACCTGAAACAGGGATGCC[G/T] TTCTCGGTACTATGTTTAAATTGTGCTGAGCCAGCAACCCCTCGAGTTACCCGGCCCTTTACCCACGCC AGCTCTGCTTGCTGCAT
EST39366 2	72 T C	AGAAACATTCTGTCTGATCAGAGGAAGATGTATGTAGAAAAATCAGAAATCTGACTGAATTCCTAAA ATCTAT[C]ACACTGAGAGGAAAAATGGAAAAAGAAATGTTTGCATAAAGCTTTTCCCTGACTCTCA GAGGGTTCAGA
EST39371 9	86 A G	CATTGGATTA GGGTGAGG TT	TGATTTGAGAC ATTTACATTT TT	AAAAAGCTGTAGCTGGCAAGTCAAGTTTATTTATGTGTGTAATTCAGTTGAGCATTTTTCAT TTGGATTAGCGTGAGAGG[A/G]AAAAATGTGAAATGTCTCAAATCAAAATGCTTCTCTTCTAAAGATTA GACATTGCCCCAACCTGC
WI-17177	23 A G	ACAAAGTGACATATCCAAACCAACC[A/G]TCCATCCCCACCTGTGCCCTATTCTTTCCCTGTGTTCTTT AGAGCCTTTTCAGCTATTCTCTGTGAAGCAAACTGCAGGAAGGCCCTCCCCGTACTCTCCCTGGAA G
EST39428 8	31 C T	GCTCCCCACA ATTTTGATT	GGTCCCTTATG AAGCCACC	AGGTTCCCTGGTTGCTCCCCACAATTTGATT[C/T]GGTGGCTTCATAAGGACCCAGGATTCGCTATT TTCTGGGTGGGCCCTAGGTAATCTGTTCCTTTGGTCCACAGAGACAAATTAAGAAGATCAGGTCT GGCTGTTGC
EST39430 2	45 A C	GGCAGAGGAA TAAGTATGTT C	CAGGGGTGCGG GTATTG	AATTTAGCAGAAACAATGAAGTTGGCAGAGGAATAACTGATGTT[C/A/C]CAATACCCGACCCCTGA CCAGTAGCTTTCCCTCAGGCCAGGCTCCGGTGGAGGATGCTCTGGG
EST39446 7b	117 C T	CTACTGACAT AGGACTTCA GAGTAA	TCCTGGAAAAAC TGACATAAACCC	AAAGCCCTGTAAACTGAAGCTAGACAACGTCAACTTTGGAAGAAAAATAACAGGAACCTATTTATAT ACGTAATACATTTTCATACCTGCCTACTGACATAGGACTTCAGAGTAAT[A/C/T]GGTTTATGTCAGT TTTCCAGGATTGTTCTCCC
EST39465 2	80 A G	AATGCAGGAG GGTGGC	CAATCTCGGCC CCTCT	ATGGTGTATTAGAGGGCCACAGGGGATGGGGAGTAAAAATAACATAAACGAACCTGAACAGAAA TGCAGGAGGGTGGC[A/G]AGAGGGGCCGAGATTGGGTGTTTCAGGGCAGAGAGGTGGAAGACCAG
EST39501 0	81 A G	AAAGATTCCCT GTAGACATCT AACATTAG	CACITGCAATT CTGAAGGCT	TGCTTACAACCCATAACCATAGGCCATGTGTTTCAGACATTTCTTGACCAAGCCTAAAGATTCTGTAG ACATCTAACATTAG[A/G]TAGCCTTCAGAAATTGCAAGTGCAGTTCAAGTCAAAACCAATTC
WI- 18387b	84 A C	CACAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATACATTTGTGGTCA CATGCTTTAGCCATAC[A/C]CATGGTAACATTGACTATGGAGTCTTGTGAAAGTGTAATGTGCGGATG GCTATGTAGACATAAAGA

WI-18387a	57 A	CCTACTTTGG	GCTAAAGCATG	CACAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATACAGTTTGTG
EST40601	78 A	CGGTGGAACCT	TTCTTGGAGA	GTCACATGCTTTAGCCATACACATGGTAACATTGACTATGGAGTCTTGTGAAAGTGTAAATGTGCGATG
		GCGTGAACCT	AAGCGTC	GCTATGTAGACATAAGA
		AGTGTATCAC	GCACACCTTC	TCCAGGATGTTTATCCAAAGCTGTGACCGTGAACATTAGACGAAAGAGGTGACTCGCGTGGA
EST41935	32 A	ATCTTCAGGAT	ACACTGTTA	ACCTGAAACACAG/GACGCCCTTCTTCCAAAGAGGCTGTGGCGATCAGGCCACTCAAGG
		AGGT	AAACTGATTT	TCCATTCACTGTATCACATCTTCAGGATAGGTAG/GATAACAGTGTGAAGGGTGTGCTCATTTTCTTC
		CATTCTGGTCT	GTTAAACATG	AGCTGTGAGTAGAGGAGTCTTCCCGAGAGTAGCAGTTGTGA
EST43091	28 C	TTATTTTGGGA	CTAC	ATGTCATTCTGGTCTTTATTTTGGACA/C/TGTAGCATGTTTAAACAAATCAGTTTTTCATAGGCAA
		CA		CCTTTGAACATCAAAAGAAATAGCAATATATTTTACAAATTTCTCATCTGTAATTC
WI-18420c	108 T	TTCCATTAAAC	AAATTCTCAGC	AGAGAGACAACAAGAAGAAATAGGGAAATGGGAAGAA/C/TAGAGTGAAATTAAGCAAAATCTT
		AGGAAGTTTC	ATTGCTATAAG	AGAGAGACAACAAGAAGAAATAGGGAAATGGGAAGAAAGACAGAGTGAAATTAAGCAAAATCTTGG
		C	C	TTCAGATTCCATTAAACAGGAAGTTTCTCAAAAAAATCAAA/T/C/GCTTATAGCAATGCTGAGAA
WI-18420a	38 C	GAATAAGGGA	CCAAGATTGC	TTTCATAGGTACTTCATGGGA
		AAATGGGAAG	TTTAATTTAC	AGAGAGACAACAAGAAGAAATAGGGAAATGGGAAGAA/C/TAGAGTGAAATTAAGCAAAATCTT
		AA	TC	GGATTTCAGATTCCATTAAACAGGAAGTTTCTCAAAAAAATCAAAATGCTTATAGCAATGCTGAGAA
		TTTCATAGGTACTTCATGGGA
WI-18425b	101 T	AGCTGATCAGCTGCTGTTACTGTGTTTTATGTGTGGCCAGGGAAGCCAAAGATCAGACACCCCTGTC
		CACCCTGTCT	CCTCCTGTTGT	CTAGACAGATTCAATGCACACAACAACAGGAGG/T/C/GGGGGTACACGGGCGGAGAGCCAAAGAC
		AGACAGATTTC	TGTGTGCA	TAGGGC
WI-18425	81 A	C		AGCTGATCAGCTGCTGTTACTGTGTTTTATGTGTGGCCAGGGAAGCCAAAGATCAGACACCCCTGTC
		A		CTAGACAGATTCA/C/TGCACACAACAACAGGAGGTGGGGTACACGGGCGGAGAGCCAAAGAC
		A		TAGGGC
		A		AAATTGAGGTCCGGGTGGAACATAAAAAAGAAAGAAAGAGAAATCAAGGGAGGGCCAAAGTG
WI-18449	129 C	C	GTATCCAGA	GGAAGCTGATTGCTGATCTAACGTGCTGTCCAGTTCCTTTTGGCTCTAAGTGGGACTA/C/TTC
		AAGTGGGACT		TGGATACAGTCAGGGGAG
				ATCGCTTCATTGAAGCCTGCTTAATTTCTCTCAGTCAACTGGTGCCCCCAAGACATTATTTTATTCTT
WI-18457	120 T	AAATGTCCAAATATCTGCCTGATGTCTGTGTTTGTGCACATTGGGGCCACAGT/C/AAATAGGCTAAA
		CCACAATGGC	TTTAGGCTTG	AGGCAGTCCACCTGCT
		AGAGGTGA	AGATGGTTCT	GGTGCTATAGCTGCTGTACACCACAATGGCAGAGGTGA/G/TAGAAACCATCTCAAAGCCTAAAA
WI-18462	39 A	G	GCACGATGGGA	TATTTACCATACATCCCTCACGCAAAAGTTTCTAATCTCGGTTTAGGGACTCCATTGAG
		GAGG	GTGAAC	TGAGGACGTGTGACAAGTCCAGCAGGGGTGGGGCCGGGCTGAGGGTGGGGTGGGAGG/C/TGGT
WI-18476	60 C	T		CACCTCCATCGTGGCCCTGGCGCTCCCTCCACTCACCCACACCTGGCCAGTCCACGTTGAGGT

WI-18491	109 G A	AACAAATGGT AGGTGGTATT	CGTGTGCATTT TCITGTAATCC	CTAATGAGATGAATACATGGAAGGCGTTAGCACAGTGCCTAAACACAGTAAGTAACCAACAAT GGTAGGTTGGTATTAACTACTATTATTAAATCCAGAAATGAC[G/A]GGATTACAAGAAAATGCACA CGT
EST50757 b	79 C T	GAGCTGAGG CTGCTTCT	ACCTTCACCC GGCC	AGCCCCCTCCACTCCACTCTGCTTCCACAAAGTCGGCTCCGAGAGCTCGAGGCTCTCTTTTATAT GTGCAGGGCC[C/T]GGCGGGTGAAGGTCAGAGA
WI-17675	103 T C	GGACATTGG CATGGTGACTT	GGGGAACCAAC CAGG	GATCTTGGAAAGCACTAGAACTAAACATCTTCACCAAGGTGCTGAAGAAAAGTGTCTTCGTTTTAAT TGCCAAAGCAGGGATGGACATTTGGATGGTACTT[C]CCTGGGTGGTTCCCATAGATTCAACCAT TGCCCTAATGGTGCTA
WI-16543	67 G T	AGATAAACTA CATTTGGGTTT	GATTTCATTT ACAGGGGACTT	GATCCATTACCTAGGGTAAATTTCTCCTGAATGTCAACAAAGAGATAAACTACATTTGGGTTTTGG[G/T]AAGTCCCCTGTAATGATGAATCAAGAACTCCTCAAGTCTGTCTTGCACCCATTTAATACGTATT TTTGTTAAGGCTGAAGTT
WI-17687	107 C G	GCCAAAAGG TTGGGAA	TTACTTTTGT CCGACCAGCA	ATCTGAGATGGAAGAGTTTCATCCCAAAACCATCTCCCCTGACCCAGTCCATGGAATAATTGTC TTCCACAAAACCGGTCCTGGTGCCAAAAGGTTGGGAA[C/G]TGCTGGTGGGTACAAAAGTAATT G
WI-17690b	79 A G	AGGCATTTTC TAGCTGTGTTT	CAAGAGTTATG GGTCTGAATC	ACAACATGTGAAGAAGATATGTTGCTTTACTCACAGTGGAGGCATTTTCTAGCTGTGTTGATTT GGCTTCCCTAT[G/G]ATTCCAGGCCCACTAATCTTGTTCTCACTCATCTGCTATGCTGCTG
WI-17690a	63 G A	GCGGAAGACA GTGAGCTGTT	TTGAGGCAATA ATCCAGCTC	ACAACATGTGAAGAAGATATGTTGCTTTACTCACAGTGGAGGCATTTTCTAGCTGTGTTGATTT GGCTTCCCTAT[G/G]ATTCCAGGCCCACTAATCTTGTTCTCACTCATCTGCTATGCTGCTG
EST51717 b	128 C T	GCGGAAGACA GTGAGCTGTT	TTGAGGCAATA ATCCAGCTC	GATCCAATCTCAGTGTCTAACTCATCATCCAGATTATTCTGAAGTGGAAACCCCTCCGACCCCAA TGGCAACATCACCCACTACCTGTTTCTGGGAGAGGCGGGAAGACAGTGAGCTGTTC[T/C]GAG CTGGATTATTGCCTCAA
EST51717 a	39 C T	TGGTCACTTTG GGGOC	GGCTCTGCCCC CGOC	GATCCAATCTCAGTGTCTAACTCATCATCCAGATTATTCTGAAGTGGAAACCCCTCCGACCC CAATGGCAACATCACCCACTACCTGTTTCTGGGAGAGGCGGGAAGACAGTGAGCTGTTCGAG CTGGATTATTGCCTCAA
EST53012	97 C T	TGGTCACTTTG GGGOC	GGCTCTGCCCC CGOC	TTTCCAGGTTGACAGGTTTATCCACCCCTTCCATCCCATGGCCACCCAGGCAGGAGGAGACAG GTGTGCTGGAGTCTGGTCACTTTGGGGCC[C/T]GGCGTGGCAGAGCCCACTGGGTTTACATTCTCTGT GGGCAGGTGTGGACAC
EST53349	96 A G	TGTTGAAAGC AGTCACAATG TAC	CATCTGGATAT CTTGTCACATT TT	AAACTGCAAATAACAAAAACAAACAGAAAGTCCAAAGGCTAAAGTCTAAGCTATAATTACACATG AAGTATATGTTGAAAGCAGTCAATGTAC[G/A]AAATGTGACAAGATATCCAGATGTTTAA
EST53389	74 A G	GGAGACCTGC AGAACTTAAA CA	GGCCTTCTAA CAATAAATGCT C	TTTCGAATGTCTCCATGACTTGACAGACTGAGAGCCAGCCAGCCAGGAGACCTGCAGAACT TAAACAC[G/GAGCATTTATTGTTAGAAAGGGCAAGTCTTACACTCAAATAGGTTTTTAACATGAAC ACATTAAGGGAGATGGCC

EST53477	61	T C ...	CGAGATTTCT TC TTTATTTA T C TATTTTCA	... CCAAAGAAAA TGCGTTCAGTA A	TTTGAGAGGTTGTGCAAAACTACTGTATTTACAAAAATGGCACAAAAGTGAATTCACAGTT/CJAA TGCACATGCATACCTCATTCACATCTTCAACAACAAAAGGTATCTAACTCTACAGAACTGAATATT AGCTTCAACGGCAGCTGT
EST64622	91	T C TATTTTCA	TGTGTATAGCA CATACTTCAGG	ATGGGGTGGTG CCGC	GGGGAGAGGAGGTAGATTGCCAAATGAGGCATTTTTTTTAAACTCCCCGAGATTTTCTCTTTATTT TATATTTTCATTTTTCATCTCTAA/T/C/TACTGAAGCCATTTCTTTGGTTAACTTTAGA
EST67268 a	77	C T C	ACGACGCCGG CGAGT	GCATTTCCGG GCAC	CTCATCTTTATTAATGCATGTATAGCACATA CTTCAGGC/C/TJGCGGCACCCACCCCATAGAGATGGTGAGGAAGTAACCTTCTGCTTCTCATTTGAAACT GTAGATCCATCGGGGA
EST78503 a	26	C T CGAGT			GAATGCAGAACGACGCCGCGGAGTT/C/TJGTGGACCTGTACGTGCCGCGGAATGCTCCGTTAGCA ATCGCATCATCGGTGCCAAGGACACGCATCCATCCAGATGA
EST80253	92	G C	ATGCACTTTATTGGTCCAGGGAGTGGGATCGAGGATCAGAGTGACACGCGCAGGGGGCTGGTGTG GGGAGCAAGCGCGCGCTGCC/G/CJGGACCCCTGGTTCCCTGAGGACCAACGCTGAATGGGGGCC CACTGGAAGATGCTTG
EST91254	73	T G	TATCTGTAGGGAGAATAACCATGCTTGCTTATGGACTATCCATGGATAACTGGTTTTTGTGTTGTG TTGTTT/GJTTTTAATTATAAGAATAATATGTGCTCATCATATCAATGCCTTCTCAGTAGAGCCCCAG ACCTGG
EST91332	100	T A	TCCAACTGAAAGGAGGGTGGGAAAAACAAACGCATCATATGTAAGCACTGAGTCCAGCCTGGCTC TTAGTAAGCATTTTAAATCACCTTCAAAAATTA/TJ/TGTGACTTACGGAAACAGGTCACCTGAATAT TATT
EST91495 b	58	T C	CTGACTCAAAGACACACTCTGAAAGCAGGTCCATCCTGAGCAGCAGCTTGATTACTTT/CJACAAG TCAGACCTGTTATTAAGACGCAGACTGGCATTTAAATCAGGCTGTGTACACCCATCCTGGGCTTT GTTCTGGCTCCTATGGTG
EST91921	114	A G	CTGGCTGAGGATCTCAAAGACATTCACCACATTTGAATCTTAGGCTGGAGGACATTTTCGTAATCTT CAGTCAGGAATAGCACACTTCCCTTCATGAATAGCAGCTTTTAGGG/A/GJTTATATCATGAGGTACA AATAAAGAGGCCCTCACC
EST92026 a	56	T C	ATAGCCAAGATTTGGAAGCAACCCGTGACCATCAACAGATGACTGGATAAATAAA/T/CJGTGGTA CATGTACACTATGGAGTACTATTACGCCATGAAAAAGTCTAAGATCTTGTCATTAGCAACAACATGG ATGGAACCTTGGAAACACTGT
EST92040 b	38	C T	TTTCCATGAGGAATAAATTTGTGTTTATATAAAACCTG/C/JAGATGAATATTTTTTTAAACAGCATG ATTCACAAATGCCAAAAACAATGCAAAATGCCCTTCAACACATGAATGGATTAAACAGACCGTGATAC ATGA
EST98276 c	69	T C	GAGCTTGCTATGTTTCCAGGATGGTCTTGAGCTCCTGGTTTCAACAATACTCCTCTCTAAGCCTCC T/CJAAAGTGCCAGGATTATAGGTGTGAGTCACA

[illegible]

TGR- A003P30	117	C G	---	---	ACAAGTTCAAAGGAGAACCTTCCTTTGTTTAAATGCAGCTGTGCTCAGAACGCTGTGATTCCTAGGA AACCATCTGGGTTTAGCCCATTAGAAAAATGCAGTTTAAAGCAGTGTCA[C/G]ACTGGCTGCCTGAA GGTACCCCTGGAGATACT
TGR- A004S34	158	C T A	---	---	GCCTGCTTTTATGTTTAGTTGCGGGGAAAGGAGGGGCTGACAAACCGCAGACATCTGGACACCAGC AAGGGTCCAGGGGAGTTGACAACTCTTTGCTCTGGCTAACAGTCTGTCATGTGACAATAGCCA AACCTCCTCATCTCTATAAA[C/T]CTTTAACAAAACAGTTAGCTGTTTACAAAACAGTTAGCTGTT TACATG
TGR- A004T44b	97	A C	---	---	AACAACAGTGTAACTTTAACAGGGGATGTTAAAGGTAAAGATCAGGAAGATAAACCCAAAATGAT TGAGTATGATAAGAAATTTGCATGGCGATT[C/J]AAATAGAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG
TGR- A004T44a	69	G A TGA	---	---	AACAACAGTGTAACTTTAACAGGGGATGTTAAAGGTAAAGATCAGGAAGATAAACCCAAAATGAT TGA[G/A]TATGATAAAGAAATTTGCATGGCGATTAAATAGAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG
TGR- A004V08	60	T C	GGCATCTCTT	AAAGGC	CCTACAATCCTATAATATTGCAAGGGTGGGAAGGATGCAGGAAACAGGCAATTCCTTAT[C/G]GCC TTTTGTGGGAAGGATCAATGGGTGCATGCACITTAGGGGACAAATTTGGGCAGTAGCTGCAAAATTC AGTAGCTGTCAAAATTTCAAA
TGR- A004V26	125	A G	---	---	TCTAGCTATAAGACCAGATTTTAATATTCTAGATATAGAATTATCCAGAATAATTCATTGAATTGA CTGATTACAAAATGTTAACAGCTGGATAAACGGTAAATATGCATTATCTTCACATGA[A/G]AAGGT TTCAGTTTATAAATGCTTAAATACTGTATCTATTGCTTAAATACTGTATCTATTGG
TGR- A004V28					CCAGGCTATAATGTTGGGGTGGCATCT[C/G]GCTCACTGCAACCTCCGCTCCAGGTTCAAGCAA TTCTCCTGCCTCAGCCTCTTGAGTAGCCGGGACTACAGGCACCCGCCACCTAACTAAATTTTG TATTTTGTAGTAGAGACATTGTATTTTAGTAGAGACAGG
	29	A G	CGATCTC	GTGAGC	TAAGTTTCCCTCTCTCTGTAGGAT[C/G]CTCCATGTTACAGTCAACTATAAACACATGGCTCATGT TCACTCTGGGCTCGCTTCAGAGGAGTTTGATATTTGGAAAGTGGTACCTTTGTTCTGTGTCTTTTCA GACCAACCGCTTCTTTCATTTCTTCAAGGCTTCTTCCAAAGGAGTTAAATCATCATCATGTCCCAATC ATCATCATGTCCCT
TGR- A004X20	25	T C GA	---	---	TTTTGAAATCTTAGAGTAGAACCCAC[C/G]ACTCTAGTAATACCTTGTAAATAAAATTAATAATAGTTT AAACACTTCCATAAAGAAATAGGGGTGCCAGCTCCTTGATTTCCCTAGGGATAAAGATATCCAT GTTAGGGATAAAGATATCCATGTAC
TGR- A004X30	26	T C	CCAC	CTATTTT	CACGGTATATGCTTATATATAGGTATATATACAGATCGTACACAATATATTTACAGTTTGACATG GGGTCCACAGTACCTTCATTTGGGTATGCAAAACTT[G/J]TGCTTTCATGAAATTTCTAATTAAAGG ACTGTTGCTTCTTTCATATTCATTTCAATGGACATTATACAAAATACAGTCTCTTTAGTGATTTAAGACGTC TCTTAGTGATTTAAGACTG
TGR- A004Z04	102	T G	ATGCAAAACT	AAGCAA	

TIGR- A004Z19	85 C T	GAGAACAACT GCAGCATTTT	AAGATGGTCAT CGGGAAGA	TAAGTGAGACAAAGTTATTGGAGGAGCTTGACACCCCTCTTCTGCCCTAGCTTGAGAGAACAACTGC AGCATTTTTTCTTTTCTTCTCCCGATGACCACTTTTGGCTGGCGGCCAGGCCCTGGGTGTC TCCCATATCGCTGTCTTAGTGAGACTGAGGATCTGGTATAAGGAAACAGATC
TIGR- A004Z42c	89 C T	TTGGGGGAGGT AGGAGACT	CAGGGCTGCCG GTCC	GTCTTAGCAGAGGAGATAACTTTGAGGGACAGCCCCAAGGCCAGGTAGCCTTCAGGGGGGGGCA GGGTTGGGGGAGGTAGGAGACTCTTGACCCGGCAGCCCTGGCTCCAGCTTCATCATCTGTGTCTCTT CATCATCTGTGTCTTC
TIGR- A005D17 c	81 T C	---	---	TATGGACTGTGTAAGTAATGATTTGGACAAGAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGCTCTGTCTAGATCTCTTGGCCTCTCTGTGCAGGATTCCTTCTCTGGGCAC GGGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAAC
TIGR- A005D17 b	79 G C	GGGGAACCC AGCAAG	GAGAGGCCAA GAAGAATCTAG AC	TATGGACTGTGTAGAAATATGATTTGGACAAGAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGCTCTGTCTAGATCTCTTGGCCTCTCTGTGCAGGATTCCTTCTCTGGGCAC GGGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAAC
TIGR- A005D44	97 G T	TTAACATTATT GAACCTAAAA CTGTTACAC	TTGCTATTAT TTAAAGCCAA AAAA	CATCAGTAACATATACACAATTTGGTCACTCAACTGAACCTTGGCTCCAATATATTTCTATACAATACTT AACATTATTGAACCTTAAACCTGTACACTGTGTTTGGCTTTAAATAATAGACAATGATTTTGG TCTATTACTTAGTGATAGACAAAGTGAATCTTGTGTAGACAAAGTGAATCTTGTGTTAC
TIGR- A005E31b	27 G A	---	---	GGAGTTCAAAATTTATAACCGGCTCTG/AJCTCACAGCTGACTGGCTAGGCAAGCTTTCCAGAC ACAAAGCCACCTGCCTGCCATGTGGATAGTACTTTTGCCTGCTTGGCCCTACAAGCCACCTTCTAT TTCATACCAATACCTTCTATTTCATACCAATAAG
TIGR- A005E39	182 G C	AGTAAGGTTA CTGCACCTTAC	---	CTCAGTGTAACAACTTTGTTAGGGAAAAAATAATCCAATGGATATATGGGAAGAGAAGTG CCAGGCTGGATGGTCTGAGACAGAAATGACCCCTTGGCTCTTATTTTGTCTTTCAACAGGACC CCACAGATAATTTGCGGTATGTCATGAGGACTGGGGATGCTCTTATG/CIGGATGCTCTTCTATTTT
TIGR- A005E42a	42 A G	AGTAAGGTTA CTGCACCTTAC	CCTAAATCAGG GGAAATTGAG	GCTGAGTTTGTATCTTAGTAAGTTACTGCACCTTACAGAG/AJCTCAATTTCCCTGATTAGGA AGGCGATGCTAATGGGTATTCATAGGTGAAGTATAAAATGTTGTATTTAAGAGAATCCCAAG CTTGGTATAAGGCAGAAATAAATGGTATAAGGCAGAAAAATAATAG
TIGR- A005E46	76 A G	CACCTGACTCG GTGCTTTAC	COCTGGCTGTG AGGTAATGT	ATGACAATGATGATAGTATTAGCCTACCGTTTGTAGCACCTACTGCGTATCAGGCACCTGACTCGG TGCTTTAC/AJGTACATTACCTCACAGCCAGGGTTGGCAATGGTCAATTTTGACAAATGGTCAATTTG ACAC
U20979	24 C T A	GCAGGGGTGA CGTATGTAGA	GGGGAGGACAC CCTAAGC	AGAGCAGGGGTGACGTATGTAGAA/CJTGCTTAGGGTGTCTCCCCACAGAGCAGATACTTGAACCG ACTCAATTCCTGTGTAAAGAGCACCTTTGTCTGCTTACGGACCTCCCCAAAGTGTGCAGAGTTCTAT ATAGGATGCTGGATTAGTCTCTTTGATATTTGTAAAAATCCCCCAAGAGCCGCATATGAATCTGCCG

X57830	106	G C	CT	AGTGAACCA ACGATCATAT	CATTGACAGAA TAAATGAGGC	A	GTGGCAACTGTGGAAAGGCACACTGAGCAAGTTTTACCTATCTGGAAAAAATATGAGATTGGA AAAAATTAGACAAGTCTAGTGGAAACCAACGATCATATCTG/CJTATGCCTCATTTTATTCTGTCAAT GAAAAGCGGGTTCAATGCTACAAAATGTGTGCTTGGAAAATGTTCTGACAGCATTTTCAGCTGTGAG CTTTC
X74070b	72	T G	TGGATC	CTTTTAAAGAA ATTTTGTGTTA	GGGCTTAAAAA TATTAGAGATC	TAGATT	AACCTGAAGAAGTTACTGGGAGCTGCTATTTTATATTATGACTGCTTTTAAAGAAATTTTGTATTG GATC/T/GJGATAAAATCTAGATCTCTAATAATTTTAAAGCCCAAGCCCCCTTGGACACTGCAGCTCTTTT CAGTTTTGCTTATACACAATTCATTCTTTGCAGCTAATTAAGCCGAAGAAGCCTGGGAATCAAGTTT GAA
Z48804	44	C T	---	---	---	---	ACTGCCGAAGTGTAGCGGCCCCCAACCTTGCCTCTCATCCACG/CJTJTAGAGCTTCTTCCCGAAGGG CCTTTAGGATAGGAGAAAGGTTTCATGCACACACGCTGAGAAATGGAAGAGCCCCCTCCAGACCCT CTACAGCTGCTCTAGCCTTAGTTGCCACTAGGAAGTTTCTGAGGCTGGCTGTAAAGTAAGTGAAGG TCCA
D28513b	133	A G	---	---	---	---	ATGACCAAGCCACCACATTTAGAACITTTGGCTGCCTTTGGAAGTCCAGAGCTGGATCTCTCAGCTCC CGCCCCAGAGGGTCAGCACTTTGGACATGGCTCACAAGCAGTTTTTGAATGACTGCATGAATGC/A GJTGCGTGCAGCATGAACCTTGTAAATCAAGAGGCTTACATAATTTTAAACCAGTTCTGTCTTC AGCTGTACATA
D29833b	85	A G	---	---	---	---	CCACTCCATCCTGATGCCCCA/GJTTATCCACAGCCTCCTTCCCAGACCAAGACCCCTATCCACCTGG TCCATTTTCCCTGTAA/GJTTCTCCAATGATCCTACCTCCTCCTACTCCTGCACCCCCAAATATGAA CAACTGCAGCAGGTGCCACCACCACCCACCAAAAGACACCCTACCCCTTGTAACTACTGCTTCTGCTAC
D29833a	21	A G	---	---	---	---	CCACTCCATCCTGATGCCCCA/GJTTATCCACAGCCTCCTTCCCAGACCAAGACCCCTATCCACCTGG ACCTCCATTTTCCCTGTAAATCTCCAATGATCCTACCTCCCTACTCCTGCACCCCCAAATATGAA CAACTGCAGCAGGTGCCACCACCACCCACCAAAAGACACCCTACCCCTTGTAACTACTGCTTCTGCTAC
D31762	82	G A	---	---	---	---	CTCCCTGCCTCCTCCTTCCCTGCCTGTGATGCTCCGTCTCAAAACAGCCGAAACCTGCTTGCAATGGGG GAGGGGGGTTTQ/G/AJCTTTCCTTCTTGGCTTCTCTTATCTCCACAAACCATCTCAATAAA GCCAAAAATCTTCTCTTCTCCCTCCTCAGGCCACCTCCTGTCTCACTCCTGTCTGTGCTGGCTTTT CTGGA
337931	64	T C	---	---	---	---	ATTATCGGAGTGGTTGACCTTACACTTACTCCTTAAATAGCAGTGAGTAATGCATTTTGAGCTG/T/CJ CCCAGGCTCTGCTCCTCAGCTCATTTCTACTCTTTTCTCTATATAACTCATCTTATTAATACAT GCACCAAGAGATATGGAGACATAAACCTGTGAATGAATGAGGCTGGGCTTTTCTGTAAATAGCTTCC TTT

D63807	101 C T	CAGCAGGACTTCAGTGCAGTATCCCTGCCCTCAGTCTCTTTAGAAATCACATCTGTGTTCAATCC ATTGTTAGAGGGAGTGATTTTCTCTGTTCCA/C/TAAGAGGAGACTTTTGTTCACAAATGGATCAC AATGCAGAGGAGTCTGTTCTCCCGCTGGCTCTCGGTGGGAGGGTGACCTGTCCAGATGAC. TGGGAACATGCGTGTGACCTC/CJACAGCTACCTCTCTATGGACTGGTTATTGCCAAACAGCCACA CTGTGGGACTCTCTTAACCTTAAATTTTAAATTTATTTACTATTTAGTTTTTATAATTTATTTTGAT TTCACAGTGTGTTTGTGATGTTGCTCTGAGAGTCCCGCTGTCCCTCCACCTTCCCTCACAGTGTG TCTGGTG
D90145	21 T C	ATTATCACTCTCAAAAATTTGGTGTGTGTTTAAAGTACTTTCTATTATGAGCCCCCT/CJGAGGA CCAGACATGTTATTATCAAGCCCCCTTATACCATCTAAT
EST14035 1a	59 T C	GCATTTTAAATTCACATTGAATCATTATTACTATTTATGATGTTTACATAACAAATTCAGTATCAT ATG/C/TJGTAGATTCAGATGTAGGTGCTCAATACTGAGCACTTATCT
EST16668 5	71 C T	ACAGACTATCGCCAACTTATAATGCTTAACTTTATGATCAATAGTAATAAATTACA/C/TJGAGATA TTCACACTTTATTATAAATAGGGTTGTGTAAGATGATTTTCCCACTGTAGGTTAACAT
EST16904 7	57 C T	TTTTAAGTACCAGAGGCACCTGCTGGAACAGGATGAAACTGATACACC/A/GJTTACTACTTACTC TTCACCTCTCAAACTGATCCCTAAAGACTTCTACTAGCAAA
EST21863 9	49 A G	GGCTGTAAGTAGAATCAAAAGTTAAGAACATTTTATGCACTTATCCACAAACATTTACTGAGCATA CTAGGTGCTGGGA/G/JTGTGACAGTGAGCAAAAACACAA
EST21885 6	80 G A	ATTTTAGTGCAATGACAAAGCCCCAA/A/GJAGAACAGAGGATCAATAAGATTGAAATGTATTACC TCTCATAAGTATACGAAGTTTAAACACAAGTATGGGAGT
EST22623 8a	26 A G	AAATGATTGAATTCAGCAAGTACATTTATGATCTATCTACATTTGTTAAACAGCACTAAAAATAA AAATTTTAAATGATTATCCATTATTACAG/A/GJAAATGTGAAAGATGGCTTTTAAACCC
EST22644 2	98 A G	CCTCATTTATTTAAAGACGGACATAAAAAT/AJATACAAACAAAAACCCAAAGTCACATTTTCAG GAGGTAAAACTAAAAAGTCTGATATGAAAATATGGTGG
EST23587 1	31 T A	AAAGATCTGGCATTATTCACATCATCTCTAAATATTTTGTAAATTTTCCATGAGTATTTTTTCA TGTCGAAGCATTTTAACTATCATTTTAGCGTAAATACCT/CJGAATAACCCATAGTTACAGAATTGG GTCGTGTAACCTCAAT
EST24246 7	106 T C	TAGTTTAAATTTCTGAACCTTTGGCTTATAAATTTTCTCAACTT/A/GJCATTTAAAAATGTATCAAT GCACCTCTTCAGTAGTACCACATGAAATATAAACCTCGTTC
EST24308 3	45 A G	CTTGAACCTCTGGTCTCAAGTGGTACGTCCTCAACCTCCCAAAATGATGCGATTACAGGCATAAG CAGCC/G/JTGCTGACCCACATTTCTTTATCCGATCTGTGATGGACATTCAGGTTGTTTC
EST24435 6	73 G A	TATTGTTGCATTATCAAAATGGTTA/CJAGTTTTCAATTTAAACTGTAATTGATTTCTATGTATAAA ACAGCTTTGAAGTTGTAATGTAGTTTCCAAATCGTTAGTTAATGCTACATT
EST25089 6	25 T C	

EST25476 9	33 GA AGAGGTCTCTTGGCTGCTCCATGGACTGTGGCGGTGGACCTGGACCGTGCTGTA
EST26183 2	70 T A AGATAATGCATTAGAGCCTGCCCTCAITTTGATCTTTGATTAACTTTGTAAGAATTGATCTCTAAATAAG ATT/AJACATTCTGGGTACTGGGAGTTAGAACAAC
EST27231 1a	28 TC AGAAAATAAGGTGCTACCAGAACTCATGT/C/GATAGCGCTTCCTTTTAGGCACATATTATAGCAATT CAGATGAAGTCTGTAAATCACACACACACTGTGCCTCTAACAAACAACACGGTGACTCTGA
EST27816 5a	26 TC CAACTCAAGGTACAAGACAATTGCATT/C/JTAAACATTTGTTATAAATAAAAGGAACATCAGATCAAT CATTAAAGGCTCCAGAGTGAACAGCATCTTCATAACTTCATGTT
EST28588 0	78 AT GTTTAATTGGCGTATGTTCCACAGGCTGTACAGAAAGCATGATGGCTCTGGGGAGGTCTCAGGAA ACTTACAATCA/J/TGGTAGAAGGCAAAAGAGAAAGCAGGCATCTCTCCATGACCACAGCAGGAGG AACAGACAGAGGAGGGGGAT
EST30226 5	25 AC TACTCACACCGACATACATATCTCA/J/CJGTAGAATTAGCTATACTGCATACTAACTTCACTTTCCCTTTGA AGGGAATATAAACTACTGAACAAGACAGACTTGTCTAACTTAAACAAGACAGACTCATTTCCCTTTGA G
EST30935 9a	59 CG AGCTATGGTAGAGCAAATTCAGTGGTGGTAAATCAAGAACTCTAAAGTTCAAGTAGAGA/C/GIAGGT GTTTTGAATGTCAAGGAAATCACTGAGGTAGATTTGGGATTACAATAAGACAGCTGCCCTGTGAGGT CATAAGAGCTTTTGTGAGG
EST32515 7	25 GA CCGAATATAAGGAAAAAATGGTGGC[G/A]TGCCCTCTAAAACCTGTTGAATAGAATAATGGCCAAAT ATTACAGTTCTCACCTTCCATGAATACTGGCACTGTTTATTTCATGTTTATATGTGAGTTTCTATGC ATAAAAATCCCAGTAAGA
EST33274 4	27 TC TGCTTTGTTCCCTCCAAATCCATAAAAT/CJGTGTGCTTCAAGAAAAATTCGTGGAAAGGACTTTGAA TACGAGTTGTACCATATCCAAGTATCTTGAATACAGGTTTCAGATAACTATGGAGATGATACCACTT GGACTAGGTA
EST33352 7b	75 CG TACACATTATCAAGAGACCACTGACATGCATCTCTCCGCAGAAATACATTCGTCCTCTCTTAGAGA AGTTTAA/CJ/GCACATAGTATTTTACTAAGAGAAATATCTTGGTGCTATATCTAGGGG
EST33424 1	126 AC ATTTTCCCACAGCAGAAGTATATTATTGTGCTGAAATCAGGTAGCAGGGAATGAATAGCTCTTGG GAACCAGTACAGAATGTTCAAAAAGATTTACAAATCTCAGTCATTACACACTGAGCAAC/N/CJAAA CAAAGGTGTTGAATCCCTCTT
EST33488 7	90 AG CCTTTGGGGGAGTTTAAAGCCAGAATGTGACAAAAGTCACTTACAGGAAGACTGGAATGTAGCCATAG TTGAACTCTAACATCGTCTATAG[A/G]ACCAATTTCCCGTCTCCAGTTAGGTTCTAGGCATACTAAGCT GCTC
EST33508 1b	45 CT AAAAACATGCTATTTGAACAAACTTTTTTATAAAGAATAAGTTGA[C/T]TGAAAAGCAGTTTTTAAAT AACATCAACTCACAATGACTTTTAGAAGCCAAATAA

EST33508 1a	36 A G ...			AAAACATGCTATTTGAACAAACCTTTTATAAAGA[A/G]TAAGTTGACTGAAAGCAGTTTTAAAT AACATCAACTCACAATGACTTTTAGAAGCCAAATAA
EST33863 4	77 C T	ACAACATAGGACTGGTTATCTTGGTTTGAATAATATGTTGCCACTTCCTATTGTTTTAAAAATGA TCATTTAA[C/T]CTTTGAACACAGCCTGAATCCCC
EST34739 3	97 T A	GAAGTATCCTCCAGTGGCAGGAAGTGAAGATCCAGATCAACAGGTTGGACCTTTTCGTTGATGA GCTGATAGCTTCTAGGCTGGGGAACTCT[A/G]GTGCTTACAACCTCAACTACTGCAGAATTTCT TGTTGGCCCTCATAAACA
EST34792 6b	104 A G	ACCTGACTGCTTTAAAGCTCTTTGTAAGCTGACCGTAGCACAGATCAGTGGCATCCACTATCAATA CTCATAAGTCTAATTTATCCTCAGGATGTTCCCTGA[A/G]GTATTGAGGAATCTTAGTCCTATTACA AAGATTTTGTGCTGTG
EST34835 9b	93 T G	GGAAATGTTCCCTTGCACAAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTTGCTTTCTGGT[G/G]GCTTAAAGAAACAGACAAATTTGTCTAAAGAT
EST34835 9a	82 G A	GGAAATGTTCCCTTGCACAAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTT[G/A]TCTTTCTGGTGGCTTAAAGAAACAGACAAATTTGTCTAAAGAT
EST35230 0	93 G T	CACAAAGGTCACCTTACTACATGAAGGAACATAAAGGCATGAGAAACAGTCATCTCAATAAATG CAAGACATGAGCATAAAAGAGGTTCT[G/G]GCTTTCCAGCGTTGTTATTACAGAGAGAAACCT
EST35337 9	33 C T	TCTTTCAAATTTTGATGAGGCATTTAATG[C/T]ATAAATTTCTGCTTAGGAATGTATCTGCT ATATCTCAGAAGTTGGGCATGTTGTTTCCATTTTACTTAGTTCAGAACCTTTTCAATTTTCATCT
EST35708 9	32 C T	CTGCCCCAAATTAACCTTTAGGCAATGGAA[C/T]AGACTTACTGTATGGGGACATTTTAAAAAG ACAGCTTAGTAATATGTCATATGCAGCGTTGCTTCCCTCTCTGAGGTTGGCACCTTTCCCTGTTGTG ATGTGCAAGTGTGGCT
EST35747 9	51 C G	ATCCAGTGCAGAGTTGTAGCTGGAGACATATTTCAACCCACAAAGGCTCCA[C/G]ATGTTAAACGT TTCCCAACATCAACCTAATACAGTGACAGCAACACCTCCCTCCTCCAGTAGGGTTGAGATT G
EST35751 9	89 C A	TGGTCCATTATATAAACTGAGGGAACAAACGGTGTGACATGGCAGACATTTATTTCAATGGAGA AGTTCTCCCATGAAACCAAG[C/A]CTTGTCTCATGATAAAGTGGAGACAATAAGAAAGCCAGGT ATATAATTAAAGCCTGTGA
EST36301 4	93 C T	CACCTGTTCAATGGTTCACTGGGCTGCTATCTGTGGGCTGATGCTCTACCAAGTGTCTAGCCTACAGC AGTCAGGAGGCAGCCATGGCCCCCTG[C/T]GCTGATGGAGCTTGTAATTTAGCCCCAACTGATCTTCA GAAAGAGGTACAACAAA
EST36519 0a	33 G T	GCCATCAGCCCCACAAAGACATGACTACCAACGC[G/T]GGCCCCCTTGACCCCATACTGGCCTCAGCAC CTAAGACTGGACAACTTTGTACCTAATGACCGCCCCCACCTGGCATATACTGGCTGGCCTCTTCTCTGT CACAGGGGCTTAGTGTG

EST36620 6	50 G A	GACTTTATTAGATAAGGGGTTTCGGCTACCCCTCAAAGCTCTCAGGACTGG[G/A]GCTAGGGTTTAAGG AAGGCTTATTTAAATATGGGAAATAAAATACAAAGGGCCACACCCGATGCAAAAGACTTT
EST36690 0a	89 C G	CCTGTGATGTGCATGGTGCTCCTGAGCAGTCTACTACTATCGTGCAGACAGCTCACGTATGTCAAGGA AAGGAAGTCTGGGGATTCTTA[C/G]AGGGGACATATCACACATATTTCTAAGTCACTGTGTGACTCGG CTTGAGCAAGTCATTTCA
EST36729 9	62 C T	GAGACAGAAGCCATCAGTTAAATGAGGTTAGGCCTCTCCTCCTAAATATACTGATTGACAATG[C/T]A TATTAGCCAGGTAATGCACCTTAGCTACCTGGACAATGCTATCAAGTGTCTGGGAAGGGAG
EST36823 6	103 A T	ACTGTCGGCCGATGATTGGAGCTTGAAAAAACTACCATGCCAGATCTCCACCCGAGACCAATTAG GTCAGTATCTCTGGGGTGCTATTCAAGCAACAATTATTTCTTTATGTTCTTAAGCTCATCATGAG TTAA
EST36987 4	126 C G	ATGATCGCTTATGTAAATTTGAGGGCGACATGGTAATGGGAGATACCCACAGGACCTGTAAATATT TAAATAATATTTAACAGCTGATCAGAGGCTAAATTACAAGTACATTTTGATGCAGTTT[C/G]GTTA GGGAATTAAGACAAATGCAG
EST37054 3	88 T C	GGTCTCACTCTCTTGOCCAGGACGGTTTGAAGTCTCTGAGCTCAAGTGACCTCCACCTTGGCTTCC GAAAGTGCTAGGATTACAGG[T/C]GTGAGCCACCACACCTGGTCCTTGGTTTAAAGTAAACCACCTGAA C
EST37269 3b	105 T G	AATAGTCTATGGCTACGGGCCCGTGGGATGTTAAAAATTTGGGATTTTAAATTAAGATTGTGAACATG CAAAACCAGCAAAATTTCTCAGCTTATATTTTGAAGTCT[G/C]AGGAGAAAAAATGGGGTCC
EST37284 2	93 G T	AAAAGACCTTTCTCAAGCAGTAAACTTTGAGCAGAGACTCAGATGAAGTAAGGGATGAACCCAGGAA GCTCTCTGGATAATGTCACTCTAGGAA[G/T]AGTAAACAGGTGTTAAAAACCTTGAGATAGCAACCCCT CTTGGCTTGCTTGAGGAATA
EST37315 2a	90 A G	AGATGGGTCTTGCTAGCTTGCTGGGCTGAACATAAGATATCCTCCTGCTCAGCTCCAGGTAGT TGGAACCTATAGTAGGAGTATCTA/G]CCCTGCCCTGCTAGAAGTCAAGTTTGATGGGCAAAATCCA CCCCAGAGCAGGACAA
EST37374 1	45 C T	CCTGCCATGATAATGTTAAAAACATATCAAGATCCTCCTCAAACTT[C/T]AAGGGTGAAAAGCATACC ATTCCATTTTAGTTGAAATATTCTTACATAGCCCAACACATTTTTTCAAGGCACCTCTAGCTACTACA GGA
EST37376 8b	101 G C	GTGACATCATGTCCTTCAATGCCCTTTCAATTAATAGTAGTTGAGCGCTGGGGCTGAAGTCAGACT CTCTGGGTTCAAATCACAGTGCTGTGCTCTGCA[G/C]GCTGCTCTCAGGCAAGTTGCTGACTTCTCTG TGTCAGG
EST37376 8a	41 T C	GTGACATCATGTCCTTCAATGCCCTTTCAATTAATAGTAGT[C/T]GAGCGCTGGGGCTGAAGTCAG ACTCTCTGGGTTCAAATCACAGTGCTGTGCTCTGCAAGGCTGTCTCAGGCAAGTTGCTGACTTCTCTGT GTCAGG

EST37378 9	63 T G ---	---	---	ACACACAAAAAATGGTGGCAGAAAAATCTGGAAAGATTCTAATAACCTCAATTCTGTGAAAAAC[T/G JAACATGCCCTCAAAAAAGAGGGGAAAAAACTTTAACAGAAACACTGTGCTGACATGATTAGCTT
EST37452 4	46 G A ---	---	---	AAGACATAAATCTGCAATGAAATCAGTTATGAAATATTAACCTCTG[A/CTTCTCAGGAGTGACAC TAATCATGGTCTGGAAGCTAGCCTATCGCATTTTAAACACCCCTTAAATCAATGACGTAGAA
EST37613 6	34 A G ---	---	---	CTAGGCATGGGCTTTACAGTCATTTATTTACC[A/GTGCATGAATTCATTAATAAACACAGCGAT ATAGCAATGAGCAAAACAGACCCCTCCCCAAATCACCCGTGCTCATGGATCTTCCATTCTAA
EST38025 4	56 T G ---	---	---	TTATTGAGTAGCTACACTGTGGCCAGAACTAAGCTTTACATGTTTTATACACTTA[T/G]TTATCTCA ACAATCTTGAAGGGTGGTATTATTTCCCGTCTTATAGGTGAAGACTCTGAGGTTTCAGAA
EST38068 6	57 C T ---	---	---	TCTACAGGTCACCAAGTATCTGTATATGCTTTAAGTGGCATTTTCATGTCACTTA[C/TCGCATGG AAGAAGCTCTCCTTTAATCCCTAACTCTCTTCTCTGGAAGACAGAACGTGCACAA
EST38420 6a	100 T C ---	---	---	TAAATCAAGGCCTCTTTTATTACCAAAACAAAAACAAAAAAGGGAACAAAATACGATGGGAGGG GAAGAGATGATGCCGAAGTGCATCTGACTGACTGAC[T/C]GTCCCTGCAGTGCCCATGGGTCCCGTGCCT TATTCATTCTCCTCTCTCA
EST38950 5	25 T C ---	---	---	TTATTGCAAAAGTAAGCAGCCGG[T/C]GGTCCCTGGATTGAGGCTGAGGAAGACATTACTTCCTG CTGGAATACCTTGGGACTTACATTTGACACAGGCTAAAAGTATGGGATGAGAGAGGAACAAAAGCTT ACAAACAAAGAGCAGCCA
EST39053 6	90 T C ---	---	---	TTTTTGTACTCTGTAGCCAGTCATTAACTGAAGTTTAAATATATCATTTTATGGGATGAGATCA TAGCTTTACACAATGCTATG[T/C]AAACAAGTTACTGAATATTTTACCTCGTGGAGTTG
EST39331 1	70 G C ---	---	---	TCCTCTTGCTCTAGCACTCAGACCAACCAAGAAAGCCCTGGAAAGCAGCCATGGAAGGAAAGTA TGC[G/C]GTGTTTGGGAGAGCTGGCACCTGGCCTCTAATCTCCCTCTGCCATTGAACAGATGGGT GCCTTGGATACATCACT
EST40544 7	31 C A ---	---	---	GTCACCATTGACCTTACATAGTGCCCTCTAGT[C/A]ACCTATGAGGCACCTAGAACTCTATTGTACTCT CACTTTATCACATTAGCTATCGAAGTTTGAAATTT
EST40548 4	37 T C ---	---	---	TTCTAATAGCATGCCCTGTGACAGGGGAACTAAGCTC[T/C]TCAAAATAACTGAAACTAAATCTGTA AGATAAAATGCTGGAAATTGAGAAGGCACATGCCCTTTGTAGTTTTCTCCAGAAGGCTCAAGGTGTTG AATAATCTGTGGGACTCA
EST40549 1	42 A G ---	---	---	TGTTTCTCTAGAGAACCCTGTGTGATACACTACGCATGCACA[A/G]ATAAAGTCACATCAAGACTAA TAATCTAAATGTTAGTTGTTTACCACCATTTCTCACTTTGAACCTAGTCCCTGCAAGACACCTTCTA CCCTGCACCTTTGGGGAG
EST40579 1	81 A C ---	---	---	TGTGAATTACACATCAGTAAGGCAGTTTACAGAAATTTTCACTCTCTACCTAAAGTCTGTGCTATCTG AGCTGGTGGAAA[A/C]GGACTGGAGACAGCGATTAAATACGGAACAAGGCTTCCAGGAAG
EST40584 3	68 A G ---	---	---	TTGTATGGTTGTAGGAATTTGGGAAGAAATTTATCTGTGAAGGAAATTTGCCACTGTAATGCACACCC A[A/G]TCTGTACTCCCAATATCCTATGTTTTAAGCT

EST51340	51 G A		GATCAAACTGTATTGCCAGGCCAGCTCCTGAAGAACTGTGAACATGAAAC[G/A]TCTCAGCCTAGA AGGATAATGTGACCTTCAATTTGCACACCATTGCTCTTTCAAACTAAGAGCCTCTCTAAGCTA GATAGCCCAAGGATTATT
J04162	134 T C		CATGGGAGTAATAAGAGCAGTGCGCAGCAGCATCTCTGAACATTTCTCTGGATTTGCAACCCCATCAT CCTCAGGCCTCTCTACAAGCAGCAGGAAACATAGAACTCAGAGCCAGATCCTTTATCCAACTCTCGA T/CJTTCCTTGGTCTCCAGTGGAAGGGAAGCCCATGATCTTCAAGCAGGGAAGCCCAAGTGAAGT AGCTG
K01506	63 T C		CTGAACTCCAGCTGCCCTACAACTCCATCTCAGCTTTTCTCTCACITTCATGTGAAAACTAC[T/C]C CAGTGGCTGACTGAATTTGCTGACCTTCAAGCTCTGCTCTTATCCATTACCTCAAAGCAGTCATTCCT TAGTAAAGTTTCCAAACAATAGAAATTAATGACACTTTGGTAGCACTAATATGGAGATTATCCTTTC ATTGAGCCTTTATCCT
L18877	69 T C		TGAGTCTGAGCACGAGTTGCAGCCAGGCCAGTGCGGAGGAGTCTGGCCAGTGCACCTTCCAAAGGOC C[T/C]ATCCATTAGTTCCACTGCCTCGTGACATGAGGCCCATTTCTCACTCTTTGAAGAGAGCAG TCAGTATTGTTAGTAGTGAGTTTCTGTTCTATTGGATGACTTTGAGATTTATCTTTTCTCTGTTGGA ATTGTTCAAAATGTT
L31848	36 T C		GCTATTTTACATATCCCAAGCCCTTAGGGCTACAG[T/C]CTCTTCTCTGGACCCCTGTAGGGTGCCA TTTGGAGTTACAGCCTAGAAGAAGAAAGGCTTTGGCCCTGGTGTGGTGSCATAGGCCTGTAATCGT AGCGCTTGAGAGGCTGAGGSCAGGAAGATAGCTTGAGCTCAGGAAGTTGAGACAAACCTGGGCAAT GT
L38517	137 G C		GGGTCCAGAAGCCTCTCAGCCAGGAGGAGCTGGCCCTGGAAGGGACCTGAGCTGGGGACACTGGC TCCTGCCATCTCCTCTGCCATGAAGATACACCATTTGAGACTTGACTGGCAACACAGCGTCCCCAC CC[G/C]CGTCGTGGTGTAGTCATAGAGCTGCAAGCTGAGCTGGCGAGGGGATGGTTGTTGACCCCTCT CTCCTAGAGACCTTGAG
L39059	123 T G		ACTTGAGAAGCAGAGCTCGCCACCTTCTGGAGGCCACTGTGATGATGAGCCAAGCAATTTGGAGCCA AGTTGAAGGGACAGGGCAACAATAACAGTAGTATTTCTTTTGTATTTTGTATAT[T/G]CGCCTGA AGATCATCCCGCAAGGCAGGCTGGAGGTGCCGTGGGCTGTGTGCTGGGATTTTAGTCTGTGCTGG GAG
L41268d	173 G A		CAAAGTTGTCTCCTGCCCATGAGCACACAGTCAGGCCTTAGGGGATCTTCTAGGGAGACAACAGC CCTGTCTCAAAACTGGGTGCCAGCTCCAATGTACCAGCAGCTGGAATCTGAAGCGTGAGTCTGCAT CTTAGGGCATCGCTCTTCTCACACACACAAATCTGAAC[G/A]TGCCTCTCCCTTGTCTTACAAATGTCT AAGGT

L48728b	111	T C	...		AAGTGAACAGAAAGATGGATTGTTCTCTATAAAAGCACATAGTATGTTTACTGGTATCGT AAGAAGCTGGAAGAAGAGCTCAAGTTTTGGTTTACTTTTCAGAAATC/GAAGAAGCTTATTCAGAAAG CAGAAATAATCAATGAGCGATTTTAGCCCAATGCTCCAAAACATCATCCTGTACCTTTGGAGATCCA GTC
M18079	52	G A	...		GCGCACAGTCCAAAATACAAATTGGACAGAAGATCTATATTGTACCAGAACT[G/A]TTTATTTCAACC CCATCAAGTATAAGGTTACTGATTGGTCCTTTTATAAACATTGGTATATTCCATTTCATGCCAA AGCAAAAGAAGTAAAAGCTAA
M19169	113	T C	...		TAGGGATCTGTGCCAGGCCATTGGCACCCAGCCACCACCCCTCCACCCCTGTAGTGTCTCCACCC TGGACTGTGGCCCCACCCCTGGGGAGGCCCTCCCCATGTGCCTGTC/GCCAAAGAGACAGACAGAG AAGGCTGCAGGAGTCCCTTTGTTGCTCAGCAGGGCGCTCCGCCCTCCCTCCTTCTCGCTTCTAATA GC
M21539	114	T G	...		TCACCTGTTCCACAGCTCCACCTGCATCTTCTCATCAAAGCCATCCAGGGATACACAGGGAGCTTCT TTCCCTTAGCCTGTGATCTGCCCATGATGATCCCCGACAGCAAAAT/G/GTTTCTTTCTGAGGCTG CCATGCTGCCACTGTCCAGGTGGAGACTGAGCAAAAGGAAGTCTCAGCTGTACCGGCCCTTTCAGAGCT TCTCTTGGGTGC
M26041c	173	A G	...		CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCTCACCTCT TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTTATTCCTGACTTC CTGATTTTCTCTTCTCAAGTGTACCTACTAAG[G/G]GATGCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041b	157	A G	...		CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCTCACCTCT TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTTATTCCTGACTTC CTGATTTTCTCTTCTCA[G/G]GTGTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041a	45	C G	...		CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTTCTCCTC/G/G]CAAAATGTTTCTCCTCTCAC TCTCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTTATTCCTGAG TTCCTGATTTTCTCTTCTCAAGTGTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M63967	57	G C	...		TAGGCAGCTGTCAAGGAGGCCAGTCCAGTCCAGCAATTCCACAACCACCTTGAC[G/C]AATGCT TGCCAAGCTGTTTAAAGCCAAGAACACCCCTTCTTTGTTCCAAATTAACCTTTAGAAGAAACCCCA CAATAAAGCAATTCAATC
M81695	34	G A	...		ACTTACTTACCCCTCACCTGTCAAGGCTGACGGGA[G/A]GAACCACTGCACCCAGAGAGGCTGGG ATGGCCTGCTTCTGCTTTGGGAGAAACGCTTGTCTGGGAAGGGCCCTTGTCTTGTCAAGGTT CAACTGGAAACCCCTAGGACAGGGTCCCTGCTGTGTCTCCCAAAAGGACTTGACTTGCAATTTCTACC T

U08641d	166 C T	CTCCTCCTTTATTTACGATGGAGGTTTAAATGGAGGATCTCCTTTTCTGTGACAAAACATCTTTC ACAACTTACCTGTTAAGACAATTTTAAAAAGATCTTTTACAACTTACCTTGTAAAGACAAAATT TATTTCCAGGCTATTTAATACGTACTTTAG[C/TT]GGAAATTAATCTATGTCAATGATTTTAAAGCTA TGAAATACAATGGGGGA
U09607	39 T C	GAGGCCTATGAGGGTCTCTACTTCAGGAACACCCCA[C/G]GACATTGCATTTGGGGGGGCTCCCG TGGCCTGTAGAAATAGCCTGTGGCCTTTGCAATTTGTAAGTTCAAGACAGATGGGCATATGTGTGAG TGGGGCTCTCTGAGTCTCTGGCCCAAGCAAGCAAGCAACCAAAATTAAGACTCTCGCATCTTCCCAAG CCCTTA
U09608	82 T C	GAGCAGAGGCAAGAGCGGCAAGATGAGTTTGGCGTTGTATTCCAAAGGCCTCATCTGGAGCCTC GGGAAAGTCTGGTCC[C/J]ACATCTGCCCGCCCTTCCAGCCCTTCCCAAGCCCTCCTCTTGTCTTTC ATTCAATCAACAAAATTTGGC
U10694	20 C G	GTGACATGAGGCCCATTT[C/G]GCTCTGTGTTTGAAGAGAGCAATCAGTGTCTCAGTGGCAGTGG GTGGAAGTGAGCACACTGTATGTCTCTCTGGTTCCTTGTCTATTGGGTGATTTGGAGATTTATCCTT GCTCCCTTTGGAAATGTTCAAATGTTCTTTAATGGTCAGTTAATGAACCTCACCATCGAAGTTAA TGAATGACAGTA
U13877b	162 T C	AAAAAGGACTCTGGTTCAAATCCAGGTTCCATTTTGTCTATCTTTGTGACCTTGACAAAGTTGTTAAAC CTCTTTGTTTCAAGAAATTTCTCCATGGAGTAACAATACTAGGTTGGGAGGATTAGTGAAGTTACATGT AAAGCACAGAGGAACAGCCCAAGAGAT[C/J]TACCGTGGTCTTACTAAAGTACATATCCTAACTTGG GGTTACCTTCAGCA
U15555	187 T C	TTTCTGCCACTTTTCACTGGTTTAAATAGCCAGCCAGTCATAATAGTAGGGAATCAGTCAAGCAA AAATGCTTTGGAAGAAATTAATAAGCAATGCTGAACATCAGGAATGTAGATATCCGTACAGAGAGT TCCAGTAAATTTTATGAGTCCACGACCCCTTTTCTAAGCAGTCTGGTCCATG[C/J]TGGTCTCATAC CTCATATGCAGGATTCATTCA
U17077	122 T C	TCCAATTATTGGTCCCAAGCAGCTTCCAACGTTTGCCATCTGGATGACAAACGGGAAGATCCACT AAAAAGTCCACGGGATTACAGAACGTCCTTGACAGCTGAGCGATGACACCACAC[C/J]TGTGTTGG ACATTTAAATTCACCTCTGCTGAATAGGAGGAAGCTTTTCTTTTCTGGGAAACAACACTGTCTCTTGG AATTA
U18543	58 T C	GCACATGCAGAATAGACTCAGCCTATGTCCTGATCCAGCTGGGTAGTTCTAGAACTTT[C/J]AGAAG CTCCATCTTTTAAATGTTTATTGTTATGTCCCTCCCTCCCGCTCCCACTAAATTTAGAGCTTTAAA AGATGCACTGCCCAATAGGACACACAGATGGTGTAGCTGAAGTTTATTAGCAATTAGGCACCTCC AAGGCTTTAGTAGAGAGGCC

U25975b	164	C A	---	---	---	<p>TCACTGCTGTGGCCTCACTCTTTTCCATTTTCTACAAGAAGCCCTTTTAGTATATGAAAAATTATT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAGAAGCAATGACTATTCTCTG AAGACAACCAAGAGAAAAATTGCAAAAAAGAC/C/AAGATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTGTGGACTGA</p>
U25975a	143	C G	---	---	---	<p>TCACTGCTGTGGCCTCACTCTTTTCCATTTTCTACAAGAAGCCCTTTTAGTATATGAAAAATTATT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAGAAGCAATGACTATTCTCTG AAGACAAC/C/G/AAGAGAAAAATTGCAAAAAAGACAGATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTGTGGACTGA</p>
U25997	61	A G	---	---	---	<p>CAGGAGAGGTTATTCACAACCTCACCAACTAGTATCATTTTAGGGGTGTTGACACACCA/C/A/GJTT TTGAGTGTACTGTGCCTGGTTGATTTTAAAGTAGTTCCTATTTCTATCCCCCTTAAAGAAAAATT GCATGAAACTAGGCTTCTGTAATCAATATCCCAACATTCGCAATGGCAGCATTCACCAACCAAAAA TOC</p>
U28413	29	C T	---	---	---	<p>ATTCTGACAGCTAAATTAGCCCTAAATG/C/JGGGTAATATTTTCTCATGTTTAAAAATGAGGTT AATATTGCATAAAATCCTAAACAGACTTCTGTATAGTTTATTAGTCAAAATGTGTTCTTGATCC CAGATGTTGTGGCCTGGGAAAGCCCTCATTGCTACAGTACAAGTAACACAAGTCGTTGTACCTCAGTT G</p>
U30884c	89	A G	---	---	---	<p>TAGGGGTAGCATTAAAGATTACAGGAGTCATTAGCAGTGATGTTTGGGACCTGCCGTATAATCTGTT CTTCTATTCCACGTTAGCCA/C/A/GJTTGTTCTTGATGAATCTATATGAGTCATAGAACACAAAACTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTTGCCACAGTTGAACACAAAGT GCTGTCA</p>
U30884a	34	A G	---	---	---	<p>TAGGGGTAGCATTAAAGATTACAGGAGTCATTAGC/C/A/GJGTGATGATTTTGGGACCTGCCGTATAATCT GTTCTTCTATCCACGTTAGCCAATTGTTCTTGATGAATCTATATGAGTCATAGAACACAAAACTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTTGCCACAGTTGAACACAAAGT GCTGTCA</p>
U31216b	78	A G	---	---	---	<p>GGGACAGCATATGTGGCACCCGCTCTCTGTGCACGTGAAGACCAATGAGACGGCTGCAACCAACA GCCGTCA/C/A/GJCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTTCAGATA CCAGCACCAAGACCCCTTACAACGTAGAGGAGGAGGATGCCAGGCGATTGCTTTAGCCCGCC TGGTAGCCCTTCCAT</p>
U31216a	70	G A	---	---	---	<p>GGGACAGCATATGTGGCACCCGCTCTCTGTGCACGTGAAGACCAATGAGACGGCTGCAACCAACA GCC/C/A/JTCATCAAAACCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTTCAGATA CCAGCACCAAGACCCCTTACAACGTAGAGGAGGAGGATGCCAGGCGATTGCTTTAGCCCGCC TGGTAGCCCTTCCAT</p>

U31416c	78 G A	AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGCGTGAGTCTTCATCTTAGGGCATCGCTC CTCCTCAG[G]ACCACAAATCTGGTGCCTCTCTTGCTTACAAATGTCTAGTCCCACTGCCTGCT GGAAGAAACACACACTCCTTTGCTTAGCCACAGTTCTCCATTCACTTGACCCCTGCCACCTCTCC AACCTAACTGGCTTACTTCCT
U31416b	68 C T	AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGCGTGAGTCTTCATCTTAGGGCATCGCTC [C]/TTTCCTACGCCACAAATCTGGTGCCTCTCTTGCTTACAAATGTCTAGTCCCACTGCCTGCTG GAAAGAAACACACTCCTTTGCTTAGCCACAGTTCTCCATTCACTTGACCCCTGCCACCTCTCCA ACCTAACTGGCTTACTTCCT
U37519a	78 C T	ACGGGTCACACAGAGAACTGAGTCTAGCCATGAGGGGCTTATGCTCCCACTCACATTGTTCTCTCC AGACCGCAGG[C]/TTCCCCAGCCTCAGGTTGCTGGAGCTGCATGACTGCATCCTGCCTGCCAGG GCTGCAAAGCAAGGCTTTGCTTCTATCTGGGGGACGCTGCTCGAGAGGCGGAGGCGCGAGAAC ATGCCAGGTGTCC
U37690	54 A G	GACCACGCTGAAACCCACCCCGCTGTGCTGACCATGGGCCCTGAGCGTCTT[G]/CCCCGAATTC ACGAGGCTGAGGCATCCGGGAGCTGGCGTAATGCTGGCCGAGTGTGTGTATCCCATACCCCACT CTGGAAGGAACCATCCAGTAAAGGTCCTT
V00540	39 T C	TGAACCGTTTCAACATGGAATGATCTGATTGACTAA/T/CACACCGAGTCCACACTTCTATGACT. TCTGCCATTTCAAAGACTCATTTCTCCTATAACCACCGCATGAGTTGAATCAAAATTTTCAGATCTTT TCAGGAGTGTAAAGGAACATCATGTTTACCTGTGCAGGCACTAGTCTTTACAGATGACCATGCTGAT A
X15943	106 A T	TCAAGAAGGTGACTGCCCTTGATGATGGGATGGGAAGATGAATGACTGTTTTACTGGGGTGTA AACCACTCTGAGCCTCTCTGAGACCATGTGGTTTTAAAAA/TATCCATAAGGGAAGGTACCCACAC CAGTATCTGAGTTCAGTAGCTAAGACCCCTAGAATTTGGATTTCATCTCTGTTTTTTCATGCTCTCCTT GTAAACCCTGAGATCATCAG
X52011b	148 C T	AGGAAGATCCCACCGACCCTTCCTGGCCTAATCCTTTAGATTAGGTACATTAACATTTAGGA ACCCAGACCGAAAAGTTGCTGAAAGGGAAGGAGACACATTACAAAGAAAGTTGCGAAAATTCGG AAATCTGTTGTGCA[C]/T/GCTCAAATGAAAACGCCCTTCGGCTTTGGGCTTTATTTTTTGGAACTG CGAGTGGCTTAGGCTAGCCT
X52011a	118 A C	AGGAAGATCCCACCGACCCTTCCTGGCCTAATCCTTTAGATTAGGTACATTAACATTTAGGA ACCCAGACCGAAAAGTTGCTGAAAGGGAAGGAGACACATTACAAAGAAA[A/C]GTTGCGAAAAT GCGAAATCTGTTGTGCAGCTCAAATGAAAACGCCCTTCGGCTTTGGGCTTTATTTTTTGGAACTG CGAGTGGCTTAGGCTAGCCT

X54741	24 A G ---	---	CAGGCCACCTGTCTTCTCTCCACAG/GJTGACAGCTTCTGAGTCACCCCTCTGTCCAGCCAGCTCCT GCACAAATGGAACCTCCAGGGCTCCAGGACTGGGCTTGCCAGGCTGTCAATAGCAAGGCCAG GGCAGAGCTGGAGACGATCTTGCTGGCAGGGCTGGGCTTGTCGAGGCCACCTGGGCCCCCTCTCC AGCAAGCAGTGC
X54869	99 A G ---	---	AAGCATTTCGGTTTACAGTGCATCAGATACATTTTATATTTCTTAAATAGAAATATTATGATTCAT AAATCTGAAAAATGAATATGTTATTTGCTCTAGJATACAAAAATCTAAATCAATATTGAAATAG GATGCACACAATTAATAAGTACAGACATCTAGCATTTGTGCGGGCTCATTTTGTCAACATGGTA
X68924	147 G A ---	---	GGCGTGTCTGACACCTCCAGAACGAGGTGCTGGGCGGTTCTGCTGGACCCCGGGAACCTCTC CTGCCGGAAGCCGGACGGCAGGATGGGCGCAACTTCCGCTGCGGCTGACTTCAACCAATCCCT TCCTGGAGACTG/AJACCTGGTCTCAGGAGCGAAGGACTGTGAACCTTGTGGCTGAAGAGCCAGA GAAATGTGAAGAAATGTGACAAAGCCTTTAAGCGGTTGTACACACTTGATTGTATATAAGATAAT/GJT CATACTGGAGAAAACTCCAGAAAGTGTGACAAATGTGACAAAAACATTTAATTAATCTCATACCTTA TTGCACAGGAAAGCATTTATACTTTGAGAAAAATTTGATAAAGAAATGGAAGATCATTAAATATCTGCT CATATCTTAACATCAGCGAGTT
X78932	62 T G ---	---	CTCAACCCATAACCTCAACACATCT/GJATCTCTCCACCCACATCCACCACATCCACCTCCATCC CCAACCCATCTCATCCCCAACTACAGCCCCAAACCCAGCCCCAGACTAATCCACAGCCATCCCCAA CTCATCTCATCCCCAACTGCAGCCCCAAACCCAAACCCAGGCCATCCCCAAACCCATCCCCAAGCC AAACTCAACACCATCC
X80026	25 T C ---	---	ACCCCACTCAAGTCCAGGCCAGGCATCTTCTGCGCTGCTTGTGGCCATCCAGTCCAGG CGCTGGAGCAAGTCTCAGCTACTTCTCTG/CJACTTTGAAAGACCCCTCCACTCCTGGCCTCA CATTTCTGTGTGATCCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCTAGAAAG
X80197b	99 G C ---	---	ACCCCACTCAAGTCCAGGCCAGGC/AJGJCTTTCTGCGCTGCTTGTGGCCATCCAGTCC AGGCGCTGGAGCAAGTCTCAGCTACTTCTCTGCACTTTGAAAGACCCCTCCACTCCTGGCCTCA CATTTCTGTGTGATCCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCTAGAAAG
X80197a	28 A G ---	---	GGCACCCAGAGTGACCAAGTCCAGCAGGAGGGCGCGCTGCGCGTGTCCGTGTTTCTTTT CAGCCCCGGAGAGTCTGACCTGGGGCTTCTCCAGCCTCAGTCCGCGCACGCTCCCGCGCTCT CTTTTCTCCCAAGC/G/AJAAACCAATGCGCCCCCTTCACTGCGTGTCCCGTGCAGGCCGGGGCTT CTTTCAGAGC
X85106	150 G A ---	---	ACACCAGCCATGGTCTAAGGACATGGATCGGGTGCCCCCAGACGTTGCACAGGGGACCCCTGCCCC CACTCTGGGCTTTTCAGATACTCTGACCAAAAAGCCTGCTTTAAACCGCAAGATGGGGCTT/GGGGG ATGCGCAGGAGGAGCCATCGGGTACTACGCGCAACACACTCACAACTGTCCAGGCTGAGATAAATCCC GGGA
X87160	128 T G ---	---	

[illegible]

1282	130 C T	GTGGATCACCACACTACAGTCTAATTCAGATGTTTTTCATTACCCCTAAAAGAAATCTTGTACCCATTAGAAATTATTCCTCATTCCTGCCCTCACCCCGAGGCCCTACTCTTTATCGCTATAGATTTGCCCTGCTACTTGACATATCATACACATGGAGCCATACATATGTGTGCCCTTCATGATTGGCTTCTTTCACTGAGAATAATGTTTTCAAGGT
6810	68 C T	AGTATCACACATACITTAATATATAGATATACACAATAAATACTCCCTACCTTGAAAACTTTA/C/TJAGAAGCATTTTAAATTTACAACACAAAGCTCAACGAACCTACAATAAGTCTAGTAGTCTGTGTTACGTGCCAAGGGATAAGGCTGAACAATAAATTAACCCCTTTAAAAATGCTATGAACAAGTACAAATTTCTTTTGTGCTGTCAGAGCAATGACCACTAAGAAATATTTTAAAGGC
6817	118 A C	CCAAGTACATTGGGTGAACGATGAGCTAGTCTAGTATTGCTTTTGTAAATCCAGTTAAGACCA TCAGCATATACAACATCATCACTAACTCAACAATGTAGCTGAGGTAAC/A/CJTGTGGATACCCCTG TGTGCTCTACTGGCCTCCAAAGGCATTGAGGGGATCATCAAGATGTTGGACACCTTGTGTTCAAATC TTGTTTCAGGTGCGGCTGTCAGATCGGCTTTTGGTTGGTCTAG
6819b	212 C	CCATTTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAACAATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAAGCCTAGTAAAGCCCGTCAGTAGT ACACATTTCTCTATGGTCTTCAACAGTTTTCATATACAAAATTTCTGCTATTTGCTTTAGCAAA CAGCAATAACITTTGTGTTTCTCTATATGACACCTAATATCCA
6819a	166 G T	CCATTTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAACAATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAAGCCTAGTAAAGCCCGTCAGTAGT ACACATTTCTCTATGGTCTTCAACAGTTTTCATATACAAAATTTCTGCTATTTGCTTTAGC AAACAGCAATAACITTTGTGTTTCTCTATATGACACCTAATATCCA
681xx	39 A G	CTGGTATGTCATAAGCAATCCATAATGTTATAGCTATTAGTATACCTATGTCACCACTTTGGGACA CAGATTATATATGTCAGACACACCCAGAAATGTCCTTTAAGATATGCAGCAAGCACAATCTGTCATGGT TTAACAAAAGAAATGAACGTCTAGG
6972b	149 G T	AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCTCCTTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCCCTGGACTCTTTTGGTTGGTAAACTATTGATTATG CACAATTCAGAG/GT/CCTGTTATTGGTCTATTCAGAGATTCAACTTCTCTGGTTAGTCTTGGGA GAGTGTATGTGTCGAGGAAT
6972a	122 A G	AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCTCCTTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCCCTGGACTCTTTTGGTTGGTAA/A/GJCTATTGATTA TTGCCACAATTCAGAGCCTGTTATTGGTCTATTCAGAGATTCAACTTCTCTGGTTAGTCTTGGGA GAGTGTATGTGTCGAGGAAT

7598k	210 A C	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATATATTTTCCCGTATTTTCCCT CAATGCAG[A/C]
7598j	208 A T	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATATATTTTCCCGTATTTTCCCT CAATGC[A/T]GA
7598i	192 G T	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATATATTTTCCC[G/T]ATTTT CCTCAATGCAGA
7598h	144 C T	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGATCC[C/T]ATTATGTGAGAGATTTTCCCTGATATGTTATCTTATATATTTTCCCGTATTTT CCTCAATGCAGA
7598g	142 C T	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGAT[C/T]CCATTATGTGAGAGATTTTCCCTGATATGTTATCTTATATATTTTCCCGTATTTT CCTCAATGCAGA
7598f	120 A G	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTATTTCTTG[A/G]GGATGCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATATATTTTCCCGTATTTT CCTCAATGCAGA
7598e	83 C T	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAA[C/T]CAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATATATTTTCCCGTATTTT CCTCAATGCAGA
7598d	77 C T	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGC[C/T]GCTAACAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATATATTTTCCCGTATTTT CCTCAATGCAGA

7598c	56 A G ...			AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCA[A/G]AGGAAC TCAATGAATAAGCCGCTAACCCAGATTTTACCTTGAGAAATGAAAATATTTCTTGAGGATGCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA
7598b	47 C G ...			AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAGGAAC TCAATGAATAAGCCGCTAACCCAGATTTTACCTTGAGAAATGAAAATATTTCTTGAGGATGCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA
7598a	30 A G ...			AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAGGAAC TCAATGAATAAGCCGCTAACCCAGATTTTACCTTGAGAAATGAAAATATTTCTTGAGGATGCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA
7998c	116 A T ...			GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTATTACAGACATCTGCCAGCTCTCCTGTA ATACCTTAATGAATGGGTGATAGTCTATCTTCTCAAGGTCCCAATA[A/T]CCTTGAGGTTCCCT
7998b	94 A C ...			GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTATTACAGACATCTGCCAGCTCTCCTGTA ATACCTTAATGAATGGGTGATAGTCT[A/C]TCTCAAGGTCCCAATAACCTTGAGGTTCCCT
7998a	75 A T ...			GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTATTACAGACATCTGCCAGCTCTCCTGTA ATACCTTAATGAATGGGTGATAGTCTATCTTCTCAAGGTCCCAATAACCTTGAGGTTCCCT
8071	119 A G ...			AAATACAGAAATTTATTAGAACTGTTTAAAGTAGAAAAAACCCCTGTCAAGAAAGACCAGGTGG AAAATGGGTTCCCAATAAAATGGAATTTTAGGGCAACAAAAGTCTAAAAGGCC[A/G]CAAAAAGAGA AATAGCACCACTGTCAATTTGAACAATGGCTAGTTACTTTTGGCATTGTTAATCACTGAATC TGGGTTTCCCTCTGAATTCACACAGAGCATGCACACACATTTTATCAT
8467b	93 C T ...			AAGGCTTTCCTCTAAACATCAGTCTACGGAGAAACTGGGAAAACTCGGATATTTGGCTTATCACTT TGACGCAAAATCCACTTTGCTGTAA[C/T]GGTCACTCCGAACTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAGGAAAAATTACTG
8467a	70 A G ...			AAGGCTTTCCTCTAAACATCAGTCTACGGAGAAACTGGGAAAACTCGGATATTTGGCTTATCACTT TG[A/G]CGCAAAATCCACTTTGCTGTAACTGTAACGGTCACTCCGAACTCCCTTCAGAGAGCAAGCAAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAGGAAAAATTACTG
8498	84 C T ...			AGGGTTACAGGGTTGGTTTAAATCAGGCTGCACACCTTTCAATCAATCTGACATCTCTATGTCA AACTGGCTTCAGCTAG[C/T]AATACTTCATTAATCGAAAAAGAAAAAATGCTTTAAGGAAAAAA AATCCAGTTTAAAGAACAAATTAACATTAGTCTTTAAATAAAGGAGGGCTAATGTTTCATGTTGCT TTATACATCCTTCTCCTCAATACAGAACCCAGGAATGTAATTTTCCCTAACTCAG

WI-18562	29 G A	CTAAGGAAAAATTAATGATGGAAATATC[G/A]ACAAATATTCACACATCATTTAAAAACAAAGTAG CTTCTCTATTTCACATAGCTTAGTTGGGATAGAAATAGAACTAATGTTTACAATGATCTTACATT TAGCATTATCAGAAACGA
WI-18618	51 A C	ATAGCAGACTTTTAAATCAATGCCAGAGACAAAGTGAGGCCGAGCTAAGAAC[A/C]CGCTCAGCTTCG TTACAATGAAGAAATGGTTTCTTTTCGATGCAAGTATAATTGTAAACCACAGTGCTCGCACAGTTC AC
WI-18683	22 C T	TAAGCTGTTCCAGGACTGGACTC[G/T]GGTCCCTTTATTGAGACTGACAGGCCAGTGGGTCCACCCAAA CAAAAATAAATTTCTCTCCAAAGCCTGCCTGCAGT
WI-18520	75 G A	GACTTGGTGATTTAATGCTTTTCCCTTAAATATGAGAAATAGGTAAATTTCTCCTTTTGTCTTTT ACTACA[G/A]CCGGAGTGGTAAATACTACTACTGCCAACAAACACGGGCATCCACTCTGTCTTCAA TGCTCTTCCGTGAGAC
WI-18563	94 A G	AAATAAGTTTTATTGGCACACAGCCCAAGCCCACTGGATGACACATTTGCCACGGCTCATCTTGCAA TACAATAGCAGGGTTCACTAATGTGAC[A/G]GACATGGTGGCTCACAAAGCCAAAGATATT
WI-18582b	69 T A	GTCTATTTCATTTAGCTAGACCCATTTCATTCTGTTTAAATGGCTACATTTGTTTTCATTGTGAGAC TT[A]GTGCCATAATTTAATCAGTGCCATATTGAAAGACATTTGGATCGTTTCCCAG
WI-18723f	94 G A	AACCTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGTCTGTAGATTTTGAAAG TGGTAACAGGTACATAGGTAAACCAA[G/A]TATATAGCTTATTTGGTGAATCTTCATCCT
WI-18723e	71 T C	AACCTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGTCTGTAGATTTTGAAAG TGGT[C/A]ACAGGTACATAGGTAAACCAAAGTATAGCTTATTTGGTGAATCTTCATCCT
WI-18723c	96 A G	AACCTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGTCTGTAGATTTTGAAAG TGGTAACAGGTACATAGGTAAACCAAAGT[A/G]TATAGCTTATTTGGTGAATCTTCATCCT
WI-18619	44 G A	TTTATTACAATATTAGGTGGCACAATACTAACAGCTTCTGA[G/A]ACAGGAGGTAAACATTTCTCA TAGACTTTGCAACTCAGCCAGAAAGTAAACTCGAAATA
WI-18715	76 G A	TTATTCACAAAAAGTGATATTGCAGAGGGTCTGGGGCTGTACATGGGAGGGCTTGGTGAGCTTTG TACATGGG[G/A]CTGGGAGACAAGGGAGCCTCCAGGTGGAAGGGTATTTTAAATAAAAAATAA TGGAGCTACAACCCCCC
WI-18535	107 G A	GTAAATAAGTTTTATTGGCACAGCCAGCTCGTTTCATATGCCATTGACATCTGCTGTTGCCCT ACACAGGAGGTGGGACCTGCTCTCACGGGAGAGCTA[G/A]TTGTTTAAAGCAGTGGTCCCAAC CTTCTGTGTCCTCCCGTG
D17525	107 C T	AGAGTGGTCAGAACACAGGCCGAATCCAGGCTCTATCACTTACTAGTTTTCAGTTCTGGCAGGTGAC TTCATCTCTTCGAACCTCAGTTTCTTCAAGATGGAAG[C/T]GCTATACCTTACCTACCTCGTAAAA GTCTGATGAGGAAAAAGATTAACTAATAGATGCATAGCACCTTAACAGAGTGCATAGCATACACTGTTT TCAATAAATGCACCTTAGCAGAAGGTGATGTCTACCAGGCAGACGAAG

DWU-133c	313 A G ---	---	---	TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGTCTCATGACTTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAAGATTCAGATCATGAATGACTGACAGAATATTTTGTGGGCAGTCCT GATTTAAACTAAGACTGGCTTGTGGTTAAATGAATATGTTGAGTTTTTGAATTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133b	236 T C ---	---	---	TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGTCTCATGACTTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAAGATTCAGATCATGAATGACTGACAGAATATTTTGTGGGCAGTCCT GATTTAAACTAAGACTGGCTTGTGGTTAAATGAATATGTTGAGTTTTTGAATTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133a	199 C T ---	---	---	TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGTCTCATGACTTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAAGATTCAGATCATGAATGACTGACAGAATATTTTGTGGGCAGTCCT GATTTAAACTAAGACTGGCTTGTGGTTAAATGAATATGTTGAGTTTTTGAATTTAATAGTAAC[CT TTCCAAATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-36	102 C T ---	---	---	ATGAGATCCTTTAAATCCTTCCATGAACGTTTGTGGTGGGCACCTCCTACGTCAAACATGAAGTG TGTTTCCCTTCAGTGCATCTGGGAAGATTCTACCTGACCAACAGTTCTCAGCTTCCATTTCCGCC CCTCATTTATCCCTCAACCCCGCCACAGGTGTTTATACAGCTCAGCTTTTGTCTTTTCTGAGGAG AAACAAATAAGACCATAAAGGGAAAGGATTTCATGTGGAATATAAAGAT
DWU-387	169 G T ---	---	---	GTGTATAAATGCACTGTTGATTTCTCAACATGGCTCACAAATTTCTATCCCAATCTTTTCTGAA GATGAAGAGTTTAGTTTTAAACTGCACTGCCAACAGTTCACTTCATATATAAAGCATTATTTTAA CTCTTTGAGGTGAATATAATTTATTTACAATG[GT]AAAAGCTTCTTTAATACTAAGTATTTTCA GGTCTTCACCAAGTATCAAAAGTAAACACAAATGAAGTGCATTATTCAA
DWU-447b	172 --- --- ---	---	---	ATTTTAGTGTCTTTGCGTTAAAAATCATTGCAAAAGTATTCTGAAGCTGCAAGCTGCCCAGTCAGAT GGGCTGTTGCCATTTAAATCACTGTAATTAATTAGTTTGAATAGAGCACAAAGCTTAGCTAATCAA CCATTATTTTCAATTTTGTGTTCTAAGAGGATTGANAATCAGTTAGTTTAAATGTCCTTTCTGTAG GCCTTCTTTCTTACAATGAAGAGATGATTCTTCTAGTTTATGGTTA
DWU-447	85 A G ---	---	---	ATTTTAGTGTCTTTGCGTTAAAAATCATTGCAAAAGTATTCTGAAGCTGCAAGCTGCCCAGTCAGAT GGGCTGTTGCCATTTAA[AG]ATCACTGTAATTAATTAGTTTGAATAGAGCACAAAGCTTAGCTAAT CAACCATATTTTCAATTTTGTGTTCTAAGAGGATTGANAATCAGTTAGTTTAAATGTCCTTTCTG TTAGGCTTCTTTCTTACAATGAAGAGATGATTCTTCTAGTTTATGGTTA
DWU-476	63 C G ---	---	---	GTAATAATCAGTTTTTTCCAGTTCTCTTTTGTGCTGCTTCTCAATAGCGTTTAAAGGTGAG[CTG]AT AAATCAACTGTCCATCAGGTGAGGTGCTGCTCCATACCCAGCGTTCTTCATGAGTAGTGGGCTATGCA GGAGCTTCTGGGAGATTTTTT

DWU-505	67 A T	TCATAC TAGGCAGTATCTCCTCTAGCTAGTGCCCATACAGAAAATTCATCACCATACAAAATTTA[A/TJGCAGTATTTTATGTTTTAAAGCACAGGTGTACCGAAACTGTGAAAAGTCTGAATTTATGGGTT CTATGCATGCATTTTGCCTAACCTAGAGAAAGAGTTTGATAAATTTTACCAGCTTTGAAGATGGAT TAACTTTTGACITTTGAGCTTTAAACTTTTAA
DWU-512	131 A G	AAAATCCAGGCATTTTCAATCTGTTTTTCATGATTTATAGAGGGTTTACACAAAAGTGCACATTTATAA AGAGCTTCCACAGTGAAGATGGAGAAGGTGAACCTGCTTTGAATATCCAGATGTTTGGTCT[AG] TGGTATGGCAGTGAGCAGGTATGTTTTGCTTTTGTCTTGCCTGCACTGAAAATTTAAATTTGCTATCAAGAGC AACTATGAACGGTTTTTATCAAGATGCTCCAGAGTGAAGATGCCGAG
DWU-525	97 A C	AACTGCATATAGATAATTATCCAGGATGTGTGGCTATTCTTTTACGCTTGTCTTCTACTGTTTGT ATATACAGTTTTTGTAAACCATATGATTGA[A/C]AAGAAGAAAGTCTATGCTTAGGCCAGTCAGTACA CCCAATTTTAAAAAATAACATATCTTCTTTTCAAAATATAGTTGAACAAGATTTCCCTAAAAAT CCACCAGGATTAATCTCTAAAAATCTAGTCTCTGATTTGC
DWU-59	94 C T	CATTTCTTTGTAAAGGTAATGGACTCACAAGGGGAAGAAACATGCTGAGAATGGAAAGTCTACCGG CCCTTCTTTGTGAACGTACATTTGGC[C/T]GAGCCGTGTTCCAGTCCAGGTGGCAGACTCGTTTTTG GTAGTTGTTTTAACTTCCAAGTGTTTTACTTCTGATAGCCGGTGAATTTCCCTCCTAGCAGACATG CCACACCGGTAAGAGCTCTGAGTCTTAGTGGTTAAGC
EST11	68 C	CTTGATCATGGGTGGAATTTTGTGTATCTGGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAG CAGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGGCA
WI-19856b	63 C T	CACACTGGCATCTAGGCCTTCGCCTGCATTGCAGAAGGAGAGCCAGGTCCCTCCTGGAGAA[C/T]G CTGGTTCCCCAGCCACACCCGCTTTGGACCCAGAGGTGTTGAGGCAGGAGGTGGTAAGACGT AGCTGTAGACCCAAAGCAACCAACCCGCTGGGACCTGCGGGAGAGGAGCACTTTAGAACATGGAA AAGTGTGGTCAATCCCATCAATTAGACAAGACACATCCTACATAATAAAAAAGT
WI-18014	40 A G	TCCATTTACATTTGGTGGCATTTGTTGAATAGCTACAGAA[A/G]GAATGAAAGTGCACCATCAGAGT GTAATTAGGTCTGTGTGACCCAGGAAGTGTCTGTTAAACAGAGATTTCTCAAGGGCAAGTGGCTTCT A
WI-18036b	97 T A	TTCCAATGTAAGAGTCAAGTACCAAGTTAAACTTCTAGAAATACAAAGAGAACATGATAAAATCTG ATCACAGTGGAAAAATTTAATCTTTTCATAA[T/A]CTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18036a	27 T C	TTCCAATGTAAGAGTCAAGTACCAAGTT[C/A]AACTTCTAGAAAATACAAAGAGAACATGATAAAAT CTGATCACAGTGGAAAAATTTAATCTTTTCATAATCTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18046	72 C T	TGTAAAGGTGACTTCTATAAGCTTCTAAACTGTCAAACTTTCATTTACTGAGATTATTTACGGCCAAT GTGTC[T/J]GTGGGTCTGAGATTTGATTATCAGCTGGGTAAGTTAACCTGTTCCTGTTTCA

WI-18083	105	G A	AGGCTTTAAACTGATAACAAATTTGCCITTAATCACATACAAAACTCTGCACITTCATTCTCCTTC CCATGTTTCTGATTTTGATGTAACCTTAAAATTTGTG/AITCCTTTAACAATATACTGTAGCTGCA AGTTGAAAGATCAGAGAGGTTATGGTTGGTAGTGAAGTCAAGTTCAGATTCAGAACTGGTCCAGTGTG TTGTTTTTTCAGCATCAG/AJTGCCACTAGCCAAAGTTGATCTCTGCAGTATCTACATGTGGT CCAAAGCTCACTCAGTATTAATCATCTGCTAATTTTCATCTTTGTTAATTCATCAGACACTGTGGT TTTCATCTCTAGAAGTTGACTT/CJGGGCCCTTTTATACCTTCCATATCTCAACTGTTAAGC GCAATCTGAACAGTTTTGGTAGTGGTATTACAGAGGAT/CJTTGTAATAAGGATTTGGAGTACTTAC CACTATTTCACTGCTGCTGAATAGTTCATAACCAACTACTGACAACAGITTAATTTTGGTTCTT TTCAAGATAATTACAATTGGAAGGGGACCAATAATCCACTTTTAAATCGAAAAATAATCTATATAC T/GICCCAATAAACTCACAGTAAATAAGCTTCAAAAAGCCTTAAGACACCAAAAGAGGAAAA GCATAGGGTTGAGGGGTGTACAAGAGGAGAACCAAGATTCAGTCCATGCCTGGAGGTTAGTCTGGGG GT/CJGGCGGGATGGACACAGACAGACACATAGATCTGGCATCTGATAGCAGGGCATACAG TCAATCTGAAAACCTTGTGTAGCCAGCATGGGGT/GJGGGAGGTGATTATGGCTGGGGAAGATG GGCACTACCCGACAGCAGCATCTAGCACACAGTGCAGGGGACGTTGAGGTGGCAGAGGGCTTT ACAGATGTCAGTTGTTGAAATTGGCCATTAAAGTATGGGGCTTTCTGTTAAAAAGTCATCCAAA AGGCTTGGGAAGAGTTTGTCTATACAACGGAGGACAGAGAAACATGA/GA/CTGGGGAGTAGGCTCT GACAGAAGGTGGGCTGTC
WI-18078	86	A T	GATTGAAGGGATTGCTTTATTAAAC/GA/JTGAAAAGCGTGATAGAGGAAGTGTAAAGATAACAA CTTATAAATACTCCCAATTGTAGAAGTGAAGATTG
WI-18244	35	G T	TAGGAGGGAAGAGGAGTGGGCTGCCTGGGCCCTCAAGACATGAGAAACGGGTGGTGGCTTCCAAG TTCTTACTTCCCCCATAGAT/CJCTGACAATGTGTCAGAAAGCCTCCAACTGGAAC
WI-18245	115	G A	TCACAAGTCAATCTCCCATCCCAATGACAGTTTGCTAAGATCATTAACITGGTTGCCAATTTTTT ATCTATTTGGGTCTGAGAAATCCACAATTTGAAGAAATCTTTTGGCAATATTGACATATTCTG CAG
WI-18261	26	G A	TCACAAGTCAATCTCCCATCCCAATGACAGTTTGCTAAGATCATTAACITGGTTGCCAATTTTTT ATCTATTTGGGTCTGAGAAATCCACAATTTGAAGAAATCTTTTGGCAATATTGACATATTCTG CAG
WI-18268	88	C T	TCACAAGTCAATCTCCCATCCCAATGACAGTTTGCTAAGATCATTAACITGGTTGCCAATTTTTT ATCTATTTGGGTCTGAGAAATCCACAATTTGAAGAAATCTTTTGGCAATATTGACATATTCTG CAG
WI-18299f	107	C A	TCACAAGTCAATCTCCCATCCCAATGACAGTTTGCTAAGATCATTAACITGGTTGCCAATTTTTT ATCTATTTGGGTCTGAGAAATCCACAATTTGAAGAAATCTTTTGGCAATATTGACATATTCTG CAG
WI-18299e	101	A G	TCACAAGTCAATCTCCCATCCCAATGACAGTTTGCTAAGATCATTAACITGGTTGCCAATTTTTT ATCTATTTGGGTCTGAGAAATCCACAATTTGAAGAAATCTTTTGGCAATATTGACATATTCTG CAG
WI-18299d	77	G A	TCACAAGTCAATCTCCCATCCCAATGACAGTTTGCTAAGATCATTAACITGGTTGCCAATTTTTT T/GJATCTATTTGGGTCTGAGAAATCCACAATTTGAAGAAATCTTTTGGCAATATTGACATATTCTG CAG
WI-18299c	67	T G	TCACAAGTCAATCTCCCATCCCAATGACAGTTTGCTAAGATCATTAACITGGTTGCCAATTTTTT T/GJATCTATTTGGGTCTGAGAAATCCACAATTTGAAGAAATCTTTTGGCAATATTGACATATTCTG CAG

WI-18298b	52 G A ...	---	TCACAAGTCAATCTCCATCCAAATGACAGTTTGCTAAGATCAATTAAGTTG[G/A]TTGCCAATTTT TTTATCTATTTGGGTCTGAGAAATCCACAAATTTGAAGAAATCTTTTGCCAAATTAATGACATATTCTG CAG
WI-18299a	48 C T ...	---	TCACAAGTCAATCTCCATCCAAATGACAGTTTGCTAAGATCAATTAAGTTGTTGGTTGCCAATTTT TTTATCTATTTGGGTCTGAGAAATCCACAAATTTGAAGAAATCTTTTGCCAAATTAATGACATATTCTG CAG
WI-18307	76 G A ...	---	TCAACTGTACCAAGTTAGCAGCAAGAGGATACCTCTTAGAGACTTTTCAGTGGACTTAAACTCAG TTTCCGCTG[G/A]TGCTATGTAAGCATCCAGATGGTTTATTTACTCTGCAATCTGCTTGGTCAC
WI-18324	72 C T ...	---	TTTGGTATGAATCTTTCTCTGACATTTACCAATCATCATTAACCTCCGGGGGGTGGGTACTGATT TATC[C/T]TAGATCCAAATAAGCATGCAGAAAGTG
WI-18350	48 T C ...	---	ATGAAAGTCACTTCAATCATAAGGGTCAAGAGAGAAAGAAATGTTTTCAGAT[T/C]TAAATCTATGAAAA GGTGTGTATCTGCTTGCAATTTAAGAAACACACAAAGTCA
WI-18395	77 G C ...	---	TCTTGACATGATCTGTGAATAACGTGATTGTGGTTGAATTTCTCGAAAAATTTGAAGAATAAAATTG ATTATTCAG[G/C]TGCAATTTGGTTTATACATATCTCTCTCTTAAATGCAAGCTATG
WI-18398	62 G T ...	---	TGCAGTGGCAAGACACTCTCTCGAGGAAAAAAGAAAGAAAGAAACAACTCAAGGGT[G/T] GATAACATTGCCAGTATAACCATAATTCAAACCAAGCAGCAGAAATTTGGAGGATAATTTGTT
WI-18396	21 C A ...	---	CTCGTTGGTATTCTCTCATCC[C/A]TTCTCTTCTGCTCTTTCTAAATTAAGAAAAAGCAATGGAATT TTAAAGATCATCTAAGAAATAAGAACTTACATATGTAACTTAACCTTATCAACTTGTACAAAGTC AATGAAAA
WI-18409a	20 C A ...	---	AAGATGGGAAAGAGGAAATC[C/A]TTTTCTTACTAGAGATTTTTTCCCTTTAAATCTTTTCAAAAT TCAAAGGATCATCAAAGGAGCAGGTGCAGAGCTCTGGGGCCAGAGGCCCCCAAGTGCTA
WI-18442	62 C T ...	---	AAAAAGGAAAGAAAGGATGGAGTAAGAGAGAGACAGAGAGGAAACAAATAAGTTTCTGG[C/T] JTTGGCTGATCTGGGTGATCAGGTGGACACTATTATCCAGAGGGAAACACACAGAGAAAAAAGG TTTATAGGTGGGAGAGAGGA
WI-18452	38 G A ...	---	TTGATGTTAATACTGTCAITCTGGAGATCGGCTAAAAT[G/A]AAGCATAGTTATTATTAGCTTTGG TATATTCTGCGACAGATTTAAACAAGTAAGACATATATCAACCTCATATTTTCCAAACA
WI-18489	102 A C ...	---	ATATAAGCTGGAGACTGTGGAGGGTGAGAGGCAGTGGGACTAGCTGTTGAAAGAGAGAAATGTAGC AGTAGTAAAGATGAAAGACTGCAAGGATTCAAACA[A/C]GGTTATGGCAATAGAGGTGAAAAAGAAA AGGCCATATAAA
EST5b	93 A ...	---	CTGGTGGGAGGAAACAAATTTGGGTATATTCAATGAAAACTCTTCAGAAATAAGAAAGGAA CAAACTGAATCACACAACATGGACAAATCTCAAATCATTAATGCTGATGGAAAGAAACCATCA TAAGAATACACAGTACAT

EST5	93 A	CTGGTGGGAGGAAACAAATTGTGGTATATTCATACAAATGGAACACTCTTCAGAAATAAGAAAGGAA CAAAACCACTGAATCACACAACATGGACAAATCTCAAATCATTTATGCTGATGGAAGAAACCACTTCA TAAGAATACACAGTACAT
EST6	48 C	TTAGCTACTTTTCAGAAATTGAAGGAGAAAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGCTCT GAACAAAGCTTTCTTTCTTTTGAACAAGACAAAGCAACATTTTGCAATGACAGAT
EST8	158 A	GGACAGGACCTCTATTCCCGCTGTGACAGCGCTGATGACTGAGGCCGCCAGGAGATACTGGGOC CTCTCTCAGGGCGTCTCCAGGACCCAGAGCTGTCTGCTTTGAGTTTCCCTAGAGCTGTGCGGGCCA GATAGCTGTTCCCTGAGTTGCAAGCAGCATGGAGATTGGACACTGTGTCTTTTGGTGGGT
WI- 18740c	104 GT	TCCTCATTGTTGGGATGATGAGAAGAAATGATTTGGGAAAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAAATCTCATTTACCATCATGTATCCAGTAGTG[GT/TAATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI- 18740b	96 CG	TCCTCATTGTTGGGATGATGAGAAGAAATGATTTGGGAAAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAAATCTCATTTACCATCATGTATCT[GT/AGTAGTGGATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI- 18985a	105 CT	CCAAAGTCTCTGTTGCTCATAAAGAAGTTTGGGATGGGAGAGAAATCCAGACCATCTTTGGGGCA GCCAGGCCCTTGCCCTTCAATTTACAGAGGTAGCACAA[CT/TTGATTCCAAACACAAAACCCCTTCCOC TTTTAAATGATTTCTGTTCTAATGCCATAGATCAAAAGCCCTCAGAAACCATTTGTGTTTCCCTCTT TGAAGCAATGACAAGCACCTTACTTTCACGGTGGTTTTGTTTTCTTAT
WI-18746	114 GA	GCCAGCAGCTGAAGTCTTTTTCTCTCTCGCTGGTGAAGAACAATCAAGATACCTTTGCGTGGATCA AGCTTGCTACTTGACCGTTTTTATATTACTTTTGTAATATCTT[GT/ATCCACATTTCTACTTCAGCT TTGGATGTGGTTACCG
WI-19112	212 GA	CCGTGTTACACACACACAATGGCAAGCATAGTCGCTGTTACGGCCAGGGGAATATGCCAAGG GACCCCTTAATGGAACACAGATCAGTAGTGTCTATCTCATGACAAACCAACAGAAACCGACGACAAA TCTTTGCGAGATTTCTCTAGTGGCTTAGAACATGGCTTTTGAAGAACACGGTGATATCTTTGAG GGTGACAAGGC[GT/CTCTTCAAACAGTTCATACCAACTGCTTTGCTCTAG
WI-19092	232 AC	TGGTGGCTGGCTAGCTAGTTTCTACAGAACATAATTTGCCCTATAGAAGGCTATTTAGATCATGT CTCAATGGAACACTCTCTTTCTTAGCCTTACTTGAATCTTGCCCTATAATAAGTAGAGCAACACAC ATTGAAGCTTCTGATCAACGGTCCGAAATTTTCATCTTGAATGCTTTGTATTAAACTGAATTTTC TTTTAAGCTAACAAAGATCATAATTTT[GT/ATGATTAGCCGTGTAAC
WI-19057i	175 GA	CCCATTATTATAGCCAGTGTCTCAAAAGTAGAGGAGCGTCTACTGGTCTTTTCAACTCCTTCA GTCTTCTGACGGCGGACTTTACCGTGACAGCGGAAGTGGTATTGACGTCCAGGCACCGCAGCCACTG TCTTCATGCAGGAACACACAGTGCCAGATCCCCACAGCTC[GT/ATCTCTTCATCTTGGTTTTGCCACA

WI-20103	188 C T ...				TGGGACTTCCAACTCAGAGGATGTGGGAATCCAGCTCAATGATACAGGATAAACTGGGATGGGCT AGGATGGACAGGCTGTGGATATGGAGTCAATGGGTCAAGTCTTATCCAGATGGCTCCAGGTACAG TGGGCTCTCTGGGCTGGAAGCTGGGTCTCCCA/C/TTCATCTGCTCAAGCTCTCTTGAAGGAGC TGGTTTGACTTCAACTTGCTAGAGCTAGCCTCATCTTTCAGTCAACTGGGA
WI-20441	111 G A ...				GCCTTACCCATTTGCACATATATACATATGCACCACCTTTGCAGTGGCAACATATATCCACACTA TAAACATACCACATTTATAATCTTGTAAAGGACAAGAAATGGA[G/A]TTGAAATAGTACCCCCAA CATATACAAGAAAGTTAGCATACTTACCCCGTTTTTCACTACATCAGAGGCCAAATAGAAATCTTT TAAGAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTTGGGGG
WI-19911b	116 A G ...				TGGTTACAAAACCTAAGCCCATATACAAAATTAGGAACACATTTAGATGCCTCTTTTGAAGAACGT TTTAGTCTTTTAAACTGAGTTTAAAAAATAACAATGCAATTTTAA/GJACACTGTTTTGAAA ACTTAAAGTGCAGCAATA
WI-20613c	165 A G ...				GTCTCAAGGGGGGAGAAAACCTGGTTCTTTTATGTACAAAAGCACAGATGTAGGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAAATGGCATGGGAGGAGGCAGTTAGAAAAACATCTAAAAC AGCTCCTTAGAAGGCCAATAATAAGTTGGA[G/A]GJAAAGGGAGTTTCCACGCAGCCAGTGTGAGC TGC
WI-20613b	156 A C ...				GTCTCAAGGGGGGAGAAAACCTGGTTCTTTTATGTACAAAAGCACAGATGTAGGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAAATGGCATGGGAGGAGGCAGTTAGAAAAACATCTAAAAC AGCTCCTTAGAAGGCCAATAATAAGTTGGA[G/A]GJAAAGGGAGTTTCCACGCAGCCAGTGTGAGC TGC
WI-19984	47 A G ...				CAGTAAAGAGTGATTCAAGTTGCAGTAATACACTGACAGGTAATA/GJ/TATAACATTAGAAAA GCAAAATCTTTTAACTTAAGGACAGACTGAACCATCAGGTATGGTCTGAGATCAAGTAATACAGG TAGGCAAGAGTTTTTCCACACTGGAAAATGAAGGCAGTTTTTCCAAATACTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135 T C ...				GCCAGTTGGAATATGGCCTATACGAACCAAGAGTGTATACAAAATGGAAGTGGTCATCAGGCAATA ATTGTTTCTTGGAACTCTGCACCGACTGTCCATGCTCTGTGGGGACTTACACATTCAGTTTGACAG T/CJTGAAAAACCAACTGGAGCTGCTTTTCCAAGAAATGTTCTGTGTCTTCAATAGGAATCCATG TTATTTCTTCTTGGCCTTAAGCTCTTATATCTTTCAAATGACCTAAGCTGA
WI-18846a	49 G A ...				GAGTGCCATACCTTCTCCAGGCTCTGCCCAAGAGCAGGAGGTGCCTT[G/A]AAAGCTGGGAGCGT GGGCTCAGCAGGCGTGTGCACCTCCCATCCCGTAAGACCTCCTTCCCTCCTCAGCAGGCCAAACATG GCCAGACTCCTT
WI-18959	123 G A ...				AGCAGTGGCCTTATTGCATCCCAAAACACGCCTCTTGACCAGGCTGCCTCCTTGTGGCAGCAACGGC ACAGCTAATCTACTACAGTCTTTTAAAGTGAATAGTGCAGAAAGAGGCACCG[G/A]GGAAGCCG TCCTGGCGCTGGCAGTCCGTGGGACGGGATGGTTCTGCTGTTTGAATCTCAAGGAGCGAGCAT GTCGTGGACACACAGACTATTTTAGATTTCTTTTGCCTTTTGCAACC

WI-20146	31 T C ---	---	---	TGAGTCTTCTGTAATTCATTGAGCAGTTAGCT/CJ/CATTTGAGATAAAGTCAAAATGCCAAACACTAG CTCTGTATTAAATCCCATCACTACTGTAAGCCTCATTTGAATGTGTAATTCATACAGGC
WI-18922	74 G A ---	---	---	TAGGAATGGTTTCACGCCCTGAGGCAATTAGACACATTTGGAAGATGCCATAACCTGTCTCACCTGGAC TTAAGC/GJ/ATCTGGCTCTAAATTCACAGTGCTCTTTTCTCCTCACTGTATCCAGGTTCCCTCCAGAG GAGCCACCAGTTCTC
WI-18763b	53 A G ---	---	---	TTTCTGTGTGTGGGTCAACCGTACAATGGTGTGGGA/GJTGACGATGATGTGA/GJ/TATTTAGAATG TACCATATTTTTGTAAATATTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA TGTGTTTTGCCAA
WI-18763a	38 A G ---	---	---	TTTCTGTGTGTGGGTCAACCGTACAATGGTGTGGGA/GJTGACGATGATGTGAATTTAGAATG TACCATATTTTTGTAAATATTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA TGTGTTTTGCCAA
WI-18771b	75 G A ---	---	---	CTCATTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCCTAGAAAGATGTTGGG AACAGAA/GJ/AAATAAACTGAGTTTAAGGGGACCTAAACTGCTGAATTCACCTGTGGA
WI-18771a	57 A G ---	---	---	CTCATTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCCTAG/GJ/AGATGTT GGGAACAGAGAAATAAACTGAGTTTAAGGGGACCTAAACTGCTGAATTCACCTGTGGA
WI-18820	70 T C ---	---	---	GGGAAAAATTTGAGACGCAATACCAATAGGATTTTGGTCTTGGTGTGATGAAATCTGAG GCCJ/CJTGATTTAAATCTTTCATTGTATTGTGATTTCCTTTAGGTATATTGCGCTAAGTGAACCTT GTCA
WI-18742b	51 C T ---	---	---	ACAAAGTCTGTAGCCCCCTCACCTTTCTGTTTTCACCTTTTGCCAATGT/CJ/ATCGGGTTTGGTTT TCTTGATTTAATAACGGTTGTGTTTCCCTTTTCCACGGAGGTTCAAGTAAAGCCGCTGCAGGAGA GTTTTACC
WI-18882	94 C T ---	---	---	GTGTGTCAAAAATGGGGTCTGCTGCTACCTTGACCTTCCCTTCTCTGCTTCTCTCTCTCATCA TCATTTCCCAACAACATCCTCTGCCA/CJ/ACACAACAAAAAGTAAAGTTTCATTTGGGCAAAAATTGA GC
WI-19970b	167 G A ---	---	---	TATAAGCCCGAGTCAACAGGACGGCTGTCTGGCCACAGACAGGGGCTGCCCTGTGGAGCCTGCCACC GGCCCCGGCAGTGCAGTCCAGCGGGGAGGAGGCTGCCCGTTCTGCCAGTTCTCACTGCGGGGACC AGCAAAAGGCCCTTCTCACTGGGTTGGTCAAAAG/GJ/ATAGTCACCTTGGCCTGGTGCATCCACAGAGGA TGTGTTCAACCCAGAAATCTTTAAACGACTGACCTTCCCTTAAAAACAGA
WI-19970a	126 T C ---	---	---	TATAAGCCCGAGTCAACAGGACGGCTGTCTGGCCACAGACAGGGGCTGCCCTGTGGAGCCTGCCACC GGCCCCGGCAGTGCAGTCCAGCGGGGAGGAGGCTGCCCGTTCTGCCAGTTCTCACTGCGGGG ACCAGAAAGGCCCTTCTCACTGGGTTGGTCAAAAGTACCTTGGCCTGGTGCATCCACAGAGGAT GTTGTTCAACCCAGAAATCTTTAAACGACTGACCTTCCCTTAAAAACAGA

WI-19067d	202 T G ---	---	TATTGCTGTTGTCACTGCTGACATTACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGATCTTCAGTGGTTCTC TTGGGCTCTAGGCTCGAGAAATGTTGTAGGGGTTATTTTTTAATAGTGTTCATAAGAAAT/
WI-19067c	153 G C ---	---	GACATAGTATCTTCTCTCAAGACGTGGGGGAAATATCTCATTATC TATTGCTGTTGTCACTGCTGACATTACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGATCTTCAGTGGTTCTC TTGGGCTCTAGGCTCG/GCJAGAAATGTTGTAGGGGTTATTTTTTAATAGTGTTCATAAGAA ATACATAGTATCTTCTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19067b	151 T C ---	---	TATTGCTGTTGTCACTGCTGACATTACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGATCTTCAGTGGTTCTC TTGGGCTCTAGGCTCG/JGGAGAAATGTTGTAGGGGTTATTTTTTAATAGTGTTCATAAGAA ATACATAGTATCTTCTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19067a	57 C G ---	---	TATTGCTGTTGTCACTGCTGACATTACGGCAGAGGCAAGGCTGCTGCAGCCTCC/JGJCTGGCTG TGCACATTCCCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGATCTTCAGTGGTT CTCTGGGCTCTAGGCTCGGAGAAATGTTGTAGGGGTTATTTTTTAATAGTGTTCATAAGAA ATACATAGTATCTTCTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19106	247 T C ---	---	TTAATCCAGCCCTACCTTGTAGTATTTTAGGAGACAGTCTCAAGCACTAAAAAGTGGCTAATTC AATTTATGGGTATAGTGGCCAAATAGCACATCTCCAACTTAAAGACAGTGGATCATGAAAAAGT GCTGTTTGTCCTTTGAGAAAGAAATATGTTTGAGCGCAGAGTAAATAAGGCTCCTTCATGTGGC GTATTGGCCATAGCCTATAATTGGTTAGAACCCTCTATTTAAT/CTJGG
WI-18944	147 A G ---	---	CAAGGCAAAATATCAGGAGCTTTTTACACACCTACTAAAAAGTTATTATGCTGAAACAAA AATGCCAGAGGATAATATTGATTCCTCACATCTTTAAGTATGTTTTACCTAGCATTTCAAAACCC AATGGCTAGAAC/JA/GJTGTTAATTAATTTCACAATATAAAGTCTACAGTTAATTATGTGCATA TTAAACAATGGCCTGGTCAATTTCTTCTTCTTAAATAAATTAAGTTTT
WI-18952	232 G A ---	---	CCCATCCCTGTGAAGGAGTAGGCCACTCTTTAAGTGAAGGATTGGATGTTTCATAATACATAAA GTTCTCTGTAATTACAACATAATTATTATGCCCTCTCTCACAGTCAAAAGGAACTGGGTGGTTGGT TTTTGTTGCTTTTTAGATTTATTGTCCCATGTGGGATGAGTTTTAAATGCCACAAGACATAATTA AAATAATAAACCTTTGGGAAAGGTGTA/JG/JACAGTAGCCCCCATCAT
WI-18932d	177 C T ---	---	CACACCTCATGCTAGCCTCAGAAACTGGAATAAGCCTTGAAAGAAATTGCTCTGAAGCTTGTA TCTGATATCAGCATGGATTGTAGAACTTGTGCTGATTTGACCTGTATTCAAGTTAACTGTCCC CTTGGTATTTGTTAATACCCTGTACATATCTTTGAGTTCAAC/JTJCTTTAGTACGTGTGGCTTGTC CTTCGTGGCTGAGGTAAGAACGTGCTTGTGGAGACAAAGTCTGTGGCTTG

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WI-19042	193 A C ---	---	---	TTTGTCAAGTGGTGGCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGAAGTTTGGAGATAGATG GATAAGGGAAATAATAGGCCACAGAGGTGAACCTTTGTGCTTCAAGGACATTTGGTGAGAGTCCAAACAG ACACAATTTATACTCGGACAGAACTTCAGCATTTGTAATATGTAATAACTCTAACCA[A/C]GGCTG TGTTAGATTGTATTAACTATCTCTTTGGACTTCTGAAGAGACCACCTCAAT
WI-18984	208 A C ---	---	---	ATTGGCCCTGTACAGTTTGCCTATTATAAAATTCATTAAAAACACTACAGGTGTGAATGGTTAAAA TGTAAGCCCTCCAGTTCAATTTTCAGTTATTTCTGAGTGCAGACAGCTATTTTCGCACTGTATTAAAT GTAACCTATTATGAATAATCAGAAGCAGTAGACAGATGTTGGTGCAATACAAATATTGTGATGCATT TATCTT[A/C]ATAAAATGCTAAATGTCAATTTATCACTGGCATGTTTGACT
WI-18951	90 T A ---	---	---	GCCTCAATTGGCGATTGATTCAAGTCCCAATGTAAACAGGGTTGGTAGTTGTTACTCATTTTGAAT ATACCTTTTCCCTATTGATTCT[A/G]ATAATAGGATCCTGGAAATGAGACCTGGTGGAA
WI-18821b	76 T C ---	---	---	TCAACTGCAGTTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC ACAGAGGCT[C/G]GGGGGTAGCCATTGTGCAGTCATGGCCCGGGGAACTTGCCAACTTCGTGTCTCAG GTGCTGTGT
WI-18821a	69 C T ---	---	---	TCAACTGCAGTTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC A[C/T]AGAGGCTGGGGGTAGCCATTGTGCAGTCATGGCCCGGGGAACTTGCCAACTTCGTGTCTCAG GTGCTGTGT
WI-19021a	20 C G ---	---	---	ACTCCTCTGCTGCTGCCAT[C/G]ACTGTCCCTTTGAACCAGGAAAAGTCACAGAGTTTAAAGAGAA GCAAAATTAACATCCTGAATCGGGAACAAAGGTTTATCTATAAAGTGTCTTCCATCACGTTG CTACCTTACCCACACTTCCCTCTGATTGCTGAGGACGTGGCATCTCTACTTACGTACGTGGGCATAAC ACATCGTGTAGGCCCATGTATGCTGGGTAGAGCAAGTAGCCCTCCCTCTG
WI-18908	70 G C ---	---	---	TGGAAATTCCTTCACTCTGGAACCATCAGAAACCCCTCACACTGGGACTTGCAAAAAGGGTCAGTA TGG[G/C]TTAGGGAAACATTCATCCTTGAGTCAAAAAATCTCAATTTCTCCCTATCTTTGCCACCC TCATGCTGTGACT
WI-19037b	155 A G ---	---	---	CACGGTTCTCTGCATCGTTACCAGAGCGCCTTCTGCTCCTAGCCACGCCCTGTATGACCGCGCAATA TCCCCAAAGCTTTGGGTCTCAAGTCATGCCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGGTC CCCTCCCTTACGAACACA[A/G]AAACCCAGCCACATGACTAGCAGCTGAGCTCTGCAGGGACCA GTGCCAGGCACTGGGGGTGGAAGTGTGGTGACACAGTGAATGGGAGTGG
WI-19037a	47 C A ---	---	---	CACGGTTCTCTGCATCGTTACCAGAGCGCCTTCTGCTCCTAGCCACG[C/A]CCTGTATGACCGCGCAA ATATCCCCAAAGCTTTGGGTCTCAAGTCATGCCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGG GTCCCTCCCTTACGAACACAAAACCCAGCCACATGACTAGCAGCTGAGCTCTGCAGGGACCA GTGCCAGGCACTGGGGGTGGAAGTGTGGTGACACAGTGAATGGGAGTGG
WI-19054	66 T C ---	---	---	TTGAGGAGGTGGGTGAACCTGCTCCTTGGCAGGATTTGTGACACTGCATTGCTGGGCTGTGTTCTT CJCGGCTCTTCTGGACCTTGACCGGTGATACCAGGCCATGTGCCATGGTATTTGGTCTCTGGGAGGG TGGGTGAATAAAGGC

WI-18972a	112 A G	AGGCTGTGGCTTATGTACCCAAAGAGGGGTCTCTGAGAAGTCTGGCTGGCTGGGATGCCCTGCCC CCTCTGGAAGGCTCTGACAGAGTACTGGGCTGGGGAAGCAG/GTGTCTTGGCTGGCCATGGAGCC TCATTGCAAGTTGTTCTTGAACACCTGAGGCTTCTGTGGCCACCCAGGCACTACGGCTTCTCTCTCC AGATGTGCTTTGGCTGAGCACAGACAGTCAGCATGGAATGCTCTTGGCCA
WI-19016b	184 C A	GTTTGCAACCAACATGTGCTCTTTCAAGTCACTTCACTGTTTAAATATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAATTTTGTAAATGTGATTAAACGAAGTTCAAGATTAGAAATACATCTGTGTC CTGAAAACCTTAGATACATAGCCGACTGTATACAGAGGTTTCATCTCA/CJA/CTCAACACTATTGAC TTTTGGGCTGGATAGTTCTGTGTGGGGTTTGTCTGTGCACTGTAG
WI-19016a	161 C T	GTTTGCAACCAACATGTGCTCTTTCAAGTCACTTCACTGTTTAAATATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAATTTTGTAAATGTGATTAAACGAAGTTCAAGATTAGAAATACATCTGTGTC CTGAAAACCTTAGATACATAGCCG/CJ/TJGTATACAGAGGTTTCATCTCAACCTCAACACTATTGAC TTTTGGGCTGGATAGTTCTGTGTGGGGTTTGTCTGTGCACTGTAG
WI-20096	21 T C	GGTTTGGGGCATTATTCT/CJ/GATAGAGACTGGCACAAGCTTTGGGCTAAGGACACCCGCCCCC ACCTCATCTAGAAACAATCTCTCGCCAGACTTG
WI-18591b	156 C A	TGGGGCAATTTTAAACAAACAGGCAAAATATCACATATACCTGAATATAAGGTAACCTCAAGCCATG AGTATAAGATTAAAGCAGTTACTTTATTTGAACAAAGGAAGTGGCATAAGCAACTCAGTGTGCCCC CTTAGGGTGGGAGCTCTCC/CJ/ACTACCACTCCCAAGGCAATCAATTTGGGAGAAAAA GTGCTTCTATCTGGCTAGCTGTGTATCTAGGGATTGCACCTTCTTACACGG
WI-19591a	45 T A	TGGGGCAATTTTAAACAAACAGGCAAAATATCACATATACCTGAAT/JATAAGGTAACCTCAAGC CATGAGTATAAGATTAAAGCAGTTACTTTATTTGAACAAAGGAAGTGGCATAAGCAACTCAGTGTGT GCCCCTTAGGGTGGGAGCTCTCCCCCTACCCTACCCCAAGGCATCATTTTGGGAGAAAAA GTGCTTCTATCTGGCTAGCTGTGTATCTAGGGATTGCACCTTCTTACACGG
WI-20310	125 G A	TCCTCCAGCTCTGTCTCCTTGTCTGAGGGTTCTGTGTTACGGCCCCCTCCAGGCATGTTTCTTCAT TTAGGTAGGAACAAAGGCCAAAGAACATACAGCCAGCTCTCTAGAGGCTCCA/G/ATCAGAA CTGGACCTTTAACTACAAAGGAATCTTGGATGAATTTTATAGGGGCTTCAGGAGCAGGTAGC AGAGCCAAAGTGCACACTCAGGCCATCTCTCCCAATGTCTCCCCGGGG
WI-20860	224 G A	CTCTCCCTAAGGAGCTTGGCTTGCAGCCCATTCAGCAGGATGGAGTCACAGACAATGAGT GGAGCTCATGCCCTCCCATGAGGAAGCCCTTAGTATTGCTGACATCTGCCCTTTATCTGCTCTCTCT CCCCAGTGTCTCAGACTTGGGCAAGCAGAGTGGTGGCAGACCCAGCCTTGAGAGCTCTTGTAGACC GGAAGGAAGGGGGCTATT/G/JGGTGTGCTTCTGGCTCTGGCTT
WI-19359a	39 T C	GACGTGGACAAAGGAGGTTTAAATGAATACTTTGTTTGT/CJ/CATGTTCAAAAAAGAGTATTAAAT ATTTTGTGACTGCATCTGTGAATGAAGACACTCAAAAGGCATGTTTCCAACTTAGGTTAATAATAA GGCTATTTGTCCACCCACTCTCGGGCATTGCTGCAATATTCTGGGCTCAAGTGGGAGGCCACGTG GGAACAAGGCCTCAGAAACAAAGGACATGCAGCCTCCTGAGCCAGTTCT

WI-19766b	93 A G ---	---	TGGCCTCAATGACTGGTACATTGGAGAGCTGTGCAGCAGCATCCTTTCTGTGGTGGGAGGGCAGGAGATGAACCATAGGAGCCAAAAGTCTA/GIGACAAACAGAAAGAGGCACACCAAGCCTGAAACCCCTC CGGACAAACAGCAGAGTTACAGCTGAGGGATGTCCTCGAGGTTCTGACCCATGAGAGGCCCCCTC ACCCTCCTTCAACCCTCTCTACCAACCAAGCTCTCCGCAGTCATGGACTTAT
WI-19766a	31 G A ---	---	TGGCCTCAATGACTGGTACATTGGAGAGCTGATGCAGCAGCATCCTTTCTGTGGTGGGAGGGCAGGAGATGAACCATAGGAGCCAAAAGTCAGACAAACAGAAAGGCACACCAAGCCTGAAACCCCTC CGGACAAACAGCAGAGTTACAGCTGAGGGATGTCCTCGAGGTTCTGACCCATGAGAGGCCCCCTC ACCCTCCTTCAACCCTCTCTACCAACCAAGCTCTCCGCAGTCATGGACTTAT
WI-20512d	126 C G ---	---	CTTCTCTGTTTGGCTTTCATTTGTGGATTGGAAAAACACATTGGAAGAAGGGACTTTCTCTGCAA AACCTTAAGAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCTTGACTGA/C/GJAAAGC TTAGAAAGGAAGTGAATGCTTCTTTGAATATGGATTTAGGGCGGGCGTGGGTGGGCTCACGCCT TATTAATCCAGGCACGTTGGGAGGGCCAAACGCGGGTGGGATCACCTGA
WI-20512c	59 T G ---	---	CTTCTCTGTTTGGCTTTCATTTGTGCGATTGGAAAAACCACTTGGAAAGAGGACTT/GJTCCTG CAAAACCTTAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCTTGACTGACAAAGC TTAGAAAGGAAGTGAATGCTTCTTTGAATATGGATTTAGGGCGGGCGTGGGTGGGCTCACGCCT TATTAATCCAGGCACGTTGGGAGGGCCAAACGCGGGTGGGATCACCTGA
WI-19599	230 C G ---	---	GGGCTTAAATCCCTCTGTTGGGACTGGTCTCCAGTTTACAGCAAGGATCGCACCCCTTTTCC ATAACCCCTTCTACATTGGAAGAGCAGCACACCTTGATACAGAATGGCTCCGTGAAGTCTTTTAAACG GACAAAGGTAATCACAGCTAACAAACGATGATGTTGGCTCACACGTAACCAAAACACCTCTTTTTC A GAACAGAGAGCGTTAAAGTAAAGGGA/C/GJTTCCAAGAGTAACACTGCTA
WI-20679	82 T C ---	---	TGTTTGAATAAAAAATTCATGGTCTTAATTGAAGTGTATGTACTTTCTTTTGAATATCCTTTTT TTCAATTAATAAT/CJCTAAACCACTCTATGTGTTCAACCTTCTGTTTAAACACTAAGATATGGGT TTTTGGAAAGGCCACAAAGTCACCAGCTCCATGAAGTGGGCGAATGGTCTTGTGTTTGGAAAGCTCT CAGGGTGTCTTCTCCAGAA
WI-19909a	29 T C ---	---	CCAGAAATAAGCCTGAATATCTCTTCT/CJTTAAAAATAATTTTTCTCTTTGCTCTTCCAA GTAAATCTTAAATGAACCTGTCTAGTCTATTTTAAATCTAGGCAATATAACACTACCTAGGGGGG TTTTCTCTTATACCTTGTCTGTACTGTGGAATCAACTAA
WI-20341	221 G C ---	---	TTGAGAGGCTGAGAGAGGCTGTGAGACATTGTAATAAGTCTTAGGGGCATGAGACATTAGGAAG GCCACAATTATGAGTAATGAATGTGAGGCTGATGAGAAGCTACTGCTCCCATTTGTTTAGCAGGA GGCAGGAAAGTGATCTGGGCTCTCTGGCAGCAAAAGCGTGTGTAATAATTTGGGTGACGTGATGC ATCCCCCATGCATTGGTTTGG/CJATGCTCCAGTGAGGCTGTGGGCAAGTCT

WI-20113	60 T C ---	---	---	TTCTGGTACATGGTAAGTGCTCAGTATTACTGAGTGAATGAGCAAGACCTGAAATACTGTC/GGA AACAGTAAAGCAAAATTACCACACAATTAGGAGGAATATTTTCAGACATAGGATATTTAAACAT CACTCAATACTGGAGCATGATTCAGCAATAATCTATTCCATAAACCCAGGTAGATAAATGTCACA GCTTTAAATATAGTTAAGTACAGTTGATCCTCGTTATTCATGGATCCGTATT
WI-20895	107 G C ---	---	---	TGATGGCAAAGTACAAGGCTCTGAAAGAACAGAGTAACAAAGAGCAGCGAGTGCAGCGTGTGGC CACTCCACCAGGAGCAACACTTGACTTCATTAAAGGCAA/GC/CTTTACTCTGTACTTTTCCCTC CCACATAGTTTAAOCCAAATAGAAAGGCATTCTATTCTCACACTACTGCTCTCTAAGGTCCTAGGAA TATACTGGTACTATAGGCAACAGATGCA
WI-20721	72 T C ---	---	---	CCTGCAATCACAAAAGTGAACCTAGTTGATATTTTGAATCATACCTTGATTTAACACCTTCAGAAA TTCTAT/C/AAAACACTAGCAACTTCCTTTTATCAGA
WI-19415c	161 A G ---	---	---	CTGGATTTAATATTTCTGGCCTAATAACCAATGTAATCAATAAAATTTGGTCAATATCTCCACCTC ATTTCTGCTAACATGTTTGCAGATTCCCTAAGTAAGGTATTGACGACTGAGACTAGTCCGGCAA GTCATGAGACCTTAGCTGATCTCAT/GAAGTCCACCTCATGAAGGAGATGATTCAACATCTCAA GCTAAGGTATAAAGTGTGGACATACAAGGCTTACAAGTTTACACTTCCTG
WI-19348c	103 C T ---	---	---	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTAGCGATGGGCCATGCACCTTCTG GCGGTGATGAAGAGACTGTTGGTCATGCGGTGA/C/TGTCCTTCTCCAGGCTCATATGGATGTCTT CGAGTTGCACAGGGAACCTGCTCTGCTTGTAGAAGCTTCTCC
WI-19348b	98 G A ---	---	---	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTAGCGATGGGCCATGCACCTTCTG GCGGTGATGAAGAGACTGTTGGTCATGGC/GA/GTGTGACGTCTTCTCCAGGCTCATATGGATGTCTT CGAGTTGCACAGGGAACCTGCTCTGCTTGTAGAAGCTTCTCC
WI-19635	98 A T ---	---	---	ATTAGTTGCTGTTGGGCCACATTCAAAGCCATCCACACAAGCTTCTGTAGGCCATTGTAAACAATG TTAAAGGTACAGTAAATAACAGTATTAT/TATCTTATTGTGTAGCACGGCTGTGAGGCTCATT GTTGAATGAAGCATCCTTAGGCAGCACGTGACTGCATGCAGATATGTGTGCTGAAAGAACTTTGCTT T
WI-19641a	46 A G ---	---	---	TCCAATTTTCAGAAACATGTTCCATGTTTATTGTGATAAGCACTAG/GJTATTATAGTCTCATGTTT TTAATTTATGAATAACGTCTGATTCATTTGATTTTGTATTTACAGAAGATGTCAGGGCTATCTCATTC AGTTATTAAATAAGGATCAGAGTAGTAAGTCAAGAATAAGTGCATAATGTGGTTTAAATTTTAAAA AATACTCAGAATGAGGTAGTATTTTAAATTTTAAATTCATCCACCCACCTTG
WI-19642b	52 C A ---	---	---	ATATAGAGTACCATCCATGGTTTCAAGCATGGCCTGGACACATTATCCCCCT/C/A/GGGTAAACCAG GACTATTGCATGAGCATTCCTTAATACGTATTTTGTATGGACACAAAGTTTTCATGCTATTAT
WI-19673b	180 C T ---	---	---	TCTGCCATGATCAGATTGTGATGAAGAACAATGATGGTCACTAGTAGGTAACCTTCTGTGTCAATTGCCT TACTCTCAGTGAAGGTGCTAGTGGATTACCTACCCCTGCTTTTGCATCACCACCTGTAAATCTAATAGT GAAAAGGCAATGATGTCTCAGTATCACTGTGAAACATTTTTC/C/TCTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACACGCTCAAAAAACACAGCCC

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WI-19873a	35	A	---	---	TCTGCCATGATCACATTGTGATGAAGAACAATGATG[A]TCACTAGTAGGTAACTTTCTGTGTCATTG CCTTACTCTCAGTGAGGTGCTAGTGGATTTTACCTACCCCTGCTTTGCATCACCACCTGTAATCTAAT AGTGAAAGGCAAAATGATGTCATGATATCACTGTGAACAATTTTCCCTTGGACCACTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACACGTCAAAAAACACAGCCC
WI-19724	35	A	G	---	TTTATTGGGAAACAAAGGATTGTAATTTGGGTAA[A]GJCTGAGTCACGGTGGCCCTGAGTAGTGTC CTAGAAAGCAACACGAGAGTTTGGTTTTCTCT
WI-19307	196	T	C	---	TCCTCTCCCCAACTAGATGGTATTGATCACTCTGCCACAATGGTACCCCTTCAGCAAGAACTG CAAGCCCTTCTTGGATTTGCCCTTATGAGAAATGGTGGCTGGGATGGAGTGACATTCCTTGTGT GGTGAACCTGCAAGAAGAAACCAAGGCAATGATTCCATAGAGGCCCTTAAAGAGACCCG[T/C]TGG AAATGGCCATGGTCTAATTTGGTGTGAATAAACTAACCTCTTTGGCTG
WI-19269	85	A	T	---	CTTCCCTCATCCCTCTTCACACACACCATCCCGGAACAAGTCTCCAGGATTCCTGCCACTGGC CATTTTGGAGTGTGTC[A/T]TTGGGTAGCAATGTGGAACCAACAGGCCCTTTGTGGAGAAATGG AGGGGTTGAGGGAGTCCAGAGGGGCTTATTGAGGGCTTTTGGCCACTTGTCTATAGGCGAGCTCG ATCTCCTCATCATCTGGACAGGTGGAAGCAATTTCCCGGGCGTAGGCA
WI-19946	122	C	T	---	CAATGGACTGAATGAGTGGCTGCTGGTGGGTGGGGGACACACACACCTTCAATACACGTCAAGGTGG CTCCAGTTTGTAGAAACAGAAATCTGCATCTCAGCCTGAGACGACAGAGAGGT[C/T]TCTTCCCTG ACCCAGCGCACTCAGGAGCCAGTCTGGTTTCAAAAACGCAATTAACCTGCCGACAGAGTTACAC CGTAGGCATCTTTAATAAATACTCCAGCAAAATGTGGGTACGGTTACTAA
WI-19956	141	G	A	---	CACAGCATGGTGTAAATAGCATCAGATTGAATGAAAAGTTTGTAAATGCAACCAATAAATAATTATA ATAAATATACATCAAGTAACCTTACAGCACACATTTTGGGCCAAGGTTTGATCTGTCTGGACCT CAATGT[G/A]CTCTCGGAGAAGCAGCCACGTTAGCAGCAGATACCTTACAGCTTGTCTACTCAA GTGATGGCCCAACAGAGCTTCTGAACCTCCTCTGGGAGGTAGCTGACAAG
WI-19076	40	G	A	---	TTGGTTGGATACTTGTCTGGAACCAAAAGCAGTTTAAAT[G/A]GTATTCAAAATACCTTTTAAAAA GTATTCTAGCACAGATTTTCTGTAACTAGATTATGTTGTAACCTTTTCTAAATCTTGTAGGAG TGTCGGTTGTTAAGAACTAGAGCTTATCCCTATCCAAATCTATCTGCGTCTCTGAAAAACTGCAGA AAGGCACTTGAAGCTGTTCTTTAAGATATGGGATTCTTTTATCTT
WI-20218	26	T	C	---	CCACACACTCTGGTTTTATAAGCTA[T/C]JAGGACAGAGCAGAGATGGAACCTGAAAAACAGGGTAG AAAAAACAATAAATGGAGGGGAACAGTGGGATGCAGAAAGATGACAACAGCCACATGTGCCCCA GTCAAATACTTTTAGTCCCTGCAGCAGAAAGATGCCAACCAAGTCTCTATACTGGCTGGGATCCTGCC ATGGATGCAGGAGAAAA
WI-20295g	154	T	G	---	CAACCTTTTGCAGGGGACGTGAATTTCTGATGAAAGTTATCTACCAAGTTTAAATTCATAATTG GGAATTCCTCTTTTAAATATCTCAGGCTTGAATGGGAGGGCTGGGCTCTACCCCTTCTCTTTTCCA TCCAGTCTATTGCCAGAT[G/C]CCAGAGAAAGCGCGGGAGGCCAGCTCTCCAGCATAGCCACTGTGG GTGGGCTTCACCTTCTGTGACTCTCTCATGCTGGGACTTGTCTTTTGGGG

WI-20361a	192 G A ...	---	---	CTGGGAGTGCTGACCTAAGTGACATTTTTTTTTATGCCAAATACAGTAATCTCCAAGCTTTTAAATGG CTTATGCAAGATGACAGAAATATGTGAAATCTGATTTGCCAGAGTTACACTCTGCACTCTCCAAGCTA CAACAGTGCCACAGCTGAGAGGTTTCCCTATACTTCTACTACTGTGACAATTTAGCG/AJATCCTTC AAATGGGAAAATTCCTAATACACGAGACAATGGTCTCTACAGTAGGCCCG
WI-20572	75 A G ...	---	---	GAGCCAAACCCAAACAAAATAAACAGAACTCTTTTGTAACTAAGTCATACCTACTTTCTTCT TCAGAAATTJA/GJTCAAAACATCATCTTTTACAACATGGAGAGCGAGGTAGGCCATAATTGTTCA AATTCATCTTCTCAAATTTAAATTTGTTTAAATCCAAAGGTGCCTATTGAATTTCTTCAAAAATA AACTGCCTATCAGGTATCATACCTGCAATGCTTCTAATATCTCTTGATTAT
WI-20588	133 G A ...	---	---	CATGACAAAAGACAAAAGATCAAGGAGTAACATAAAATTAAGTTGAATAAATAGTATACAGCAATC TTCACTTTTTAAAGAAAATGTGAGATCCTTTGTTGGTTTTTATTTCTTAAGTACAAAATGCTAAACI G/AJGGAGCCGAGCTCTCCGCATTGAGG
WI-20593	79 A G ...	---	---	TGACCTCATACTGGGTTCTGGTTAGAACACAGCCACTAGAACAACTCCAGTCTTTTTCAGTCTGTTG CTGTACTTCAGI/GJTTTAAATCTGGGAATGAGCATGCAGCAATGCTCCACCAGATGAGGAAGAAA AGCTGTTAAAGGAACCTCAGGATGTTGTTAGGAAGGGGAGTGGATGCCAGGCTTCACCAGACTAT CCAGAAGCCATCCATGGGATTTGGTCTGCATCTGTGAGACACTGAGCT
WI-19765	57 T C ...	---	---	TTCTTTGCCAAGCCTGTTCTTCAAGTTATTCAGAACTGGGTGTATACCTTGCTCTCAI/CJATGTATCT TGTCCTGCTGCTTTTAGGTTAGCAAGGTGTATGAATACTTTTAAAGTTTGTGTTCTTTTCTCCTCGT GGTATCAGTGAATACTGATCTATTCTCTGGCTAGGGTCAATTTACAAAATTGCCATGGAACCTGAGC AAAAGGCCACGTTGGGATAAAATCACTACCATCGACGCCACCAAGTATT
WI-19066i	239 A G ...	---	---	TGACAAAGGGAGAGAGGGAATTTCTACTATTGCAAGGAAATCCTCAGTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTACGAGGAACCTGG CATATGTTCTTGGTGGTCAACCTGTAGCTGAATTAATCTCTCCATATCCGGATGCTCAATTACAGT ACCATTCGAGGCAAACTTTTCTTAAACGCCCTTCAGT/GJGTTCTTTTA
WI-19066g	184 C T ...	---	---	TGACAAAGGGAGAGAGGGAATTTCTACTATTGCAAGGAAATCCTCAGTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTACGAGGAACCTGG CATATGTTCTTGGTGGTCAACCTGTAGCTGAATTAATCTCTCCATATTCI/TJGGATGCTCAATTAC AGTACCATTCGAGGCAAACTTTTCTTAAACGCCCTTCAGTATTCTTTTA
WI-19066f	148 T C ...	---	---	TGACAAAGGGAGAGAGGGAATTTCTACTATTGCAAGGAAATCCTCAGTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTACGAGGAACCTGG CATATGTTCTTGGTGGTCAACCTGTAGCTGAATTAATCTCTCCATATTCI/TJGGATGCTCAATTAC AGTACCATTCGAGGCAAACTTTTCTTAAACGCCCTTCAGTATTCTTTTA

WI-19066e	147 G C ---	---	TGACAAGGGAGAGAAGGGAAATTTCTACTCATTGCAAGGAAATCCTCAGCTTAAGCTTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTACGCCAGTCCAAATCTCTACGAGGAACCTGG CATATGTTCTTGCG[G]TGGTCAACCTGTAGCTGAATTAATCTCTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAAGGCCTTCAGTAGTTCTTTTAA
WI-19066c	100 G A ---	---	TGACAAGGGAGAGAAGGGAAATTTCTACTCATTGCAAGGAAATCCTCAGCTTAAGCTTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCG[G]ATCTCTTAGCCAGTCCAAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCAACCTGTAGCTGAATTAATCTCTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAAGGCCTTCAGTAGTTCTTTTAA
WI-19066b	87 C T ---	---	TGACAAGGGAGAGAAGGGAAATTTCTACTCATTGCAAGGAAATCCTCAGCTTAAGCTTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTACGCCAGTCCAAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCAACCTGTAGCTGAATTAATCTCTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAAGGCCTTCAGTAGTTCTTTTAA
WI-19066a	72 C T ---	---	TGACAAGGGAGAGAAGGGAAATTTCTACTCATTGCAAGGAAATCCTCAGCTTAAGCTTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTACGCCAGTCCAAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCAACCTGTAGCTGAATTAATCTCTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAAGGCCTTCAGTAGTTCTTTTAA
WI-20660	105 G C ---	---	TTTACAGCGAGTTTTCCTGCTCAATAAGTATGAATCTAAATAGATTAGGGTGAAGAAAGAAAATGTG TGCTAAATAAAATCTCCCTTTTGAATGATATTTTG[G]TAAATAAGGGAAGCAATTAATATTA CAGACATATTTACAAGGTTCTGAACATGAGTGATTCCTACTGTTTCTGTACAAGATAGAACAAA AAGCTATCCACCGCCGCCAAATACTGTTTAAACAACACTATGTTTAAAGA
WI-18768	120 C T ---	---	CTGCTGCCAGCTTCTCTTGGCCCTGCTCCAGATGGCGTCTCCTGGCAGCCCTCCCTCAGTCTTCC TCCACCGCCTCTTCCCTCCAGCCTGCCCTGCATGCATGTGCACCCCTTGGT[G]TTCGGCTCCATCGCC TTGAAAGCTCTGAA
WI-19087	37 A G ---	---	TTCCCCAGGGTCTGTATTGCAGCTAAGCTCAAATG[T]A/TATTAACTTCTAGTTGCTCTTGGCTTTG GTCTTCTTCCAATGATGCTTACTACAGAAAGCAAAATCAGACACAATAGAGAAGCCTTTTCCATAAA GTGTAATTTAATGGCTGCAAAACCGGCAACCTGTAACCTGCCCCTTTAAATGGCATGACAAGGTGTGC AGTGGCCCATCCAGCATGTGTGTCTCTATCTTGCACTACCTGCTCC
WI-18790	49 A T ---	---	GAAAGCCAGAGATTAGCCCCGATTCGGCATCTGTCAACCAGGACAGAA/TJGCATGGACAAGGGA TGAGCTTTACAAGATGATGCACITTTGGAGATCAGAAAATTCATATTTAAGCAAAGTGATACAAACA CAGTGATTTGGGAATGCT
WI-18987	35 G A ---	---	AGGAGGCTGTTCCAGGAGTCTGCCACAGCCTC[G]A/GTGGCCCAAGCCAGACACTCACCCACCTT CCCCAGTGCCCCGTGGATCCTGGTCTAGGCTGGACACAGGATTCAGAAAGACACAGGCTGCACA GAAAGAGCCAGATGGACCTGAGTGTGGTCAACAGCCCCCTACACTCAAGGCTGAGAGGGCCTCAGGAA AGTCA

WI-18919	26 C T ...			TGGATGAAACCACAGGGATTCCGGAC/CTGGCAGACCCCATTTTACTTCACTTTCTCTACAGTG TTGTTTTGTTGTTGTTGTTTTATTTTTTATACCTTTGGCCATACCAGAGCTAGATTGCCCAGGTCT GGGCTGAATAAA
WI-18741c	64 G A ...			CTTCTGGTCAAGGCTTGGACATCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTC[G/A] CTGGAGTTCAAGCTTGAATTATATGCAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-18741b	38 G C ...			CTTCTGGTCAAGGCTTGGACATCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATATGCAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-18741a	23 T G ...			CTTCTGGTCAAGGCTTGGACAT/CTCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATATGCAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-19179a	170 G A ...			TCAGAAGCAGACATGGCATCTGTTCCCTGCTGCTGTTGGTTGTACCTTTACAGAGACCTGAATT TTAGAATTGCCAGTCTGCCAGAGTGAGTGAGTAAATCTCCTTTCAGGTAAGATAGGCTATCTC AACACTGCTGAGTGATTCATAAACATATCAACCA[G/A]TAGCATTAAACCATTTTATTCCTGTCCTT AGTGCTGAAGATGCTCACCAGTTTCTGTACAGTAAGGCAGCATGCT
WI-19212	46 T A ...			CCAAGTTGCATCCATGTTGATTTCTGATGAGACTAGAGTGACAGT/AJGTTTCAGAACCCAAATGT CCTCAGGTAGTTTGGAGCATCTCTATGAGATGGGATTATGCAGATGCCCTATGGAATGACAGCTGC ATAATTAAACATATTCAAAGTCTCTTACAAATTTATTTCCGACGATGTGACGTAAAGTAGACCCA ATGGGAGAGAAAAATGCCGTCTTCTTCCCTCTTTCTGCACTGCCATAT
WI-19183	210 G C ...			CTGTTGAAGGCTTCTCAGGCAAACTCCAGCTTAAAGCCCTAGACAGGTAAGGACACACATTGGATG GCAGCATGGTTCTTCCCATTTATGGGCATGAAATATGTGTTTGAATAAGGAACAAGCATTATT CCTTGGCAACAGCCTCACTTAAGAGGCTTTTGTGCTGAGTCAAGCAACACACTTGCCTGCTGCCCC CTTGGAG[G/C]TGGCATTTGACCTGCTCTCACTGGTAAGGTGACTTGGTGGC
WI-20014b	214 T C ...			TTGAAATCCCAGTCTCTGGCCCCCAGGCAGGCTCTGCACATAGATGTCTTCTCTACTGGGGTC GTTCTGGCTTTTGTAGAACTTGGTCTGAGATGTTCTTCCCTGTCCATTACCATTCGATGTTCTTT TGTTCAAGAGCAATGTTCTTGTATTCTGAACTGGAAACTGAACCAAGTTTGCCTTTCTCCTAGTCACC AAGCATACTT/CJTCCTGGCTCCCCAAGTACTTAAATGTTCTCATCTGT
WI-19041	198 T C ...			GTCTCCCCAGAGTCTCTGCACCCCCAGCCCTGTCTGCTGTAGGGGATACAGAGAAGCTCCCCG TCTCTGCATCCCTTCCAGGGGGTGGCCCTTAGTTTGGACATGCTGGGTAGCAGGACTCCAGGGCGTG CACGGTGAGCAGATGAGGCCCCAAGCTCATCACACCAGGGGGCCATCCTTCTCAATACAGCC/T/CJG CCCTTGCACTCCCTATTCAAATAAAATTAGTGTCTCTGCTGCTGT
WI-19135	20 G A ...			CAGTTACCTGCTTTGCCTC[G/A]AAAGTGTCAATTTGTATTTTAGTATTAACCTGTGTAAGT GTCTGTAGGTACGTTTTATATATAAGGACAGACCAAAAAATCAACCTATCAAGCTTCAAAAACT TTGGGAAAGGGTGGGATTAAAGTACAAGCACATTTGGCTTACAGTAAATGAAGTATTTTATTAAC GCTTTTGCCCATATAAAATGCTGATATTTACTGGAAACCTAGCCAGCTTCAC

WI-19236	54 GA	TACACAGAGGTCGCACTTGGACTCTGAGGGTTGGGTGTGGAAGGGGAAAGG[A]GATGGAGAC CTGCTCCCAAGCTCTTCTGTGACCCGGTTACATGGGAACAGGGTTAATCTGTGTAGGGAGGT CACCTTACCTTTTTCATAGGGAAGAGTGTACACTCTGCTGCTATCTCAGGGGAATGGGAAAG AATCTTCAAGGGCAAGAACTCGTGGGAGGATGCTGTGTATGTAATACT
WI-19144	222 GC	GTCCAGTCTTCCAGAAAGCAAGACTGCCCTTCATTCAGCCTTGTGACCTCCAGCCTTCTAAGG CTCAGCCCCAAGGACTCTGGTGGCTGCCAGCTTGTAGCTATCTATCTATTCATTCATAGCCAA ACAGGAGACCCCTTTCAGGACTTGCAGACTTGCACACAGGAGGCTGTAGCCAGGAACCCCTCTTCCCTGGT CTGGCTCTGCTGGAGCGG[G]CTGGGAACCAACACCTTCAGTGTGGTG
WI-19139b	110 CA	CCCGTCTAAGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACGTGATTTACACGAGGGTAGAC GGCAGATGCCTGACAGAGAGTGGGTTGGCAGACAACACACTAG[C]AATTTACGGGTGTGGGCAC ATGGGTGTGGCACCTGGACGTGTGCAGCATGTGGCGGTCTCTGTGTGAAGCCACCGTCTCTCTTGG GGGCCGCGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG
WI-19139a	66 CT	CCCGTCTAAGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACGTGATTTACACGAGGGTAGA[C]TGGCAGATGCCTGACAGAGAGTGGTGGCAGACAACACACTAGCATTTTACGGGTGTGGGCAC ATGGGTGTGGCACTGGACGTGTGCAGCATGTGGCGGTCTCTGTGTGAAGCCACCGTCTCTCTTGG GGGCCGCGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG
WI-18910	112 TC	GGCTGGGACCTTTAGGAAAGTGAATGCAGGTGAGAAGAACCTAAACATGAAGGAAGGGTGCCCT CATCCAGCAACCTGTCTTGTGGGTGATGATCACTGTGCTGTG[C]GGCTCATGGCAGAGCAATT CAGTGCCACGGTTTAGG
WI-19235	173 AG	TTCAGGAGGTGGAGTTCGTGTCAGCTCTCCTGCTGTGATGTGGAAGCTTCTGATATTGAAGAAACA CGAATGTCTGTAGCTTCTCTTCACTGCCCCAGTATTGCTGTGATTTATCAGCGATGCCCTCTGT CACTCATGCCCTTGCCTAATGTTTCAAAATGGTGGAA[A]GJGCTTCATGTAATATGATCAGGACCCACC TCCAGTTCTTCTGAAAGTGTGACAGTGTCCAGCCGGTTCTGCAGCACTA
WI-19222	179 CT	CGTTTTCCCTAACTACCCAGTTTAGTTGGGATGATTGATTTCTGTGTTGATCCCATTTCTAA CTTGGAAATTGTAGCCTCTATGTTTCTGTAGGTAGTGTGTGGGTTTTTCCCCCACCAGGAAGT GGCAGCATCCCTCCTTCTCCCTAAAGGACTCTGCGGAAC[C]TTCACACCTCTTTTCTCAGGGAC GGGGCAGGTGTGTGTGTGTACACTGACGTGTCCAGAAAGCAGACTTT
WI-19117	134 AG	AAATATGCAACGCGAGGAGGAGAAAGAAATGCACCTAAGACAAGAACATTTCTCTCATAGAACATTG ATCTGTTTACAGGAAACAACCTTGCCTTGAATTTACACAGTGAGACTGTACATAATTGCATGAA A[A]GJTAGCTATTTTTTCTAAGACATTTTTCATTCATGAATTTTCAAGTTTTTTCATCTGTACA CATTTCTTAAACACATGATACCAGCAGCAACTGAAATGAATGCCGAATTTG

WI-19134c	263 C T ---			CTCCTGTTGTCGACCTGACAGGGTGACACAGCCCCCTTTACACTCTGTCTCCTCTATCTTCTCTGGGTAGA TGCCCTGGGTAGGGCTGAGTACTGAATGGTCTTCCATCCAGCAAGGGGTGCAGCCAGGGTCTCAG GCCCTTCAGAGCCAGGGCTAGAGGATGACGGTGGCTAGAGCCAGCTGCACATATCTTTTCAGAGCAC TTCATCCACTTGTCTCCTCTACCCCTCGGCACCCCTGGGTGGAAAGGG
WI-19134a	162 T C ---			CTCCTGTTGTCGACCTGACAGGGTGACACAGCCCCCTTTACACTCTGTCTCCTCTATCTTCTCTGGGTAGA TGCCCTGGGTAGGGCTGAGTACTGAATGGTCTTCCATCCAGCAAGGGGTGCAGCCAGGGTCTCAG GCCCTTCAGAGCCAGGGCTAGAGGATGACGGTGGCTAGAGCCAGCTGCACATATCTTTTCAGAG CACTTCATCCACTTGTCTCCTCTACCCCTCGGCACCCCTGGGTGGAA
WI-19224	112 C T ---			GGTTTACCAGTCTTCCAGGGAACCTCGATGAAGTGTCCAAACAAATGAGCGAGTGAACCAAGA AGAGGATGACATTAGATCCAGGAGATACAAAGAGGAGATAATCTCTCAGGATGCCTGTGAAGA AAGATCCCTGGATCCAGGATGATTATAGGACAAGTTGTTCATAATCCAGAGGCCAGAAAGACTTCC AGGGAACCTCATTCAAGGAGGTGAAATGATGGATGACTCTCCAAAGATGAAAA
WI-19201	179 T C ---			GCAGCTCCTAAGGACCCTGGCCATTAGCTCTTGCTTTTGATGGCATTCTTTCCACCTTGCTTCTC CTTTGCTCCTGTGTAGTGTGGCAGGTATGACAACTCCTCAGTGGAAACACAGCCCTCAGACTGCC CTTCCGCCCCCACACTTTGCCCTGCAGGTGCACCGAAGGAC/TCTGGGGGATAAAATTCAAAAAA GTGTGATGTGCTGCTCAGAGGTGACACTCCTGCTGCTTGGCCTCAA
WI-19034	45 T C ---			GAAATGGCTCCACTCAGAGCTACCCGGTGTAGGATAGGGGAAT/CJACTTCTATTACATTAAAG GCAACAGCAGTTAGTAAAGGTTTACAGTGTCTTCTGCTGTTTGAAGTGCAATATAAATTTTTTG CTAGCCCATGATCAATCGACTTCTATTGTTTATATACACTCAGCATTTAAGTTCTGTCGAATTGAC ATTTGCTACTTATAAACTTAGTCCCTAAGTCTTCTTATGCTGTGCTATATA
WI-19102	25 C G ---			TGTTCTGAGTCACGCTGAGGAGAG/CJCTTCACTCAGGAGTTCATGCTGAGATGATCATGAGTTCA TGCAGGTATATTTTCTTTGGAAACAGATGAAGCAGAGGAAACTCTTAATCTTAAATCGTTCT TGATTAGTATCGTGAGTTTGAAGTCTAGAACTCCTGTAGTTTGAAGTCAAGGGGAGAGGTAT AGTGAATGAGTGTGAGCATCGGGCTTGCAGTCCCATAGAACAGAAATGGG
WI-18548b	65 A G ---			AAAGGAGGGAGAACTCTTTTACATAAATGCCTTGCATCATCCTCCAGTCCCTCCTCAGTGGGAA/A GJAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18548a	62 G A ---			AAAGGAGGGAGAACTCTTTTACATAAATGCCTTGCATCATCCTCCAGTCCCTCCTCAGTGGG[G/A] AAAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18700	97 T C ---			GGCAGCAGCTTTTTTAATTTGAACACTTCTTCTTGAGGACACACCTTCAGTACAGTTAACAAATGGT TACACCTGAAATCTGCTGAGAGCAGAGCTT/CJAGATCCACAATTGCAAGGCCACTGCTGGCTCA CTTCTCTACA
WI-18501	121 C T ---			CAGAGGGAAGTTTATTGAGTCAGCCACAGAGGAACAGAGAAACAGACACAGGAGGTTCTGTGT GCATGGAGGAATCAGGGCGCCGNACAGCTGAACCTCGCAGGACAGAGGGGGC[C/T]GGACAGCA GCGCATGCGACAAACATTCA

WI-18017	87 C A	ACAAAGAAATGGAATAGGTTGCGAAACCTTATCTGCATGTACAAAGTAATCCCGTAGATAA GGAGAGCAACCCNGGAACA[C/A]ACTGCTGGATAAATCGTTCAATAAAATTATATCTCTTTGCAT CAGAGCTGGTGGAAATCAT
WI-18148b	101 A G	TTATTGCGTCTCTCGATAACCTCTCTTTGGGACTATGAGATCATCACCAGATGTGAAACGAAAGCA GTGATTTAGAAACCNCGATTCTGAATATCC[C/A]GTGGCGCATATGCAAGGAAGATGA
WI-18254	64 T C	TATACGGATCATGTATTTGTGTGACCACTACTACCAGTCAATTTGTAGAGCAGTTAAATCAC[T/C] GCCAAATTCCTCTCTGCTTCTGTTAGTCACTCTCTCCAAACCCAGGNACTTGGCAACCTGTTT TCGGTCTCTAGACATTT
WI-18265b	117 C A	CAATGGGTGGACTGAGTGATAAAACGCATATTGAGAAACAGACGGCCTCTGGCCNCTCTGCGTCC AAGGCTGTAAAGGTCTCAGGATTGCTGCTAAGTGAGCCATGAACCTGGCTG[C/A]GTTTTCAACCTTTTC CTTGGGTGGTTCTTCAG
WI-18295	40 C T	ACCACACATTTGTTGAGAGCCTATTGTGGAGAACAAACAG[C/T]TTGGGAAGTAAAGTTGATTACT TCCTCTCCAAGGATGATATGTTTAATGAATCCCTTNCCTTAGCTTCATTCTTCATAATGCCAAA
WI-18459b	64 T C	GGCAAGAGACAGAGATTTAATTGAATAAACTCCAGGCTGTGACACGGTGGGAGACACAAAT/[C]GAGTAATTAACAACATAATTTTANATGACAGTGCATTAATTAACGCTCCTGGGTAAGCCAGAG GGGAGGAGGGCGCTTTCA
WI-22585	56 A G	TTTATTTAAATTTGCATCCTGAGATAATAAAATTTATCTGACAAGTGAACAAATG[A/G]CAGAAGC AGCAGTGAAGTTTCGGAGAGGCGAGGTATCCTTCATTTTGGCACAGCTGTATATAGATTGA
WI-21155	36 A G	GGCTGTGGAGTAACAGAACTTGATGGAAAATGG[C/A]GTTCTGTGTAGATGATTCTAAAGCTTTTC AGACAAATGGCAGA
STS-F02766b	88 G A	GCCTTTGCTCTTTGCTGCTCAGAGGCCTCAGATGGATACGAGCAACTTCCTTTTGAACCTTTTAT TTTCTGGCAGGAAGA[G/A]GGATCCAGCAGTGAGATCAGGCGAGTTCTGTGTGCACAGACAG GGAAACAGGC
WI-19888a	98 C T	GGCAGGATCAACCCATAACAGAGAAATAACTCCTTATTGGAAACAAGGTTTATTTTGATATGATG AAAATATTTGGAACTAGAAAGTAGCAGTGA[C/T]TGGACAACGTTGTAAAGATATTAAATGCCACT GAACTGTTCAATTAATGGTAATTTTCATGTTATGTTGATTTTCCACCTCAATTAAGAAATGGAACATGT CTTATAATTGTAATACATGAGANCATATTTATGTTGGAAGTGAACACAAG
WI-21485	82 C T	TGAGACCATCCTCCTCAACAAAGAATCAGTCAGTTCAGCACCTAATTTCCACACTGAAGTCTACG CAATTTTCATGCAGA[C/T]TGTGCACACAGTACAGTGCACAAATCCAGAGGGCAACACATTTGTAATT CATATCATCCGTTTCCAAA
WI-20601a	125 T C	TCAGAATTGCTTCCACTGCCCCCAACCAAGAAATTTAATGAATGCNCTTACAAATGAGATGACTT GAAGTTAAAGAAAGGTACCTTCCTTGGAGGTTGCATGACAGGATTAGTCTCTGTTT[C/T]CTTGGT GCAAGTTTGAACCAAGTATATGATACCAATTCATCAGAGCATCTGTTCCCTGTCAGATCCCCACTAG

WI-20561b	94 T C ---	---	CGTTGCTATTTAAGATGGCTGTTTATAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATTATTG TACTTCAGATGAAAAATCCTTACATGTC[G]GGAATCAATGTCTTTTAAATTTTCAGATAAAGAAATTT NCATTTGAGGAGACATACAATTGTAA
WI-20561a	25 A G ---	---	CGTTGCTATTTAAGATGGCTGTTT[G]TAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATTAT TTGTACTTCAGATGAAAAATCCTTACATGTGGAATCAATGTCTTTTAAATTTTCAGATAAAGAAATTT NCATTTGAGGAGACATACAATTGTAA
WI-20116e	69 T A ---	---	GCTTCATTTTCTGTCACCCACCCTGTCCACAGTTATGTTGGCCTTCAATATATGGCGTTAGAACAT AT/AATAATCTATATCATATATTTATACACACAAACACATCTTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCTCTCCCATGCCACTTAAAAATGNGCAGAGTTTGTCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI-20116c	59 T A ---	---	GCTTCATTTTCTGTCACCCACCCTGTCCACAGTTATGTTGGCCTTCAATATATGGCGTT/AJTAGAA CATATATAATCTATATCATATATTTATACACACAAACACATCTTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCTCTCCCATGCCACTTAAAAATGNGCAGAGTTTGTCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI-20116a	22 C G ---	---	GCTTCATTTTCTGTCACCCAC[C]GCTGTCCACAGTTATGTTGGCCTTCAATATATGGCGTTAGAA CATATATAATCTATATCATATATTTATACACACAAACACATCTTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCTCTCCCATGCCACTTAAAAATGNGCAGAGTTTGTCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI-20466b	133 G A ---	---	AAAGATTGCAGTCCTGGGACACAGTTTGGAAAAACACTATTTATAAGGTTGCACATATTACAACACAG NTCCCAAATGGTGAACTGGTATTTCTAAGATGAAAGCTTAATGAACATAATGAAGTGAATAAACGC[C] G/AJTGTAACATAATGTTTAAAAAGTTAGAGCTTGCTCAAGTCAGTACAGCTCTTAAGATAATAAAT ACAGTAACACTACTTTTTATTTCTTGTCTTTTATCCCTTTTCAGGTTGATT
WI-21444	39 A G ---	---	CTGGGCAGCAAGTAACCATTTTAAAGAAATACTCTCAAC[A]GAGTCTTTTTTATGGGGTATTTCA GTTGTTAACAAGTTAAAACTATTGGAACATAATCTTTGTATTTTATTCGAGGAAGAAGAAATCT ATAAGATTGACTTACTCATTGTTGACTGGTTTTTTGAAGCCTTACTGGGG
WI-21034b	148 T C ---	---	AGAATGGACAATGATGCAGATGATTGTGAGCATTTTGTAGAGCAATTTGATGAGAAAGTGGTGATTAGAAGGATACAG CATAAATTTAATTGTAACATGCTTATCTAGCTAACCTAATCTGTTCTGTAGAATTAAGTGGTCTGAGG GAGATTGGATAGAT[C]GGCTAACCTATCTCAATTTTAAGTAATGTGAGCAA
WI-22091c	205 G A ---	---	GGCGTGTATTGATGCAATGTCCAACCACTCAAGCTATCATGAAATCCAAATATTTCCCACTAGAG ACATGCAGAGCAATGTCAATGTAACTAACAAGCATATTACCTCCCCCTTAAGTGAAGTCAATAATTC ATTACTGTGTGTAGCTTTTAAAGGTTTAAAAATGTAGCAATTAAGTGGTATTTTACTTGAGGGCA ACA[G/A]AATACGGCTTAACAACACACTAATCATGAGGCTCAGGGATTG

WI-21805a	45 A T ...	---	CAACTGCTCTGAGGCTCTTCACTAGCTGATTTATAATCCTATATTATJAAAAAAAAAATCTATAGTCTG CAGTCTTTTGACATACTTCTCAAGGTGGATATGTTGGTGAATGCAGACTCCATCAATATGTGTGGTT TTGTTTGGCTTTTGTAGCTTAAGTCTGTTTGNAAATCCAGAGGAATATGATTGAGGCCAGAGTTA CATTGGTTCATAAAATTCGAACAGTTGAAGGCTGTTTTGTTAATTGCTG
WI-21778b	155 T C ...	---	AAAAATCCATAATTATTGAACCCAAAGTTACAGAGAAAGTTGTAACCTTTTTTATTGAATTATTGAC TCTGCCCGGTGTCTGCTGCTTCAACTCCAGTCTGTCAATGCCCTGTAGGTGGGTCCCCAG GTCTGGGCTTCTGAGGTCCTTCTGCTAGAGGAGGAGGAGGCTGGT
WI-20907	241 A C ...	---	TGAGTCAGTGGTCAGATGGGCGAGTTGCGCTCAGCTGCAGTCCCTGACTCCGGAAACACTGTGCTCT CAAATGATCTAGAGCTCATCTTGGCGGTACATGAGGGCGAGTTGTTCTAGTACCCATTTAGCCC ATGGCTCTTCAAGCCAAATTCACACTGGGAAAAACACACCCCTCACAAAGATGCCCTATCCATTTGAGTTC ATACAGGTTTTAGTAGCTAGAACTAAAAAACATTTTTTA[A/C]AATTATCTA
WI-21449b	222 C T ...	---	AACAGCAGCAGTCACCTCCAAATGCAAAAAAATTACAAATTTTAGAATAAAATTATAATGTTTA TAATGGGGTTCAGAAGANTTGAAGGTACAAAGATCAATACGCGCACTGGAGCGGCTGGAG AAGCCAAAGCCCACTGGTCAGGGTCCAAAGCTGACAAAGTCCCAACCTGAGAGGTCTCCACACCC AAATCATACCCCTCAGCTTCCCA[C/T]TGACAGAGCCAGTGTCTCTGGGTTAG
WI-21558a	157 G A ...	---	GCTTACAAGGAAGCCTGTGGACAGCGAGNTGGTGGAAACCGACTCCAGCTGGAAAAACCTGCCCTC CCATCCCTTAGCGCTTCTTGGCTTCCGGCTGATTTCTGACAGAGTTCTGGCCAGGGCAAGG AGCTGTGGTGGGGGCGAGTATG/AJAGCCAGGGACTCCCTTCCACAGATGAGGCTAGGGCTGCAA AAGGGCCCGGTGAAAGAGAGATGTGGTCAAGGCTTTATGGGTCTCTCCACC
WI-22187b	178 G A ...	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGCGGTGGCTAGCAGAGCTCATGNGACCA GTCCTGGGCTGACCAATGGGTGATTACATTTAAAAACCAAAACCAAAACAAATACCAAGA ACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTG[A/A]AATTTTCATGAAAAATTTCC CCTAAACCATAAACAAAACTGTCTCTTACCCCAAAAGTGTGGAGGAAAG
WI-22187a	110 C A ...	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGCGGTGGCTAGCAGAGCTCATGNGACCA GTCCTGGGCTGACCAATGGGTGATTACATTTAAAAACCAAA[C/A]CAAAACAAACAAATACCA AGAACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTGAAATTTTCATGAAAAATTTCC CCTAAACCATAAACAAAACTGTCTCTTACCCCAAAAGTGTGGAGGAAAG
WI-21809b	148 G A ...	---	TCATGAATATGCAGCCTCCATAATCTTCTCCCTTGTAAACACGTGCAGTCCGTTCAAGCTGTAAA AACAAGCCCAACCCAGACATCACAGAGGCAAGAGCAGTGGCAGTGAGAGGGAGCCTGTAAAG GATGTTTCAAAG[G/A]AGGGTCCCGGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG

WI-21609a	42 C T	TCATGAATATGCAGCCTCCATAATCTTCTCCCTTGTAACAAA[C/][GTGTCAGTCCGTTTCAACAGCTGT AAAAAAGCCCAAAACCCAGACATCACAAGAGGCAAGAGCAGTGGCAGTGAGAAGGGAGCCTGTGA AAGGATGTTTCAAAGGAGGTCGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGCTGAGACANTGGCCAAAGAGGAGTTGGAG
WI-22512a	104 T G	ACATTCGAGCCAGTTTTTCCATATTGCTCCACTGCCTAAATCCCTTGGTGCCTCCCTAGGGCTTCA GGGTAAGCCCTGACATCATGTCCTTTGTGATCTGTG/JACCTCACCCATGTCTCCACCTNAGTTCC CACATTTCCCCACGCTAAGGGCAGGCAGCTACACTTGACTGCA
WI-21028b	139 A G	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGCCCTTTTAAAGGGCTCA CAACACTAAAGATTTACATGAAGGGTGTGATTGATTGAGCAATCTAGGGGATGTGACAGGGG TTTC/JGJTGCACTGGTACAGAACACACAGGGAGTTTCACAATTTTTTTATACAATGCTTGGGAAT CTACGG
WI-21028a	121 A C	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGTCCTTTTAAAGGGCTCA CAACACTAAAGATTTACATGAAGGGTGTGATTGATTGAGCAATCTAGGGG/JAC/JTATGTGACAG GGGTTTCATGCACCTGGTACAGAACACACAGGGAGTTTCACAATTTTTTTATACAATGCTTGGGAATC TACGG
WI-18829d	58 A G	ACAACTGCCTGTTACAGGGGGAAAAATCCTAGGNAATAACTTATGTGTACTTCTTG/JGJTTTCA TCATAAGACAAAGCACAAGCACCACCCATGCCTCTGAGGAACATTGGACCATGCACCCCTTGAAA AA
WI-18829b	35 T A	ACAACATGCCTGTTACAGGGGGAAAAATCCTAGG/JAATAACTTATGTGTACTTCTTGATTCTCA TCATAAGACAAAGCACAAGCACCACCCATGCCTCTGAGGAACATTGGACCATGCACCCCTTGAAA AA
WI-20964	87 G A	AGCCAACTCAAGGCCAAAAAATTTCTTAATATAGTATTATGCGAGGGGAGGGGAAGCAAGGA GCACAGGTAGTCCACAGAATA[G/A]GACACAAGAAACCTCAAGCTGTGAGGTCAATTTGTAAATTA AAGAACTAAGATTAGATGAACACACACTCAGAAATACTCTAGGAGAGCTGAAAAAAGAAAGAAC AGATGTTAACAAAAACAATTAAGGCTGCTGGGGAACCTGAGTCCATGTTAAGCTTG
WI-20059a	59 T A	CTCTGAACCTAAAGGGCCGTGAAGGCATGATTGGTTTTGGCACACAGAGTGGATAACCAAT/JACAT TGGCTGGAATGAGGTGTCAGGAAATAAANTGCACAAATCTAACACCATGTTGAAATCATGTCTGA GTTCTGGAGAAAGTTAAGGTAAATAATTACAAAGACTGACATGCAACTCTTACCTTACATTATT CATCTACAGACTATTTCTCCCTTAGGAGATGAGGAGTATGGGCCCTTAGGT
WI-22130b	165 C T	TGTTTTTGAGGGCTGTAGCAGACTACATAATGAGCGGTGAAGCGGCTGCCCTTCCCTCTCCTGACAC CAGCAAGGGGGAGGCACCATCACGGCCCTGCCCATCATGCATCCATGATTACTAGCACTAGGAA GCCAACGGGAANAGACCCCGGCGCTTGCTC/JGJTGTTTAAATCCAGGTTAAGCTATACACGTTTAA ATACATGTCGGAGGTTACATGGTCTCATGCAAGTCCCTGTGATGGGAATGAC

WI-21681	117 G C	GCTAGTCTCCACCCCTTTAAATGTACTCTAGGTACAAAATAAACATTATACACATATAAGATCAGTCTTTCCAACTTTAGAAATGATAAATAAGAAATGACATTTTAAATAAAATA[G/C]TTTAGTCACAGTCACACAAAACCTACCTTCTAAGGAAAACGTCCAGTGAAGCCGTTAAATTTGTGCTTTCAGCTATGAAGGA
WI-21980a	25 T C	TCAGTTTAAACACATTTCATCAAGGAT/CJAGATTAAATTAATGTGAGGTGAGCATAAAAGGGAGATTATAAACAGAAATGTGTTTCTGGGAACCAAGTTTCAAGTGACTCAGGATAAGTTTTTATTAAATTTTCATGGTGAAGCCCTGGGATAAAG
WI-21636	71 A G	TGCTTGATTAAATGTGGTGTACATTATCCTATTTTCACAGATGGAACACAGAAAATACCAGCTTTTTAA[A/G]TAGCAATATCTATTATAATAATATTGAAATAACACCATAATAATATCATCTAAAGGAAGTAATCTAATGTGTGATTTTCAGAGAGGGAGAAAACATTACCTCTAGAGCTAGGCTATTGTGC
WI-22457a	112 G A	TCATGCAAACTCCAATCTGAAGGTGTAGAACTAGGAAGGGACAGGGATTTC
WI-21524b	97 C T	TTGCTATAATTTCTTAAATGCAAAAGAGTACATCACAGCAGAGTATAGCCAAATCACTCATTAGACAACAGTAAACATACTGGACACGGTTTCAGGCATGAAGGATACA[G/A]CAGTTAATTAACCTAAAGGAACAGAGTCCCTGCATTCCTGAAGCATAGGATGGGAAACAGTAATGCAGATTAAATACCTGGGGCCAAAACCACTGAACCTCACCCAGCTGAAAACACTGAAGGATACCTGGGTAAAGGA
WI-21524a	35 A C	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAATAGCCTGATGACGACCTTCGCGTCATCTTATAATGGTTAATAACAGCATTCCTGTCTACCC[C/T]GATGATGCTTCTCTCTGCAATGGACTATTTGCCAGTTGCAACAGGGCTAAGATTGTGCACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTCCTGTCAGAAAGATTCTTGACTTCTCCAACTTCTCCTCCAGGGGATG
WI-22652a	32 G T	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAAT[A/C]GCTGATGTACGACCTTCGCGTCATACTATAATGGTTAATAACAGCATTCCTGTACCCCGATGCTTCTCTGCAAAATGGACTATTTGCCAGTTGCAACAGGGCTAAGATTGTGCACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTCCTGTCAGAAAGATTCTTGACTTCTCCAACTTCTCCTCCAGGGGATG
WI-21703d	197 A G	TTACCTTCCAAACCCAGGCCACTTTGGAGAAAG[G/T]AAGAGAATGCTATTATCAATAAGCCAAAGACAATAGGGGACTACCTGGGGTAGACCAAGATGGGCAGTCACCATACACCATCATCTCTGCCACAGAACC
		...	TTTGACATGCTGCCCTCCCTACTCCGCACTCACCTGTCTAATTTGGACCTGAAGCTTCAGCATCCCTTCTTAGGG
			CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGGAGTGGTGGTGGGCGAGGGCTCTGCATCCCCCTTCTCCTCAGCACAGCACCATCTTCACCCTCCTGGGAAAGCAGCATTTGGAGCCTACACCACTTGTCCTTCTCACCAGGGTAAGAAATGCAGGTATTTGCAGAGGGGAGTGAGTCTGGGA[A/G]GTGGGCAGAGCACAGCTAGGGGCAAGGACTTAAGGGAACITTTGGGGGAAGAG

WI-21703c	134 A G ---	---	CAACAGGCTCATGGAACAGAGCCCTAGGGATCCAGGAGCATAGGAGGTGGTGGCTGGGCGAGGGCTCTGCATCCCTTTCTCAGCACAGCACCATTCTCACCTCCTGGGAAAGCAGCATTTGBAGCCCTACACCAAGCTTGCTTTCTCACCAGGGTAAGAAATGCAGGTATTTGCAGAGGGAGTGAGTCTGGGAAAGTGGCAGAGCACAGCTAGGGCAAGGACTTAAGGGAACCTGTGGGGGAAGAG
WI-22663c	139 G A ---	---	CCCTTGTCAGTCTGTGCCTCGGCTTCTCACTGCACTGGCAGGTAGCCGGCGCTCGCTAATCTTATTCOCAGTCTCGGTGAACATGGGCTCAGTCTCCCGGCTCAGTGTGGGTTTGCAGTGGTGCACCTTACAGGC/GA/GAAGAGCTTCCCTCATTTGCTGAGGGCTTTCCCTGAATCCGCTGTGAATGTGGGT
WI-22663b	55 C T ---	---	CCCTTGTCAGTCTGTGCCTCGGCTTCTCACTGCACTGGCAGGTAGCCGGCGCTCGCTAATCTTATTCOCAGTCTCGGTGAACATGGGCTCAGTCTCCCGGCTCAGTGTGGGTTTGCAGTGGTGCACCTTACAGGCGGAAGAGCTTCCCTCATTTGCTGAGGGCTTTTCTGTAATCCGCTGTGAATGTGGGT
WI-22663a	38 C T ---	---	CCCTTGTCAGTCTGTGCCTCGGCTTCTCACTGCACTGGCAGGTAGCCGGCGCTCGCTAATCTTATTCOCAGTCTCGGTGAACATGGGCTCAGTCTCCCGGCTCAGTGTGGGTTTGCAGTGGTGCACCTTACAGGCGGAAGAGCTTCCCTCATTTGCTGAGGGCTTTTCTGTAATCCGCTGTGAATGTGGGT
WI-22668	99 A G ---	---	TCCTTTATCCTGCTGCCTGCCTGAGTATCTGGGAATCCTACAAGGATTTGAGGGAGGCCCTTGGGATCCAACTTAACAAATAGTTTTCTGTAAATATT/GJTTCTAGTCCATTTAGATTGTGTAAATGATCTAAATGGNGTAACCATTTAATATCAAAAGTATAACAGCATTTAAGTCAGCTTTTCGAAGAAACTTTTATT
WI-22631a	52 T C ---	---	AAGATATAGTGGCAGGACAAGATTGGTCACGAAATCCTGGCTTCAGTTCGATJ/CJAGCACCATTTTCAAGTTTTAGGCAAGTATTTAACCTCTCAGGCTCATTTTCTCTTTTGTAAATTTGTGATAATGGACC
WI-20258	157 G T ---	---	TATGTACCATCATAGGGTACTTGGACAAATCAACTGAAATTTTAAATCCACACTTTTCAAGGAGGGGAGCCAGCTGCATGCTGCCAGGCTCACAGCAGCGCGGCTACTGTGCTGGTGGTTTGGTGGCAGGTGGAGATGGTGACGGCGATTGGAAACCGTAAGGCATGACAACGGAGGCGCGGGGTTTCAG/GTGGGTTGACGAGGTGCATGGCTGGCAGCGGCGCTCTACAGAAGGAGGGAGCGCAATTCACAGCCTCTTGACGTAGTTCCGGGGAAAGTACC
WI-22714	212 C A ---	---	ACTACACATATGCTGATTTTCAACAGTAAAAATAACATTTTACATTTGTAGAGAAAAATCTAGGGTCTACTAAATAATCTAGTACTTGTTCCTGCTCCTGCTAATCTGACAGGAGTGTGTGGGAAACGAAAGCTGTAAGAGGATTCAAAGGGGCTAGGATTTGCCACAGATCCTGTAAAGGAAAGGATGAGGTGAGCTTACCAACCCCA/CATGTAGTAGGGGCCAAACATCCTTAACAAGCTAGTTGCT
WI-22734b	44 G A ---	---	TGGGGCTACTTTAGATGGGATGGGCTCAGGGTCTGGGAAGGCCCTG/AJCTTTAGAAGACATTACCCCAATGATGAGAGGCCAGTCGTCGAAGCCATAGTTTGGATGGCGAGACTTTTCCGGCAGAGGAAATAGCAAGTGCAAGGGCCCTGAGGGAGAAATGAACCTTGGGCTTGTCTACAGGTTGAAAGCGGCCGGTNTGGCTGAGGTTTAGTGATG

WI-22724	117 A G	TGATATGATGCTGAGATTGCTTCCAAATATGCCTAGGAAGGGAAGTGTTAGAGATATAGGA CAATCAAGATTGTCAAAATGTATAGTAAGCTGTTAAAGCTTCTAAGGGT[A/G]GTTATTCTATTTT TGGGATATGTTGGGAATT
WI-22750	48 G A	TGTAACCTGTGTTTCTGAAAGTTGAGGGAAGCTGAGGCAGCTAAT[G/A]GGCTCATACAAAGGT TTGGAAGACCCATTCTGACTACCTACCTAAAGGAGAGTCAGCATTTCTGACCATTTCTGACTGTGCT
WI-22775a	60 A G	TGCTGTTTCTTTAGTTTCATGACGTTTATCACAATGTGCTACTGTTCCATTGTTTACATC[A/G]TAGTA GGAAAGGGGAAATAAACTCCCTAAGGGCAGCAATAATTTCTGCTTTGAATCCTTCAATCAGGCAAA TATTTGTTGAGCACCAAGGGCCAGATGGAACTGAGGTATGTAGGTGTTGGAGCCAGGAAGGAAG GGT
WI-22808	143 C T	CTTTAGCTAATGAAACTGGCTATGTGGACTATGATAGACCAAGAAAGCTACCCAAAGTCCTGAGGGAG CCTAGTCTCTCTAAATGCAGACAATGTACCCATGACAAGGGCTACAGCTTGGCTTTAGCAACCAAGGA GGATGAAGA[C/T]AGCAAACTGATTAAAGAGAGTAGGTATAAGAACCAAGGGAGAGTGGGGTCCAAAT ATC
WI-21016	207 G A	TCTCTGCTGCTTGAGCCCTCATCCCCACCCCTCCAAGCCCTCATGCCACCAACACCCGTGTCACAT CCCCATCCTCCCTGTCTGCTCCCATCTCAAGTCCAATTCGAAGCCAGAGCCCTGGCAGCTTTCTG GGAGACAGCATGAAAGGAGGGAGTGAGATGGCAGAGATGGGTGGAGCCAGTGGGCTGTGGGTC CTG[A/T]TGGCTGGTGATGIGGGGGCCAACTCCTGAGGCCAGAGTTCA
WI-21031	31 C T	TTGAACACCTGACCTGACCTCTGACATGTGG[C/T]CTCTGTGCCCAATTTGTCTCCAAGGTGGCACA TCTTCATCTTTGTTATATATCTGCAGGAACACTCAGTCTCTTCAGCAGCCGAGAAACACACACA
WI-21314	122 A T	CCATATCCAGTCTCTTTGAAGCTTTCTATTGACTTTTAGGGTTCAGTTATTATATCCTTTTACACTAT GACTTTTCATTGATTTTATTTGTTCTTCTCCATTCTCTGTCAAACCTTTTC[A/T]TTTGTATAA ACTGTTTCTAAACTTCACTTAATTCCTATCTGTATTNCTGTAGTCCCTGAACTTCTTTAGAGG
WI-21186	95 G A	AGCGAGCATCAGAAATCACCTAGAGGGTTGACTAAACAGACTTCTGGACCCCAACCCAGAGCTTCT GATTCAGTAGGCTGAGGTGGGCTTAC[G/A]AATTAGTATTTCGAAGACCTTCTTAAGTGTTCAG ATGCTGCTTGTCCCGGGGAACACACTTTGAGAACTATTGTTCTAAATGTTCTCTCTCTTTTAA GGAGAGACAGGAATTCAGAGAACTGCTAATTTAAGCATAATGTATTGAAT
WI-21187a	94 A G	CCACGATAACTATAAAGCAGAAAAATTAGCTTTGAAAAATCAATAACATATTTAGTAACACACATT CATTTTATAACACACATAAAGACACC[A/G]GNTCTCAGTAATGCTCTAGTCCAGGGTTCTCAA AGTATGGCTTCAGACAAGCCCCATTTGCATCACCTAGGGGAATTGCTAAATGCAGATTCTCAGGCC CTACCTACTGATCTACTGAATCAGAACTCTGAGGGTGAGACCAAGCAACCTGT

WI-21190	39 T C ---	---	TTTCCCACATACCAATGCACCTGTTGTATAAACTATTGCTGGGGTAAGCCCTTCTTTGGAGAC CAGTGACATAGACATGATCCCATTAATATATTAACAAATAATTAATAATCTGTACTATTACTGC TTTAGTTATCTAGTGTATTGAGAAAGGAGAGTCAGCATAGTTATTTTCCATGTAATAAAAGCTT AACACA
WI-19937d	186 G A ---	---	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAACTTGAAGGAAA GAACTATTGCACAACCAACCAATGTACATATCTGATTAGACAAGCAAAAGCACCTTCATGTTGTCT GTAAGGTGTTCTATGGCAACAGTGATGACATGGTGTGTTCTCAGCAAGTC[G/A]TCCAAACCTTC CAAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-19937c	185 C T ---	---	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAACTTGAAGGAAA GAACTATTGCACAACCAACCAATGTACATATCTGATTAGACAAGCAAAAGCACCTTCATGTTGTCT GTAAGGTGTTCTATGGCAACAGTGATGACATGGTGTGTTCTCAGCAAGTC[G/T]GTCCAAACCTTC CAAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-21117b	227 C T ---	---	GAAAACGGGGTGCTAAACAAAGAAAGTCTCAGATCCCACCTGAAATCTGTTTCAGTTTCACAGGCTC TCTCCAGAAAAATGCATATGTACCAATTTGCATGTACATTTTCAGAGCCCTTCAAAATACATTTCTGGGG TCCAATCACATACTTCAGGTTCAGACTCCTAGCTCCCAATATTCCTACAGTTCTGAAGANITTAGCAGT CCTCTCATTTCTACAGTCTGATTTC/TTCCTACTGAATCTTGGGTGGAG
WI-21122a	42 C T ---	---	TCACTTTGTATCATAATCCCCTGTAAAGCTAAAGTTATTCAIC/TTAAACAGGAACCTCTGTTTTTCC TTATTCAAATGTCAAGCCTGACGCTTACTGTACATATTGCTAGCAGGAGACAACTGGAAATACT AAACAATACTGGAATTCACATTACAGACAGACGAAACCAACATGGGATGCCACACATAACTTCCT TTGTAGGTTTCACAGAGAGCCTATTTGTGGGTGCT
WI-21254	53 A G ---	---	CAGTTTGTGTACAGGAAGGGCCCATGAATGTGGCGGAACTATTCACAGGAG[G/G]CAAGGAGAAG CTGTTCTCTGG
WI-21054	23 G T ---	---	AAGGAAACTGCATGGGTACAAAT[G/T]TCCAAATTCATACTTAACAAGGTGGGGAACGGGTCAATTCT TGGCTGTCTCCAGAACAAAGGGCGAGTCTATGCACCTCTG
WI-21059b	181 T C ---	---	GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATTCCTCCACTGAGCCTGGCTGAA CTACAGCTGCCAGCATTTCTGGGCTTGCAATTTCCAGCTTCGTCACATCTTAATTTCAAGCTGAAA AATCCTGGGGAAGAGACATACTTCACTGAAGTCATTTCTCTATTCT/GIATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT
WI-21059a	63 C T ---	---	GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATTCCTCCACTGAGCCTGG[G/T] GAACTACAGCTGCCAGCATTTCTGGGCTTGCAATTTCCAGCTTCGTCACATCTTAATTTCAAGCTG AAAAATCCTGGGAAGAGACATACTTCACTGAAGTCATTTCTCTATTCTATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT

WI-20442	37	T C	---			TCCACGTGAAGGAAGAAAAAANGGGGGGGGCTT/CJTAAAGGTGGCACAATTTAAGAAAAAT ACCATCCATTTTCTCAGTCTAATCTGAATCCATACATTAAACAAAAAGTGCAAGTGATGAGACGAA CA
WI-21235	43	T C	---			GTGACAAGAGGTGAAGCAAGGGGACAAGGGGCAGCAGGGCAGTCT/CJCTCGGGCCGATGTTCCAGGG CAAGCTACGTA
WI-22012a	57	T C	---			ATCAGAACTGCAATCTGCACATGAAAAGACCTGGGGGGAATGCCTACATCTGGAATTT/CJATTAC ATCAACGTTAAATTTGTCCGACCAGTCTTCATTGCTGATCACATTTTGATAATGACAGATCCAACAT GAACTCCTGAAGCAAAATGAATATTTACCTTGCTTTTCATGCAAAATTTAGGGACCAAACTCAAAAGG TTTCATCCATGCTGGGACACCAAGATCTAAGGAATTTGACAGGGATCTTCT
WI-21149a	167	G A	---			AGGACCTGCTCTCACACGTTCCCTCACCCCCACCAGCTTTTGGCAAGATAGTTGACTAAATACCACCT AAATAGTGGCTTTTTTTTTTTTAAACAATGACCTTTATTTATCTTTAACTTTAACTGAGTCTTATATA CAGACCTGCCCAACTGGAAAGCTTTTACAC[G/A]TGCTTCAGAATCGGCGATTTGCACAAATGGTT TGGGGCAGGTCTGTGTTAAACATGGGATGGGAACCCACAGGCTCTACCTG
WI-21376b	188	A G	---			GGTGCAACTTGGAAATAATGGTTTAAAAACAGGATAAGCATTAAAGGAAAAACACTTTCAATGTGTC TTCCATTGATGAATTTGTTTTCTCTTTATCCCGCAAGTGAGTTTCATGCTCGGTGAAACCA GACAGTGTGAATCTGTTCCAGCCCAATCTGCAGCATTAGGGATGAGTTCTC/A/GJGAAGTGATTCT GAACTGACACGCACTCATGTCTGCATGGGAACCTCTGSSGAGAAGCCCT
WI-21382d	125	C G	---			CCATTGCAGTCCAGAGATGAGAACTGGACAGAGGCAAAATCATGAACAGAGGGAGTCAAGAGA AGGGTTTTCTAAGATGGAGAGTGGGGGGGTTTGATCCAGTGGGATNGGCTTCCQ/C/GJAGGTT GCAACCCAAAGGAAGTCTCTGGAAGCAGCACCAGTCTGTAATGGGAGCAGAGAGCTGCCATCCTC AGTCAGGTCCGAGTCCAGGTCCGAGGAGAGCTGCTGCTCATAGTCTCGCAC
WI-21437a	201	G A	---			TCCCTGAGGTGGAGTCCTAGCATAGTCCCTCCCTCAAGAGGGGACAAGGGGTCAGGGGCAGAGC AAAAATCCAGTCTGCTTCAACCACGAGACTGCCCTTTGGGATGGAAGTTTCTGGAGCTCCCTCCATT CTATTCTGTGGGCAGGAACATGCCAGGCTGCTGTAATGGCAGGGTCACTTTACCAGGGC[G /A]CAGGCATAGTGTGGCCCTGCTGCTGCTGGGGGCCACCTGGGAACAGT
WI-21202b	156	A C	---			CAAAATAGAAATTTCTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTTGATCT GTTTTATGAACATGATTTTATAAAATGGTCACAATATATTTTAACTGATTTATTGAGGG AGGAGGAGAGAGTTGACCAA[A/C]GTCTACATGCATAGACAGTCTTAAAGCGTATCTCAAAACATG A
WI-21202a	61	T C	---			CAAAATAGAAATTTCTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTTGATG TCTGTTTTATGAACATGATTTTATAAAATGGTCACAATATATTTTAACTGATTTATTGA GGGAGGAGGAGAGAGTTGACCAAAGTCTACATGCATAGACAGTCTTAAAGCGTATCTCAAAACATG A

WI- 21627b	153 A G ---	---	GCATGAAAGAATCCAAATCAGACITTTATTCAATAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTCATTATGGATATTTATGCTAGGAATGACAA CAGTAAGGGCATTGCAA[A/G]TCCAAAGTCATCTAATAATTAAACCATAATTTACATAATTTGTAGG GACAGTACTAATACTCTACAATAAATAAGGGTTTAAAAATGTTGCTTA
WI- 21627a	106 A G ---	---	GCATGAAAGAATCCAAATCAGACITTTATTCAATAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTC[A/G]TATGGATATTTATGCTAGGAATGA CAACAGTAAGGGCATTGCAAAATCCAAAGTCATCTAATAATTAAACCATAATTTACATAATTTGTAGG GACAGTACTAATACTCTACAATAAATAAGGGTTTAAAAATGTTGCTTA
WI- 21399a	75 C T ---	---	GGATTGAGTCCCAACTTGATCTCAAAATTCATCTTGCATGTAACAAGCTCATCCCTCTAAAGTT TCAGTTT[C/T]TTCACCAGTAAAGGAAAGGTTGGACCAGACATGTTGGACCGTAATTGCTTGGTAA CTGCCCTCTGCATTGTCTCTGAGGTTGTGTGCCCTAGGACTAGGTAGGATCTCTCTTGTCTTCTGCC TTACCTAGGCATAGTGCCTGATAGCAGGCTGAAGCCCAATTCATCTTGT
WI- 20328a	68 G A ---	---	CGATGCTGCTAAGATAGGAGGTTAATCTTTACATGGTGAGTGGTCACAGAGACAAGACATCAAT C[G/A]TCTGTTAGCAGCGAGAGAGACACTTTAAGTTGCCCAAGAGTACAAATCCCATCTATGAGAC AGCAGTGTGGCTTCTTAAAAACAGTAAACCATAAAGGAAAGGATTTAGAGGTTTCAGACATT AGGAACAANTGTGGCCAGAGATACACAGAGCCCTTGAAGGAAAGGCCCTACT
WI-21249	155 T C ---	---	TTCTGGCATCAAAATGTACATGTAATCCAAATTTAACAGATCAAAATGTTACACTAAGTTTCACT TAGTATCTAAGTATCCAATCACAATTGTATCTAAGTTTCACTTTTAAAGAACATTATAAGGTAATT AAAACTCTAGGTGTATACTTA[T/C]ATGGAACTAGTTTATTTCCNATTTAACTACTGTTTCAATTCGCGTA AAGTATGTTGTCCCAATTTTCAGCTGTTTAAAGGAATTATAAAACATTGAGA
WI-21504	147 C T ---	---	TGACACAGCATCAATTTTCATGAATACCTTTGAAAGGGCCATTAGAAAAAATAAGAGCCAAATTTGGGTC ATTTGAGAAACATTTTCAGCACAAATTCAGTGGGGGCACGGCCGTTGGCTCCAGCTGGGTTTTCOC AGATGCAACAAT[C/T]GCGGTTCTGGCTTCTCCACTGGTGGGATGGGATCGCGCCTTCGGAGCTCT CAGGG
WI-21242	115 G A ---	---	CTGCACAGGGAGGACAGCTGCTGGCAGGGACTAATAAACCCCTTCACCTGGCCATGGTGGTGGTGT CTCTATGGACCGAGGCCCTGAAACGCGGGCAGGGAGGGGCAGAGAAC[G/A]CACTAGCTTGGGGGTG GGCACAGCTTCAGACCCCTT
WI- 21475c	181 A G ---	---	TAGCCCTTCTGCCAACATCTGGCAATNGAGGCTGGGGTGGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGCTCCAAACCCAGGCTTCTCACTTGTCTACTAAGCACAG CAGTCTGAAGCTTGGGACCTGGGACGTGGCTCTTTGGAGAAGGCA[A/G]AAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTTCCCGTTCTCCACCCTATTTCTCCCTGAAG

WI- 21475b	117 A T	TAGCCCTCTGCCAACATCTGGCAATNTGAGGCTGGGTGGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGTGGCTGCCAAACCCAGGCTTCTGATCTGTTGCTTACTAAGCA CAGCAGTCTGAAGCTTGGACCTGGCAGTGGCTTTTGAGAAAGGCAAAAGCCACAGCAGCAAC ACTTAGAGCAAGACCTTCCGTTCTCCACCCTATTCTCCTCCCTGAAG
WI- 20893d	207 A G	TGTTTGTTCCAGCCACATCTTCTCCAAAGGAACCCACCCAGCCCGTGTGCAGGCTTGTGCAGGG CTGTCTTCGGCGTTTAAAGTCTACTGAGGAATACAATCATTTGTACGTAAGTTTCATCACCGCACTCC AGCGTCAGGCCAAACCTTTCGGTGGACCTGGGNAACCTGCCATTCTCTCTCTTTTACAATGCAGT TTCAGACATAACATTGGTAGAGTAAACAACAACCAACCAAGCCTAAATG
WI- 20893c	179 T C	TGTTTGTTCCAGCCACATCTTCTCCAAAGGAACCCACCCAGCCCGTGTGCAGGCTTGTGCAGGG CTGTCTTCGGCGTTTAAAGTCTACTGAGGAATACAATCATTTGTACGTAAGTTTCATCACCGCACTCC AGCGTCAGGCCAAACCTTTCGGTGGACCTGGGNAACCTGCCATTCTCTCTCTTTTACAATGC AGTTCAACATAACATTGGTAGAGTAAACAACAACCAACCAAGCCTAAATG
WI- 19941c	71 C G	GAGCTCAAGGGAAGACCCCTTACCAGATAGGGACTAACTGGAGGGTGGAAAGGAACAAGGTGAAA GGTATC/GJGGTCTGTGAGACAAAAGCAGGGGGCTGAGAACACAGAGCAAGGTGGTTGGAG GGAGCAGCAGGAGGTGCAGGAAGGAGATGGGGACATTTCCTATTCCAGTGCATGTCCCTTAAAT AAACTGGGTACAGGAGCATTTNGAAGAGGAGAACCAAGGACAGAAAGCAAGCG
WI- 21552b	166 C A	TGGGTACATGGACAGATGTATATGTTTATGGTTATATGAGATATTTGATACAGATACACAATGTG TAATAATTACTTCAGAGTAATCGCATCTCTTCACCTCAAGCATTTATCCATAGTGTACAAAGAA TCCAAGTACTCTTGATTATTTAAAATGTA/C/AJAATTAAATTTATTGAATTTAGTTACCCC ATTGTGCTATCAAAATATTCATCTTATTCATTCTTTGTAACCTATTATTGTA
WI- 21552a	66 G A	TGGGTACATGGACAGATGTATATGTTTATGGTTATATGAGATATTTGATACAGATACACAATGTG /AJTAATAATTACTTCAGAGTAATCGCATCTCTTCACCTCAAGCATTTATCCATAGTGTACAAAG AATCCAAGTACTCTTGATTATTTAAAATGTACAATTAATTTATTGAATTTAGTTACCCCA TTGTGCTATCAAAATATTCATCTTATTCATTCTTTGTAACCTATTATTGTA
WI-21512	54 C G	TCCTGCTACTTCATGCTCCCTCCCTGCCCCAGAACCTTACAAAATATTTCTGTC/GJTAGAGAGGA AAGAGCTGGTGCTCTGAGGGAACGTCCAGGTCCGGGAAAGGCACCTGCTGCTGTGATCTGTC TCAGTATGGGAGGTCTCCACTCGCCCCACAGGCAGCCTCGGGGCCAGAGATGAGATATGCTGTA TCCAGTACAGGGGCTGCTGCTGGGTGCTCCCAACAGCTCTCTTTGGGGG
WI- 21513b	192 G A	CACATAGTTTCTCAAGAAGAGGATGAACCTGAAAACTCTCTAAGGCGAGGACAAAAGCACTTCCATT ATTCTTAGTTTAGACCAGAACTCTTAAATTTTATATTCTCTTTAATAACTGTCAAAATACACCAAATA CTTAGAGGAAAAATTTACAGTATACCAAAACATTTTAAAGATAAAGAGGCAGTGTAA[G/AJAGTAG TATCTCTACATACCACAGTATACAATGATGCCCTTCTGTCAGGTTTAGGAAC

WI- 21514b	133 C T ---	---	---	TTGAACCTCTGAAGGTGGCTTATGTCTGACCTCTCTTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAGTATCTCAACATTACAAACCCCAATCTTCAAGGAAGGAGCACATTACCATGGAGCJC /JACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCCTTATGCAGGAAATAAATGAGG ANITTAAGGCTCAGATGGGTTAAGGTGATTGTCAAGGGTCATAAGGAACT
WI- 21514a	100 A G ---	---	---	TTGAACCTCTGAAGGTGGCTTATGTCTGACCTCTCTTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAGTATCTCAACATTACAAACCCCAJ/GJCTTCAAGGAAGGAGCACATTACCATGGA GCCACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCCTTATGCAGGAAATAAATGAGG ANITTAAGGCTCAGATGGGTTAAGGTGATTGTCAAGGGTCATAAGGAACT
WI-22020	27 C G ---	---	---	ATGAACATGTTGCAGTGGGATGAATC/GJTTATCATGATGCTAAGTGAATAAGCCAGACACAAA AATCCAAATGTATCATTTACCTGTATGAGGGTACTT
WI- 19576a	113 A G ---	---	---	TTTCATCGGTTCTTAATACAGTACAATCCTTTTGTGAACAAAAGTCACACTGGCAATGATTATTACA GATCCAAATAGACTCAGGCTTCAGACATAAAAAATTAACATTG/JGJCTAGTTCAGTGATTAGT CACAGAANTTAACATCTGCCAGATGTACACAAATTTGGTAAAAACTACAGCTTCTCTCCACGGGA G
WI- 21695a	141 A C ---	---	---	ATACACAGGCCACAAATTGCAGGATGGAAGGCAGTGGGCACCTTGGAGTGACTACACATGGCAATA AGCAGCCTATCTCTTACCACACAGAAAGTTCTTGGGGCATGTGATGGTAGGCCAGACCTTTCCAA GGGAATA/JCTTACTACACTAAGCCTACACTGTACTGTGAGATCATGGTGAACAAGGCCACAGGC AGTGGGAGGAATGTGATGACTTCACTGTGTTCAAGNTTCTAAGGCCACGAT
WI- 21574a	235 C T ---	---	---	AAACCCAGAAATTTAGGTACTTTTGATTTATGAGGAACCTCACTATAGGAAGCAACTTATGAGTG TGTAATATTTGATCTAGCAGCAACTTCCACTGATCTGGCAGGTGACAGCTCTCAGTGAACAGCGC TCATCACCTAAAGTGAGAGGCTGTCTATTCTCATTTGTGAATGTCCCTCAGAGTCACTAGGGAGCCATT GGGCAGGCCAGGGAACCTTACTGCCTACTTCTCTCTGCTCAGGTGGGA
WI- 21644c	151 T A ---	---	---	TGACTGCCAAGATTTAGGCCCCAACTTAGGAGCAAGGTCACCTTAACCTTTCAGGAAGCTTGGGT GTGACCCACTGCATAAATGGATTTTCAACATANTATTTAACAGACTCAAAGTGATACATAAAGCTTG TTTCATAAATAAGGGA/JTTCATCAAGATCCATGGAATGATGCAGTTTAAATGTGTTCTCAGC TTGCCTACTGACCACCTTCTCTTTTCTAAATATGGCAACAGCAGCAAGTC
WI- 21614b	55 G A ---	---	---	TGCTTTAACCTCAAAGTCCAAATAAACATATAGACATTTTGANTATAGCTATC/GAJTTTTAACA AACCTCATATGATCACTGTGCAATTTTCAGTCACCTAAATACGGAACCATGACTATTAATAAACA TTTACTGTGTGGGTTTGTGGGACTGAACATTAACCATACGTGATTTCTAAGGTACTAGGGAGTT GGAACAGTACTACGGGTCAATGGTATTTTGGGCAGTTGGCTGTGTGGG
WI- 21615b	151 C T ---	---	---	GACCGAGAAAAACTGCAAGGCATATGATGTTTGTGGAAGTATCACATGACTATTTCAAGCTTATAGA GAAACTTGCAAAAAAGTACAAAGATGGCTATTTTAAATTTTACATATTAAGATAAGGATGGACT CTTTCACTGAGTATTATC/JAGGACACAAATCGACGGATGTAATCTATTTGANTTATACCATAGGCC TATTCATATTGGCCAAAGGGAAGGTAGGATGGGTACTGTGGAACGGA

WI-21981	61	T A	---	TGTCATCTCATTCTGGAGAAATCATAGATGTGGCAGAAATACATATCTTGAAGAAAAAAATTAAGTCTCCTTATGGTACTGTGATTTCAATAGGGTGTGGGATAAGTACATGACACATGCATGGGATAGA CACTCTGTTCTCTACAGATCCGTCTTTGGGAATTACAGGAACATAAAGGATATAATGGATGGGTT ATTACTTTTACATGTGGACAATCTAGTTGTAGCGTTTAAGGTTAAATTTGG
WI-21660	120	C T	---	TCCCAACTAGCCTCTCAGTATTTAGATGAGGATAGAACAGATACGGTGTAAACACGCCTCTCCACTGCT TACTGTGTACCAAGAAAGGCAGAAAGCAGCTCACCAAGCCTAACCTAGGOCJCTGTGCTTTTTCAG GCTTCTCAGGATGCCACAGCACATCTGCGGAACCTGGGATGCAGGAGAGAACAGGGTCTGTCTTC AGGAGSGTACAGC
WI-19105c	211	C T	---	TGGAAGTAGCCCTCTGACAGAAAGAATATTTGTGGTCCATGCGTTGAGTCTGTTAAGAAGGA CACTAAGGCACATGGCTGGTGATCTTTGGTCATAGACACGGGTGAGCTCATGGTGAACCTCCTCTT GTCTGTAGGTTTCCAGGGCTGGCACAGAGGTGAGGGCAGAAATNTGGGGTCCCAGTGGATCTCCCC ACAACTTCCTGTTCCAGGGGCAGGATTTCCACCCAGGGCCAGGGTGCCCC
WI-19105a	33	T C	---	TGGAAGTAGCCCTCTGACAGAAAGAATATTTCTGTGTCCATGTGGTTGAGTCTGTTAAGAA GGACACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGAACCTCCTC CTTGCTGTAGGTTTCCAGGGCTGGCACAGAGGTGAGGGCAGAAATNTGGGGTCCCAGTGGATCTC CCCAAACTTCTCCAGGGGCAGGATTTCCACCCAGGGCCAGGGTGCCCC
WI-21760c	81	C A	---	CAAACTAGTCACTCTACTGATGCAAAATGATTTGGAGGTGCTCTCTAGCTTTACAATAAGNGGAGG GACCTCTGACTGCA/C/ACCTCTGTCTCAGTTTCAGGGCA
WI-21760a	35	A G	---	CAAACTAGTCACTCTACTGATGCAAAATGATTTGGAGGTGCTCTCTAGCTTTACAATAAGNGG AGGGACCTCTGACTGCACCCCTGTCTCAGTTTCAGGGCA
WI-21569b	198	T C	---	TCTGCCATATTGTTCCAGCACACTATTACTGTTATTCTCTTTGAGGAAAAACAGGNATTAAG AAATCTGGTTTGAATTTCCATGATGCCCTAACTATGTTAAAAATCCTTTTCCTTACCAAAAAAGBA ACTTCTTAATCACAGAGAAACAGAGGGAAGACTGAGATATGTTGCAGAAATTTATCTCTAC[T/C] AGAGACAATTATAGTTTCAATAATCTTTCAGGGTTGTGCTTACTTGGGGGGC
WI-20934a	72	T G	---	CCAACATGCAACATAGTCTTCTTCTTAAAAAGTACATAGTAAAGGTATGAAAAACATTTGTATTCA GAGAA[T/G]TCTAAGACAAAATGGTCAAATATTCAAATGGCTGGCACTAGTGGTAAATTCAGCAGAC AAACAGCATGAGAAAAAGCCGGGAGACAGTAATAATACGTGCCCATTTGCAATGAGTTACCCAATC AAGCCCTTTTACCTCTTAAGATGGCAGATTAGAAGACCTTNTTCCCAAGGAGA
WI-21561	55	T G	---	TTTCCATTTTATTCAGCCGGGCCATCAGAACAAATAGCATCTATACCTTCGAAACQ[T/G]CCTCTTAAC CTCTCCAGGCAAGAAAGGAAAAGTGATCATATTGAATTCCTCAGAATGGTGGGATCTCAAGACTT TTTAGAAAGTGCTTATTAAAGTAAAGAGGCTTGAATATAATGATGATAAATGGTAGCCCTTTCTGGA AATAATTTTGTGTAATCTGTTTAAAAAGATTTTTTGGATGCATTGTCCCCA

WI- 21961c	200 T G	AGCTTTGCTTGAAATTTGGTACTTACTACCTTGCAATCTCTTATTATTATTATTACTTTTATTT TTCCGTAAGTTATTGGGTACAGGAGTATTTGGTTATATAAGTCTTTAGTGGCGAATTTGTGTGATT TTGGTGACCCATTACCCAAAGGAGTATACACTGCACCATACTCGGTCTTTTATCCCTCGCCCCC[T/G]C TCCACATTTTCCCCTCAAGTCCCAAAAGTCCATTGTATCATCTTATGC
WI- 21961b	73 G A	AGCTTTGCTTGAAATTTGGTACTTACTACCTTGCAATCTCTTATTATTATTATTACTTTTATTT TTCC[G/A]TAAGTTATTGGGTACAGGAGTATTTGGTTATATAAGTCTTTAGTGGCGAATTTGTGTG ATTTGGTGACCCATTACCCAAAGGAGTATACACTGCACCATACTCGGTCTTTTATCCCTCGCCCCCTC TCCACATTTTCCCCTCAAGTCCCAAAAGTCCATTGTATCATCTTATGC
WI-21956	26 T G	CCCACCTTGGGTCTCTTCAAGTGAAT[T/G]TTCCTTCTGTTCTTAAAGCCTTTTAAATGAACCT TCCATTCTGTTCTGAACTTGCTTAGTCTGTTTCTGCTTCTATGCCCTCAGTCGAATTTCTTTCTT CTGAGCGGCAAGGACTGAAGTTGCTGTGACCTGTAGGGTTTCGACGCGGTAACTCAGGGTAACTC CTATCTCTCCACCGGTAAACAGAGGGTTACATTATGGGGTCCAGGTT
WI-21966	148 G A	CAACATACATTATGGCTGCCTTTATTTAAGAAATGTTTACTGAGAACTGTACTGTAAACAACATAT TTTTGTAGAAGCATGAGTGAGTGTGTGTGTGTGCGCGCGCGCACGGCATGGCACTGAGG GGATTGCAATGGG[G/A]AACAGGATAAAAGGTATAAAACCTTGGTCCGAAATCTTTGCTTATTAAAC CTTGGCCCTGCTCCTCACAATGTTTCTACACTTAATTCATAAGAGAGGTAGA
WI- 21930c	148 G C	TATACTGGTTTTGGTTACATGGATGAATGCTAATGGTGAAGTCTGAGATTTAGTGATCCCATCA CCTGAGTAGTGATGATGATCCCACTTGAGGCTTTTATCCCTTACCCTACCTCCACCCCTCCCCAT TTTGAGTCT[G/C]CATAGTCCATTATACACTCTGTATGCCCTTTGCATACCCATAGCTTAACCTCCC
WI- 21139a	165 T C	GCTCTAGTGAAGAAATTCAGGACGCGGTCTTCAGAGCAGAGGGCTTGGTTCAAGTCCCTGTTCTGCCA CTTACTAACTGCATGACCTTGAGCAAGCCACTTAATTTCTCTGCTCTCTCTGTGAAATGGGTACAA TGTGGGTCAGCAGTAAAGGAACATACTA[T/C]GTACAGCACTTCAGCACAAAGCCTGGGCACACAG
WI- 20317b	217 G T	CACATGCAATGAAATACACAGGTAAACATTTTAAACAGTGGGGACAAATTTAAGTACGTGGCCAGC TGTTGGTTGTCTTGTGGTCATTAAAGACAATGTTAAGANTCAGGAGTACTTAAGTGTAGTGTACAA AATTTTGTCTCTCAGTCTTTCATTAAGTAAATTCATAAGATGATATACATATTACTGCAGATAAA ACCATCATCAGAAA[G/T]TATTAAATTAATTCATATTTTGGGCTACTCT
WI- 22082b	179 G A	CAGGACTTGGTTGCTGTCCCACTGCACATAATGTCCCTTTTGTGAGTTATTGGTTGTGTGCG TTTTCTTTTGCATAAGAAATATGTCATTTAGTCCAGAGGCTCTGCTTTATCCGGATGACGGAGG GTACACGGGGCTCCGCTCAGTTCGCGCGAAGGACGTATT[G/A]CTGAACCTGGGACGAGTCTACTC CTCCCCACAGGAGGCCACGATTTCAAATCCTCTTTGCTGTCAACCTCT

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WI-22082b	67 C T ---	---	CAGGACTTGGTTTGTGTCOCCAACTGCACATAAATGTCCCTTTTGTGTTGAGTTATTGGTTGTGTCG/
			TTGTTTTCCTTTTGCATAAGAAATATGTCATTAGTCCAGAGGCTCTTGCTTTATCCGGATGACGG
			AGGGTACACGGGGCGTCGCTCAGTCCCGCGAAGGAGTATTGCGTGAAGTGGGACGAGTCTACTC
			CTCCCCACAGGAGCCACGATTCAAATCTCTTTGTGCAACCTCT
WI-20993	139 A G ---	---	AACACAACTCCATGCTTTCAAGATCCCACACCCAGATACTAAGACATATTAAATTTACAGCAAT
			TAAACAGTGTAGTTTGGTACAATAACACATATAGCAATGATACAAATTAGGGGAAAAACCCCTGG
			GCCTTCTA/GTAAACAAGTGAGTATACATTAAAGACAGTATTGCAGAATGGCTTCAGGATTAAATTTGA
			TTAATTTAGAGAGGCTATTTCAGGCTTCTCCTAGCTCATCCACACATCACC
			AAGCGATTTTATTAAATGATTTGGACATACTGTAGGTCAAATAATTTCTGAAGATAACAATTA
WI-21723b	125 A G ---	---	TGGACTTTAAAGCTCGACATAAAATAGTAGCTTCAAAGGGTTAGTCATATCCCCA/G/CAACA
			GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAACTCGGAAATC
			ATT
			AAGCGATTTTATTAAATGATTTGGACATACTGTAGGTCAAATAATTTCTGAAGATAACAATTA
WI-21723a	82 G A ---	---	TGGACTTTAAAGCTC/G/ACATAAAATAGTAGCTTCAAAGGGTTAGTCATATCCCCAACAACA
			GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAACTCGGAAATC
			ATT
			CAACAGATGCTTGAGCCAAAAAAGCAACATAGGCGAGAAATACAAATTGAGAATATCTTCATGTTTC
			AACCTTTAATCTGACTTGCCTTTTACTATCCTTT/G/CCCCATTTCTCTAATCTCTTTTGCCTTACAA
			TATATTACCTTGTAGGTATCACCTCATCCTATAGGAATGCCTTCTAGTTAATGTCTGCCCCAAACA
WI-22132	99 T G ---	---	ATACTAACCCATTGAAGGATAACTATGGAACCTTTAAATGGGACAGTGGG
			TGACAGATCACACCACATTTTGTGTAACCTTTTCTCCTTCAAGAGTCACCTTAGCTTAAGCCAGAA
			GATTCTCTTAAAGAACACATACACAGATGTGCACACAC/G/AGAGGGCAAGTACAAAAATGTAACC
WI-21006a	106 A G ---	---	CCACCAAGTGCATGTGAATGAAGTGCAAAAAGGCTTCATTTGCAAACTCTGAGGATCATTTCTCT
			CTGCTTCAGGAAAAATAACAGAAAGGTCCTAACTGCCCTAGGCCT
			CTGAGGCTGCTCTAACTTCATNTGACGGAGCGAGTTTCTGGCTTGGAAATAACTGAAAAGATTGAT
			TTTCTCTTTGTGTACAAAGGATTCAAATAATTTACATCTTCTCTGCCAGTTAAACGTGCCGTGG
WI-21761b	138 C G ---	---	CTC/G/CAATACACACCACCAAGCCAAAGCGTAACCTTGGCTGCCCTCAGGAAGGCTGGGAGGAGTGCAG
			ATGGTA
			AATGAAAATGCCACCCAGAGTTAACAGCTTGCCATGCATGCAACTGTGTGCGCAAAATCAAGTTGT
			TTTAATACCAGTGTGCAGCTTTGATTCCTCCATGAAATTAAGCTGTGTGCTCACTGTTTACATAA
WI-21079c	166 G A ---	---	CTCAGGCCACCCCTGAAATATCTGCTAGTGGG/G/AAATTTACAACCCACTGACCATCTCAGCTCAAA
			GCCAGATGACTATCACCTACACATCTGCCAGGGTAATAGGCATGGGCAAT

WI- 21079a	50 G A ...	---	AATGAAAATGCCACCCAGAGGTTAACAGCTTGGCATGCATGCAACTGTGTG/AJCGCAAAATCAAGT TGTTTTAATACAGTGTGCAGCTTGATTCCTCCATGAAATTAAGCTGTGTGCTCAGCTTGTTTACA TAACTCAGGCCACCCTGAAATATCTGCTAGTGGGAAATTTACAACCCACTGACCATCTCAGGCTCAAA GCCAGATGAATATCACCTACACATCTGCCAGGGTAATAGGCATGGGCAAT
WI- 22129a	45 T G ...	---	TCGTAGATTTAGCCATGCCATATATTTAACTTTTAAAGGAAAAGT/GJTTATATAACAGTCATTGCT TGGTAGAATCCAGTCTGCAATAAGTTAGCTCTAACAGTTAACATTGAAGCTTTATACCTTATATTTA AATGTTAGCAATCTCTACTACATTTTCAAAATATAAATAATTTGGTTGCAAAATCCAGNAAAGGGCA TTAACCAACATGGGACTGATCTGGGGCTTCCACCTGACTAAGGTTTTA
WI-21941	79 A G ...	---	TGGAGTTAAGTGGGCTCTGCTATTTCCCCAAGAGGACTCGGAAGATGTTGATTCAGGGGCAGAGT GAGGGCAGAC/A/GJGGATGAGGCTCTCTGTAAAGTCCACAGACGCTCACAGATGCTGGGAGGCT GGGACTGCCAGGTTGGAGCCTACCCAGAGAGCCTCACTGCATTGACCCACACCCACCTCACC CAGCACAGGCACACGCGAGGGCACACGACACACGNTGCACCTCACACGC
WI- 18916b	42 C T ...	---	AATGGCATCCCTGTGATACCAAAACATCTTCAGCAGCTCAGC/CJTGCGCTTCCACTTCTTGGTACCC GGTTAACTGCCAGGNGGTGACAGTGATGCCAGGGCTCGCCCACTACTGCACCTGGACACAGCCTCACCC AATGCCACCTTCATA
WI- 18916a	35 G C ...	---	AATGGCATCCCTGTGATACCAAAACATCTTCAGCAGC/AJG/CJCTCAGCCGGCTTCCCACCTCTTGGTACCC GGTTAACTGCCAGGNGGTGACAGTGATGCCAGGGCTCGCCCACTACTGCACCTGGACACAGCCTCACCC AATGCCACCTTCATA
WI- 19828c	200 A G ...	---	TTCCCTTCTCCCCAAGAGTGGGCAGAAAAGCTTTGTTAACCTCCTTTTACAGATGAAGAAAAACAA GATCAGAGGTGCTAAGTGTGTAGCCTAGTGCCAGGNCCTTCTGGCCCCAATTTCTGGGTTCTCCCCAAG CCCATGCTTCTCCACTTCTCACAATCTTTACTTCTCCTCTGACCCCTCACCACCCCAAAATJAG JCITTTAATCTGGAAAAGAACCCAGCTGCACACTGGGCACACTTGACCT
WI- 21863b	47 C T ...	---	CACAAGAGTCTGTACAACCTTAGGGACACCCAGCCCTGGCCCTG/CJTAGCTGCATGCCACCCTC ATATCCACCCCATCCACGCTCTCTGCCCGACACCCACAGGCTCCCTGCTCTGGTTGAAGTATTTT CTCCAAGGCAGGAATGAGTCTTGATCCAAACACAGCATCT
WI-19860	51 C G ...	---	TTGACCTAAGCCTAGCATAAAATTAGCTAAGTAGAATGTTTCCAAAGATG/CJCTGCATCAGTAT CTCCATCCCACATAATTTCTGTTGATTTTGCCATTACCCCATAAATGGTGGGATCTACCTCCCT CCTTGCAATTTGAGCTGNGCTCTGATCCTGTCTAAGGATCTGAAGCC
WI- 19889b	80 C T ...	---	ACCCAGCTCCTTTACCCCTGTGGCTTTCAGTAGGCTTTGGCTAATGGCCANTGAAACTGCAGGGCAAG AGGAGTGAGGGG/CJTAGACAGCATTTATTTCCCTCTTTCACTCCCTGTAGCTTTGGTAGTGGCTGTAT TTCCTACTGATAGTTCTTGCCCAACAGTCGTAACTATTGC

WI-19891c	172 C G	TGTTGGTGTGAGAAATTCACAGCTTACTACAAGGAAGCTGAGAAATTCGTTGGTGCCCCCTCCCCCCCCG ACTCCTCTGTCTGGGAAACGTGGCTTGNCTCCAGACACGTGTGATGCCAGCTCTCCTCAGCGG AGCTCCGATCCCTCAATTTGCCATCTGTCTGACTC/GJCGTCTCCCGGGCGTGGGCGTCTGTGT CAGCGAGCGGGCGGAGGAAGGAAGGAGATCCAGGGTCTGTCTG
WI-20155a	81 C T	GCACCTGTAGGGGTAGCTTCCATGGTTCTCCAGCACGGGTGTACATTACCTTAGGCTGACCAT TCCCTTGGGGGGG/C/JGCAAACTGCTTTGAGGAAATNTCCAGGAGGAATAAACTAGAAGACGC ACCTGCTATTTCAACCATACTATGGAGAAATACAGCTAATGAAGTGGTGGCAGAGCTTTGGCCGTGTGA GTGCCCCAGGGTAAAGTCTCTCTTCTGTCCAGTCCAGAGCAGAGACTTCTC
WI-20270b	91 T G	AGCCATACAATGCATTGCAAGAAACAAAGCAGCTGTACAGGAGTGGGACGCGTCAAGTGTACAAT ACATTCATGTCCAGGATAAGGAGCA/T/GJACACCAGGATTTATACACGGTGGCAGCGGTATAGGCA CGATGATACAAATATAAGTATATTTCCATCTATATAATACACAGCTGGGTGGGAAGGATGCT GGGTGATCTTGTTCCTCCGAGAGGGCTGGGAGGCGAGGNGGGTGGTGGAA
WI-20270a	53 G A	AGCCATACAATGCATTGCAAGAAACAAAGCAGCTGTACAGGAGTGGGACGCG/C/JTCAAGTGTAC AATACATTCATGTCCAGGATAAGGAGCATACACGAGGATTTATACACGGTGGCAGCGGTATAGGCA CGATGATACAAATATAAGTATATTTCCATCTATATAATACACAGCTGGGTGGGAAGGATGCT GGGTGATCTTGTTCCTCCGAGAGGGCTGGGAGGCGAGGNGGGTGGTGGAA
WI-20622	130 T C	CCACTTCAATATTTACAAATGCTCAGCGCAAAATATGAAAAGCTTCAACACTTCCCTTTGTA ACTGCTGCAATAAATGCAACTTTAACAAACATACAAATTTCTCTGTATCTTAAAAGTTGAA/T/C/ TACTAATTTTATGATTTACTCATATTTTATTCATATACATTTTATGACATCATTTGCCAATACATA CATTATTTCTNTAATTTATTTTACAATAAGCCAACTCTGTCATGCAG
WI-20768b	190 C T	TTCCACTCAAACTCCACCCCACTTCTCTGGAAGGAGGGCTAACAGGACCTCCTGCTGCTGCTGC TCACGACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAACTCATTCTGTATATCACCCTCTA CAGGAGAGGCTATTTCTGGGACCCAGAGNTCAGCACACATCTGCTGGGA/C/T/CAGGGACTC GTAATTCGCTTGGTCCAACTCTTCTATGGGTTTAGCTGCCCTCATTC
WI-20768a	71 C T	TTCCACTCAAACTCCACCCCACTTCTCTGGAAGGAGGGCTAACAGGACCTCCTGCTGCTGCTGC TCA/C/T/GACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAACTCATTCTGTATATCACCCT CTACAGGAGAGGCTATTTCTGGGACCCAGAGNTCAGCACACATCTGCTGGGACCCAGGACTC GTAATTCGCTTGGTCCAACTCTTCTATGGGTTTAGCTGCCCTCATTC
WI-21909	153 A T	TGTTGCTTTGTGCCAGGTACTCTACTGCTTTACATAAAATATCTCAATTTCTGTACATCTAACGGCAA CTAAGTATACGCTTACATCTGTAGTGGCACCTAAATAAGGATATTTGGTCACTCTTTAAAGAAA TGCTTAAACATACCAAAG/ATJAGTGGAAATCAATAGATAAAATATTTAAGTCTTACAAAGCGTAC GACACTAAAGTAATATAGGATACCACTAAATTTATATTTCTATGTATGGAAG

WI-22202	128 A G ---	---	---	TGTTGCTTTGGTTGTTTCTTCTGGAACATATTGGAACACTTGTTTTCATAAGCTGTCTCCTGACAGT GGCACAATCCCATCCATCTTCAGGCCTTTTAATAAGGTCAATTATGAATCTGAATTTCTTGA/GJTAAAT ACTCTGGTGCAATTCATCTGCAAAAGCAACTGGCACAACCACTCTGCGGTGAGCTCTCGG AGAACATCTAATATTAGTCTAGTCTCTGTCGGAACCTTCTCCAGCTCAC
WI-22189	70 C T ---	---	---	CCAAGGATGAAATTTCCACATTTATTTNCTTTTATGTGAATAGAAATGGCAGTGAAGTGTCTCTATG AA/CTTGAGCGAGGAATGGGCATGGCGCTGCGGTACGACCTGGACGTTGTGCTTCCAAAGTACAC TATGTGTGGTGAGACAAAGGGT
WI-22283	109 T C ---	---	---	GGGGAGGCATCATAGAAAAAACCCTCAGCCAGAAGTTAGGACATTGTGATTCTCAGCCACTAACGA GCTGTATGACCTTGGTCACTAGGCCCTCTGCAGGCTCTGTGTG/CJTTCATTGCAAAATAAACCCCA GACCGGGTCATCTTTAGTTCCTTCCAGCTCTATTATTTATGATTGCTCTTAGTCTTTATGAGCCA TGTATGATTATCAGTCTCCCTGATGCACTCAACTCCAAATGATGCAAAAG
WI-2290a	136 C T ---	---	---	GACGTACTCTGAGGGCTCTGCCAGGTGGATTAGGTGAAGAGAGGTTTTATGGSCCTCTAAGCACCG GCCAGTAGTGGGAATGCCATGCATGGGTGAGTGGGATCTGGGGGGGTGAGACCTTGCTTTT [C/J]TTCCAACTCTCTCTTTAGCCAGAACTTTGCGAGAGCCCTTTNATTTCTCTTCCCTCTATTCC CCTCCTTTCCCAATGTGCTAAGGTCCCAATTCAGAGCCCTCCAG
WI-22292	53 A G ---	---	---	CCAGTGAAGGGTTTACAGCCATAGTGAGGTTCCCCCATTTGCTCAGTACCAGA/A/GJTTTGAGTAC GGTCGTTTAAAAATACTTATCTGACCACAGTGGAAA
WI-22387	186 C T ---	---	---	ACCTTGACACCTGCCATCCGGTGCCATCTCTCTGGCTGGCACATCTATACCCACTCTGGCTCTGAAAG GCTTGTCACCAACCAAAATGGCAGCTGGGGCTAAGGCATATTAAACAAAGCTCCAAAGGACCCCTT TCACTTGGGCTAGCATCCAGCTCTCTCTCAGCAAGGCGAGATTGTGGT[C/J]CCTTTGTGTTTTCTG AACAGGGCCCGAGGCGAGCCAGGCATGCOATCACTGCAGCACTCAACCCCT
WI-22395b	127 A G ---	---	---	GCCGTTCCAGTATTGATAATAATTTGTGTTTAAATTTCTATACAGAAATGGTTCTTTCTTGAATATTT GTAGGGATGGATGAATTGAAAGTGAATTAAGTCAAGATAAGGGGCAACTCTTTAAT/A/GJAAG GAAATGTTACCAATCCATAGTGAAGAGTAGAATATGTTCTTTTAGAGTAGNTAGAAAGTCCCCAGG CTCCT
WI-22405	90 A C ---	---	---	TTTATGGCTCCTGAGTGCCTTCACCCAGCTACACTTTACCTTGATCTATAAAAGTGAATTTAGAGT AAATACATTGGCTGTAAAGTCG[A/C]GATCAGGTGCTCTCCACCAAAAGCAAAACAAACTGCTGA AATGTGCAAGGTTTCTCAGTG
WI-22419b	67 T C ---	---	---	CCCTCTGGACAGTTTGCTTATGTGTTAGACAATCAAGNCTGCCCTTCCAGGCACAGCCAGTGCTT /CJCTGGATGGCATCAGCACAGGCTCCCTGCCCGGCCCTTGAAGCATGGCTGTGTGCACGAT
WI-21342d	59 T C ---	---	---	ATTTTCCCTTTCTGTGTTTCGTATTTTCCCTTTTGTGAGTAAATNAGCAATACACTGAT/CJTGGA ATCTGCATGATTAAATAACATTAAACAAGTTCATAAACACACCCCATATCAGAGTATAAAGCAAGAG GTTGAAAAATATCCCTAACCGAATGCAAAATTAGGTATCCCTCAAAATTGCACATTCTCCTCCTAGTT T

WI-21763b	154 A G ---				CATACCCCTTTAGGTGCCACATTGATCTTAGTTAACAGTCTTGTAGTCCCTCTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACTTCCAAGTGGAGCCAGGCTCAGACTGTTCTCAGTCACT GCTCTCCACAGCTGATT/G/CAGACATTGCCTGTCTTCTACCCAGCAGCTGTCTAGTGCACCTT GA
WI-21763a	135 T C ---				CATACCCCTTTAGGTGCCACATTGATCTTAGTTAACAGTCTTGTAGTCCCTCTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACTTCCAAGTGGAGCCAGGCTCAGACTGTTCTCAGTCACT T/C/GCTCTCCACAGCTGATTACAGACATTGCCTGTCTTCTACCCAGCAGCTGTCTAGTGCACCTT GA
WI-22440	64 A C ---				CAGTCCATTGAGTCCCCAGTCGAGGGTGCACTTCTCTTATCTTGTAAAGCCACTTGGGTAA[AC] TCCATTCCAGCTCTGCACCTTCTCCAGTTTCTCATGTGAGAGTCCCTGGAGGGAGGCTTCTTGG AAAT
WI-22449	74 T C ---				CAATGAATGTTGTGGCATATGATTTNCCATTGTGTGACAAATTTATTAGCTGGCATCCGAATACAGTAC TTCTTTT/C/GAAAAAATACACAATGGGAAGTACACTGACA
WI-21965a	112 A G ---				CAGGTTCCACCAGAGGCTTTATTTCAGCCACTCAGGACCTGGCTTCTGCTCCAGGCACTGAACA CAGTCAGGCTCTTCTAAACACTGGCAGGACCTCCCCACAGC/A/GJCCCCACAGGTTCTCTGTT TCCCAGTCTGATGGATTGAGCAAGACCTTTCACACATTACCCACTACCTGCTGGAGAGGAGGTC ATGAGGCAGCTGTGTGCTGCCAGCTCAGTGTGACACACTGCCAATGTGC
WI-21687c	115 C G ---				CACCTGGCAGTTGATCAGATTGTAGGAAAAATTAACCCAGATGGGTCTACATTTTNTTCAAGTTCA AACCACATGGTTTCTAGTCAGAAAGTCTCATGGACTTTCTTCTTAAG/C/GJTGTTCTATGATCAGAC CACCTCCTAAATGTGGCTTTACCCATTACAGGCTACAGTTGAATCAGGCAGGAGCAGCTGCTGGAG AG
WI-22374a	149 T C ---				AGCTTTACAACAAAGCGAGGGTTTAAGGAGCTGAGAAGAAATTCACAACTATTGACTATACAGAG TCTTCAATCCAAAAACAGTTAATAGTAACCTTGGTGGCACATACAAATGCATTGAATACTCTGTAT TATTCAGTAACATAAT/C/JAGGNTCCTGCATCATTCTCTTCCACA
WI-22250b	132 C T ---				ACTTGCTTCAGGCAGGCACTTCTGGGATCTAAACTAGAAATCCTTGAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCACTTCACTGTAGTGGTTATTATGGGTTCTCTGCCTCCTGGCTGTGTATG[C/T] GGANCCAGGAGTGGAGGAGCCGTGGAAATAGACAGGGGAG
WI-22250a	89 A G ---				ACTTGCTTCAGGCAGGCACTTCTGGGATCTAAACTAGAAATCCTTGAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCACTTCACTG/JATAGTGGTTATTATGGGTTCTCTGCCTCCTGGCTGTGTATGC GGANCCAGGAGTGGAGGAGCCGTGGAAATAGACAGGGGAG
UTR-04932-2b	192 G C ---				GCAGCCATCCTCTCTCCAACACCTCCAGGCCACCTGGGGCCAGAGCACCTCATGCCAGCAGCAC CTACGTGGCCCGAGTACGGACCCGCTGGCCCGAGTTCTGGGCTCTCAGGACGTCCAGCAAGTGA GCCAGAGGTTTGTGGGACTCCAGCCAGGGGATGAGGCCAGCCCGAGAACCTG[C/C]AGTGCTTC TTTGACGGGGCCCGCTGCTCAGCTGCTCTGGGAGGTGAGGAAGGAGT

UTR-						GCAGCCATCTCTCTCAACACCTCCAGGCCACCCCTGGGGCCAGAGCACCTCATGCCAGCAGCAC CTACGTGGCCCGAGTACGGACCCCGCTGGCCCGAGTTCTGGCTCTCAGGACGTCGCCAGCAAGTGA GCCAGAGGTTTGC/TJGGGACTCCAGCCAGGGGATGAGGCCAGCCAGCCAGAACCTGGAGTGCTTC TTTGACGGGGCCCGCTGCTCAGCTGCTCTGGGAGGTGAGGAAGGAGT
04932-2a	149	C T	---			GTGAGGAAGATGGACCTGGACAGAGATCAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTTCCACCGCCCTTGGCACTGTCTCTGGCCCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTCCTCAAGATGCAGCCAGGAGCCTCTCTGA AGGACAGTCTGGTTACGATGCTGAGCTTCTTAGAACCTTCCATGGTT
stFIBBb	412	G C	---			GTGAGGAAGATGGACCTGGACAGAGATCAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTTCCACCGCCCTTGGCACTGTCTCTGGCCCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTCCTCAAGATGCAGCCAGGAGCCTCTCTGA AGGACAGTCTGGTTACGATGCTGAGCTTCTTAGAACCTTCCATGGTT
stFIBBa	341	T C	---			GTGAGGAAGATGGACCTGGACAGAGATCAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTTCCACCGCCCTTGGCACTGTCTCTGGCCCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTCCTCAAGATGCAGCCAGGAGCCTCTCTGA AGGACAGTCTGGTTACGATGCTGAGCTTCTTAGAACCTTCCATGGTT
stIGLV2	61	T C	---			GTGAGGAAGATGGACCTGGACAGAGATCAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTTCCACCGCCCTTGGCACTGTCTCTGGCCCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTCCTCAAGATGCAGCCAGGAGCCTCTCTGA AGGACAGTCTGGTTACGATGCTGAGCTTCTTAGAACCTTCCATGGTT
stSG1001	70	T C	---			GTGAGGAAGATGGACCTGGACAGAGATCAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTTCCACCGCCCTTGGCACTGTCTCTGGCCCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTCCTCAAGATGCAGCCAGGAGCCTCTCTGA AGGACAGTCTGGTTACGATGCTGAGCTTCTTAGAACCTTCCATGGTT
7a	33	G A	---			GTGAGGAAGATGGACCTGGACAGAGATCAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTTCCACCGCCCTTGGCACTGTCTCTGGCCCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTCCTCAAGATGCAGCCAGGAGCCTCTCTGA AGGACAGTCTGGTTACGATGCTGAGCTTCTTAGAACCTTCCATGGTT
stSG1002	63	A T	---			GTGAGGAAGATGGACCTGGACAGAGATCAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTTCCACCGCCCTTGGCACTGTCTCTGGCCCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTCCTCAAGATGCAGCCAGGAGCCTCTCTGA AGGACAGTCTGGTTACGATGCTGAGCTTCTTAGAACCTTCCATGGTT
3						GTGAGGAAGATGGACCTGGACAGAGATCAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTTCCACCGCCCTTGGCACTGTCTCTGGCCCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTCCTCAAGATGCAGCCAGGAGCCTCTCTGA AGGACAGTCTGGTTACGATGCTGAGCTTCTTAGAACCTTCCATGGTT
stSG1009	36	G C	---			GTGAGGAAGATGGACCTGGACAGAGATCAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTTCCACCGCCCTTGGCACTGTCTCTGGCCCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTCCTCAAGATGCAGCCAGGAGCCTCTCTGA AGGACAGTCTGGTTACGATGCTGAGCTTCTTAGAACCTTCCATGGTT
stSG1011	107	C A	---			GTGAGGAAGATGGACCTGGACAGAGATCAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTTCCACCGCCCTTGGCACTGTCTCTGGCCCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTCCTCAAGATGCAGCCAGGAGCCTCTCTGA AGGACAGTCTGGTTACGATGCTGAGCTTCTTAGAACCTTCCATGGTT
stSG1012	89	T C	---			GTGAGGAAGATGGACCTGGACAGAGATCAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTTCCACCGCCCTTGGCACTGTCTCTGGCCCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTCCTCAAGATGCAGCCAGGAGCCTCTCTGA AGGACAGTCTGGTTACGATGCTGAGCTTCTTAGAACCTTCCATGGTT
stSG1017	42	C T	---			GTGAGGAAGATGGACCTGGACAGAGATCAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTTCCACCGCCCTTGGCACTGTCTCTGGCCCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTCCTCAAGATGCAGCCAGGAGCCTCTCTGA AGGACAGTCTGGTTACGATGCTGAGCTTCTTAGAACCTTCCATGGTT

stSG1019 3	136 GA ---	---	GGACAATACTACCTAAGGACAAAATACTATTATTAATAAAAAAGTCTTCTAGTGTATATTGTGTAACACATTTCTGGAGCTGGTAGGAATAACCATTTTATTTTCTGTAGTGCCATCTATACAAACCTTTTAC TIG/ATTTGAAAACTGAGATTAAAGTTGCAAAC
stSG1020 2c	143 GT ---	---	AAGCTAACTTAGGTGAATGGTGCCTCAAGGTCTTTCCGAGGGAAGCTCAGTCCCTGGCTTGGGAGAGTCAGCCTTGGTACCTATAACGGGCTCCAAGCTAAGGGCTCAAGGAAGCAGTCCCACTGCTTCTCGCTGTCA/GTTCAGAGACCACAAGGCAGATGCCACTGCTGCTCTTCTTCTGCTACTTTCT
stSG1020 9b	75 AG ---	---	TCCTTTCTCTCTTTCACTCTCAGTCACCATGATTCAAAATAAACTAAATTCCTCTAAGATCCCACTTTATTTTTAA/GCTCCAATAAATGTAATTATCAGCTGCTGAATT
stSG1020 9a	34 CT ---	---	TCCTTTCTCTTTCACTCTCAGTCACCATGATTC/TAATAAACTAAATTCCTCTAAGATCCCACTTTATTTTTAACTCCAATAAATGTAATTATCAGCTGCTGAATT
stSG1021 8	29 TC ---	---	TACTAGACATGCAAAATGAGAAGATTACA/T/CJGTGAATATTTAAAGAAAGTTATATTTGTTTGACATAATATGCATTGTACCCGGGCATAATAAAGTTAAAGCCAGTTATTCTGA
stSG1025 2	108 AC ---	---	ATAGGTTTCAGGAACAAAATCATTAATGGAATAATGAGAAGAAATCTTTATTTTGGACCAATTTTAGGCATTAAGAGTTTCTTTCTCTCTTCCCTTGATCA/CJAGTGAAGATATGATAGGGAATTCAGAAATTTCTCTCTTG
EST10915 0	123 AC ---	---	CTGTATTAATTAAGAAGGCACCTATTAAATGAGGGAGGAAAAATCTACCTGTACACAAAAATCTGTAGTTAACAGCATCTTCAATAAAACCTTTAAAGGATAATGGTTACGATCATTTTAAAG/CJATTTTAA GAACTGAGTTATTTGGAC
EST11023 1	166 TA ---	---	TTTTTGTAAACCAACCCCTGAAAGTTCCACATGTGAAATATAGATACAACAGTGAACAAAAATATGGCCCTCCCATGTACATTGGTTACCTATGTACAAGTATCCTATACACCAGTAAACAGCAGGC AATTAGTCAATTAAAAAAATAGTACATGTTAT/AJGTGTAATAAAATTTAAATTTACAAAGGCTTTTCCACTCGTGGATTGTCTCTTTTGGAGGGAGTAATCCTGG
EST14096 8	71 GC ---	---	GGGATGTATATTACAGATAACACAACCTACAATAATACCATCAGACATTGAAACATAAGGCCATTCTGTGA/GCJTATTTTAAAACTGGTGTTTTGCACATAATGATCTTAAAAAAAATGAATTACCAAAACCAAGATTCTCTTCTAAATGAAAAATTTAATGCAGGTACAGGATAACTTTAGGGCTATATCTAATCTGAAG
EST22113 6c	125 CA ---	---	TGCAAAATGTGAGAAGGCAGCGGGGCCAACCCCTGGACCTCATCTCTGTCTAGAATGTGAGGTCTGCAGGGATGCTTAAGTCTCTCTGCGAGAGACCCGAGGTGCAGAGATGATTCTTCTCA/CJCCCTTC TCTCAGGGTCTGGAG
EST22555 7	60 GA ---	---	TCAAGCATGTGTGAAGGCACCTGCCCCGCCAGACCCCTTCTAACCTCTGCACACTGGAAGGT/GJAAAACTGGGAGAGAGAGACACTCCCTCCCTAGCTTCTACCTGGGACCCCTCCAAAGATGAGCATTCATCTGGAGACCAAAATAAAAAAGGACAAAAAGACCAGGGCTCAGAG

EST22917 6	74 C T ...				GTAAACCTTGCAACGCCATGCTAAATGAAGCCTGACTGACCAGGGGCTCTGGGCTCTCAATGCA ATAGAAA[C/T]TGACATGGGCGCAAAAGACTTCCAGACAAAAGCAGCGAAGGGTAGAGGATATAG GTTAGCATCATCTGGTTGTGA
EST38458 6	65 A G ...				CAAGTTAGAACCATGCATCAGCTTTTCATCCATGGTGTAACTTAAACCTCAGGCTGCTCCTACTCA[A/ G]TGTTGTTGCTAGCCTCACTCGCACACAGGAAGCTTGGAAATTTGGAGGCTCCAACTCACTCTCCA
EST36745 3	56 A G ...				GAGGGGAACTTCAAAGAGGATTCCAAACAGTGAAGCAGAATCATGGGGCAAAAGT[C/A/G]CTATGG GGCCAGACTGAGGTTGGAACACACAAAGCACTCCAAAGCTGGGCCAATCCCAACCGCTGGTGAAGCCGC ACAGCAGGAGTAGCCAT
STS- R37410c	201 A T ...				TGTGACCATACCAACCTATGCAATAAAAGAAAAAATCCTCACTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTTCAGGCTTTTTGAAGTGTGAATAAAGTTTCATAGCATTTTGGGA ATTTATGGTTTGAATAAAATACAAAATGTGTGATCTCCTGAGACACATTTATAACATTCTGGTATG T[A/T]TTTGTGAGTGGTGTCTAGTGGCCAAT
STS- R37410b	139 G T ...				TGTGACCATACCAACCTATGCAATAAAAGAAAAAATCCTCACTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTTCAGGCTTTTTGAAGTGTGAATAAAGTTTCATAGCATTTTGGGA ATTTATGGTTTGAATAAAATACAAAATGTGTGATCTCCTGAGACACATTTATAACATTCTGGT ATGTATATTGTGAGTGGTGTCTAGTGGCCAAT
STS- R37410a	48 C T ...				TGTGACCATACCAACCTATGCAATAAAAGAAAAAATCCTCA[C/T]TTAAAAAACAACAA AAAAACCTTTGCAATGCTATCATTTTTTCAGGCTTTTTGAAGTGTGAATAAAGTTTCATAGCATTTT GGAAATTTATGGTTTGAATAAAATACAAAATGTGTGATCTCCTGAGACACATTTATAACATTCTGGT ATGTATATTGTGAGTGGTGTCTAGTGGCCAAT
STS- R42778	74 C T ...				TATCGTGGGAAGTTCCAACTCATCTTATGCTGCTTTTCTACTTGCTAATATTGGATGCTTCTTGCCA GGCT[C/T]TTAAATTGTGCTGAACCTGGGAAGAAACCTTCTACTCTCCACAACCCCTGAA
UTR- 04350	125 C G ...				CAATCTGAAGAGATGCATAGCGGATTGGTGGCTTTCAGCAGCTGTGGGGAGGTGGGACTGAGGAGCG ACTGCTAATCAGTATGGGTTTCTCCCGGGATGGTGAAAATGTTCCGGACCTAGATA[C/G]TGACGA AGGTAGCAGCACACTGTGAGTGCACCTAA
stSG1026 6	55 T C ...				GAAATAAACTAAACCTGCAAGCAAAATCACTGTTAATAAGAAATTGTTCTTCTGTTT[C/G]GACAGTTG AAGTGGGTGTGAGATGGGCATAGCAATGAACAGTGGAGCCCAATGAGGTCTCAGAAATGCGGGGCAAA CTCCTCTGTGAAAATGTAT
stSG1028 2	70 T G ...				GTATAATCAGCATAGCCAAAGCCCTTTTAAAAATAACCAATACTATCATTTTATGAAATCTTTACA AGAT[G/A]AGCACAGTAGTACAATATTTAAGCATCTCAAGTCTCCATTTAAGAGTTGACTATC
stSG1031 0	128 C A ...				CACCTTAGATATGAGGAAATGGTTTAAATGGACACAAAGGAGTACGCCAGTTGGAACCAACATAG TTTCATACCACGTTGAAACCATGTGTTTATATGCAAAATACAGCAAAATATTTTTCACCT[C/A]TTTG TCAATGCCAATGCATTGAAAGGCCCAAGAAAATGAGAAAAGGATAACAAACTTTTGATAAAAAAGGTA AGAATTTCTGTGTG

stSG1033 1b	116 T C ---	---	TTTAAAGCTACATGTCTGAAGAATGATGCTGCTGATTGAAATAAGGAAGAAAGGATGCATTTCGG GCTCCAACTGTCTAGGAAGGCTAGACCTCAACACCAACCTCCATTC/GCATTTCCTCTTTGG CTACTATGTCTTTCCCTGACTTCTGCTCTCCAGCTCTCTGGGCTGCTGCTTCCACCTGTTTCATCTGA CTTAGGACCTCC
stSG1033 1a	107 A T ---	---	TTTAAAGCTACATGTCTGAAGAATGATGCTGCTGATTGAAATAAGGAAGAAAGGATGCATTTCGG GCTCCAACTGTCTAGGAAGGCTAGACCTCAACACCAATTCACCTCCATTCCTCTCTTTGG CTACTATGTCTTTCCCTGACTTCTGCTCTCCAGCTCTCTGGGCTGCTGCTTCCACCTGTTTCATCTGA CTTAGGACCTCC
stSG1243 b	225 G A ---	---	ATTGGCAAATGGGAAATGACACCAATCATTTGATTACAGAAATGTTTTATAATCCTCCTCTTG AAATTATGTTAGGCCAGCATGGTAGCTTATGCTGCAATCCAGCACTTCGGGAGGCCAAGAGA AGGATCGTTGAGCCAGGAGTTCGACACCAAGCTGGGCAACATAGTAAGACCCCATCTCTGTTTTT TTTAAAAAAGAAATTCGTTC[G/A]AAAGTATTTTCAGACCAAAAGGAGGT
stSG1345 b	60 G A ---	---	AACTGACGTATCACAGGGGCAAGTATCTCTGTCAATAATTTGAACCTAGTTTGTCTTAC[G/A]CGCT TCACATTTAGCATGGGCCAAATTCAGGAGATGCCATGCAATGCCATAAATGGGGCAA
stSG1345 a	54 T G ---	---	AACTGACGTATCACAGGGGCAAGTATCTCTGTCAATAATTTGAACCTAGTTTGTCTTACGCGCT TCACATTTAGCATGGGCCAAATTCAGGAGATGCCATGCAATGCCATAAATGGGGCAA
stSG1385 b	117 T G ---	---	TTAATGTCATCCAGGGAGGGGCCAGGATGGAGGGGAGGTTGAGGAGCGAGAGGCAGTTATTT TGGGTGGGATTCACCACCTTTCCCATGAAGAGGGGAGACTTGGTATTTT[G/G]TCAATCATTAGAA GACAAAGGTTTGTGAACCTTGACCTCGGGGGGATAGACATGGGTATGGCTCTAAAAACATGGCC CCAGCAGCTTCAGTCCCTTCTGTCG
stSG139	69 T C ---	---	TCGTCTCTTTCCAGTGTCTTCCAGAGCATCCCATGATGTTGTGACCGACAGCACTTTGTGTCT TTC/GCTTTGAGCACTTCCCACTCTGGCTGGTGTGCTGCCACTGATTGTGTACTGTCTTGCTGCCC GATCTGTTCCAGACAAGGCTGATTCAGAGACTCCACGTGGTCAAGGCTCTGTTTGTCAATCCCT TGGCTCCTCCACTTCCAGTTGGCTTCTGTCTCTCAGTCTCTCCATGTGGCAACCAAGATGGC TACTGTGTCCAGGTTACGTCCTCTCAGCTTGGAAATCCAGCAGCAAGAGATGTCTCACTCCCA AAGTCCATAACTCAATCCTTGGGAAG
stSG1427	103 T C ---	---	CCCTGGAGTTTCTGAACATAGGAAGAATGCAAGTCATGTGTAGGTCC[G/G]CTCCCTTGCATGA AATGTGGGAGAGGAAATAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCCTACC GCA
stSG1471	50 A G ---	---	CAAAACCAAAATCCTCCACGATATATTACTATTTAGTCTAAGTTC/JTTTAAATCAAGGTTGAGA ATGACGAATCAAGAAATTTCTTACATACATAAATGCTTTCCTTAGTCTGCAGATGGTA
stSG1483	44 T C ---	---	CACACCCACAAGTTTCATGCTAATGCCAAGTATCACTCTTGAGGACAAAGGCAAAACCAAGTGTGCA [C/G]AATGTGGAGGATGTCTGTGAGCTGTAGTTACTAATGCAGGAAACCCCAATGCAAGAGGAA AATGCTGA
stSG1696	67 C G ---	---	

stSG1847 b	95 G A	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACCCCTAAATGAAAGAATTT AGAGGTTAAATAAACAAGTGAGAGACC[G/A]TTTACTTACATCAGTTCGGTTTATAGACATTTGAA TCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAAATTAATAAATGATCACTGTGCT TCAACACAACTG
stSG1847 a	49 C A	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACC[C/A]CTAAAAATGAAAGA ATTTAGAGGTTAAATAAACAAGTGAGAGACCGTTTACTTACATCAGTTCGGTTTATAGACATTTGA ATCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAAATTAATAAATGATCACTGTGC TTCAACACAACCTG
stSG1897 a	83 A G	CTTAATGCCCTTCTCTCTCTTCTGCACAGGAGACACAGATGGGTAACATAGAGGCATGGGAAGTGG AGGAGGACACAGGACT[G/G]GCCACCACCTTCTCTCTCCCGTCTCCCAAGATGACT
stSG2022 a	86 T C	TGCTTGAGGTTTCAAACTGAGATATCTATGGCAAGTTTATAAAAAGTAGACTTATGATCAAGGTACAA TTTTAACATTAAATATACAT[C/A]ATCCATAATCTCATCTATTTAACATTAAACACAGGCTTTGTGT TGTTATTTTTCTCCCTACAATATTTCTGACTCTGTAGGACAGTGGGCTCAGTTGGGGGTTGAC T
stSG2076	104 C G	AAACGTTGTCCCAAAAATTGTGTTACAGTTTCACAAGTATAAAATAAGACTTCTGAAAAAAGTTTACA ATTAGTTATAAAACACTTAAGAATAATATTTGACATT[C/G]ACATCACAGTGGGGCATTTT
stSG2108 c	71 A G	TTGAGCAACAATGATTTCGGAATTGGGAGCTCCAAACCAAAAATGATTGAGGGGCTCCACAGAGA GAG[C/A]GTTAAGGGGAAGACTTTTATAGGACAACTGTAGAAGTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTATTGTTGTTCTATCTTATGGGAAAGTCTGTAGTTATGTAATTGTAAG TTGTTGGGCTGTGTCTGA
stSG2108 a	49 T C	TTGAGCAACAATGATTTCGGAATTGGGAGCTCCAAACCAAAAATGATT[C/G]AGGGGCTCCACAG AGAGAGCATAAAGGGGAAGACTTTTATAGGACAACTGTAGAAGTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTATTGTTGTTCTATCTTATGGGAAAGTCTGTAGTTATGTAATTGTAAG TTGTTGGGCTGTGTCTGA
stSG2141 b	173 A G	TTATTCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTATTTTAAACAAATGACTGCGTGTAC TGAATCTGACTGTGTGAATAATCTCAGAATGGCAGCACCCTGGCATGGCATGGTCAGGTGGGT GCAGTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAAG[G/A]AGTTCCCTATTATTATTTAAGGC AGTTTCAGAGCACCTGGCATTCTGTTGCTCTG
stSG2141 a	113 C T	TTATTCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTATTTTAAACAAATGACTGCGTGTAC TGAATCTGACTGTGTGAATAATCTCAGAATGGCAGCACCCTGG[C/T]ATGGCATGGTGCAGGTG GGTGAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAAGTCCCTATTATTATTTAAGGC AGTTTCAGAGCACCTGGCATTCTGTTGCTCTG

siSG2148	50	A G ---	---	TGGGAACAACCGGCTATAGTCTGAGTCATATTTTGTAGACCGTGATTTC/GAAGAAACAATAA ATGTGGATTAGAAAGGAAACATCCATTACTGTATTTTCGATACCTTGTGATGTTCCACAGACGAGCTC ATCAC
siSG2175	68	C T ---	---	CTCAATGAGGACTCCATCAGCCAAAGCGGTTTATATGGCAGATGAGCTGTACAAATCTGTTGTGCT IC/TGCCGCGTACTCAGCTAATGCTACCGGGTTGGAGCGCACACCGAGCCAGCCACCTTTTCCAT ACCTGGCAGAGGGAAGGAGTGGAAGACCA
siSG2189	41	C T ---	---	CAAGTGGTGAAGCTGGGATTGAGCCTGATATTCACACTA/C/TCTACATCCCTCCAGTATAATA GGAACCTCATCGCTAACTTGAGCACCTTAGTGTTCTGAGTACTTCGTATAGGTTATCTCAATCCTACTC CAGCTTTGCGAAC
siSG2200	49	T C ---	---	TGTTGATGACCATAGAGGATGCAAAAGCTCCGGGCTGGTCTGTATGATG/CJTATATTTATGTAT AATGCTTACCTGATGATACCCACATATTACTAGCCTTATAGATGAGGATGGATGGCAGCTTGGCTG GTCAAT
siSG2243	85	G T ---	---	CATTTCTGCCTCCTCTCCAGTACTACCCCGTCCAGCAACTGCCTCTCGTATAAATAAGTATCAA GATGGTCAGTAGAAAAG/GTJAGAGCATCTCCTCAGCCCTGGAAGACAGTGTGGAGCTTCAGCT
siSG2257	65	A C ---	---	TCAGTGATTGTAGGAGCTGGCTAAGTCATGTCTAACTCTGTGAGGCGGCTATCAGAAGGGCAG/A CJCTGTCAGGAACCTCGCCAAAGCACTGGGCTGTCTCCTCAGGCAGAAATTCCTCCT
siSG2306	67	A G ---	---	GTCATCAGCGTAGAGGTCACTGGTATAAACAACAGTAGCTATATGATATTTGGGAACATATTTACA [A/G]TATGCTCCCATTTGGGTTTCCAAACTGATACAACCATGAGGTGAACACTTTCAGTGTTCACAG TTCTCCAGAGA
siSG2334	70	T G ---	---	GAAAACTACCCACAGCATCATGTTAAAAGAAGAGAGATGAAAAGAAAAAATCCCCGCAAAAAACA AAAAAT/GTGCAGTGGAGGGGCTGTGGAGGGGTGAATG
siSG2339	63	T C ---	---	AGACGAGATGGTGAATCAACAAGACCTCAAAATGCTTGACTGCGAGAAGTAAGTGTGAC[T/C] GTTCTCAGAGTCAACATTACGGTGACTGTCTATTCTGGCTGTCTCCTATTCAATCA
siSG2465	76	C T ---	---	CAAGACTAAGAAGCGCCAGTGGTCCCACTCAAAAAGAGATTTCTGATTCTACCTCAAAATG CAGAAACCA/C/TJACAGATTAAAAGAGAAACACACACACACTTTGAGAAACTCGCCCTTCCTC ATCTTCAAAGTGTGGGGTATGCA
siSG2549	140	T C ---	---	TTGCAGGCTTGATTCCACAATAACAAAGTCATGTATAGAGAAATGTGAAATGATCTTGAAAAACCAA GATATATAAATATTGAAGTCATTTATGCCCTTTGATGACTGGTTAAATATGCAAGCAGCTAAAG GAATATT/CTACACACCCACCCCTTTTAACT
siSG2577	123	T G ---	---	AATTGCCAAATGGAAAATCCAGAGGATTTTAGACCAACTTTGCCCTGTTCATCCAGTTTGGT CCCAATATAGGCCCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAAGCA/T/GJGAACAATC CCGGCCACAGATTAAITATT
b				

stSG2577 a	121	CT	---			AATTGCCAAATGGAAATCCAGAGGATTTTAGACCAACTTTGCCCTGTTCATCCAGTTTGGT CCCAATATAGCCCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAG[C/T]ATGAACAATC CCGGCCAGATTAAATT
stSG2700	58	GA	---			ATCTCCTCGACTGCTTTAGTGGGAAAGGAATCAATTATTTATGAAGTGTCCGGCCCC[G/A]AGTCAC TCAGCGTTTCGGGAAATAAACCACTGTCCAGAGAGAGAGGCTACTTGAGCCGGACACCA
stSG2724 b	101	TG	---			AAACAAGCTTTGTCATTTTCACACTACATTTTGTGTCTTTATTAATATTTGCAATGCTATAAT TTAATACTTATATCCAAATGCTTGCATAATCA[T/G]TTTTTTAATCCTGGGTGTGAAAGAAC
stSG2776 a	65	GA	---			GTGGCCGATCTTTACTTTTCCAGAAAAGCGGTAAATAAAACCTGTAGAAAGTCTCGAATATGC[G/ A]TATTGGCCCTTTGGAGTTAGGCCAGGAACCTCAACAAGGACACTGCTGGCCAAACCACAAAA ATATCCACTAATCCCGAATATAGTAAACCCTGTCTTGTCCGAATG
stSG2791 b	109	GT	---			AAGGAAAGTGGAGGGAAGGGAAGAAATTACAATGGTTAGAAAAGAGCAACTAAAGATTATTTT TATTATACCTCTGAACGGTAAACTAGCAATTTTAAATAATTT[G/T]GGGTCCACTTAAATCTATTA AAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
stSG2791 a	100	AG	---			AAGGAAAGTGGAGGGAAGGGAAGAAATTACAATGGTTAGAAAAGAGCAACTAAAGATTATTTT TATTATACCTCTGAACGGTAAACTAGCAATTTTAAATAATTTGGGTCCACTTAAATCTATTA AAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
stSG2826	85	CT	---			CCGCAATTTCAACACACATTTCTATGAAAACCTAAGGGTGGATCATGTACAAACACAAAAACAAGC TCCCTCCCTCCAAAAACA[C/T]GAACAAAAATAAGAAAGAAACCCATGAAATGCCAGGTTTA ATTTTTTCC
stSG2850	88	GA	---			ATGGTGCATTGTAAAGGCAATTAATACCTTTTCAGGCAGGGGCTGGCAATTTAATGAGCTGA TGTGTCCCAAGGAGACGGCC[G/A]GGCTCACACATCCCATCAATACTCTCTCCCAT
stSG3031	71	TC	---			ATACTCAGGGGGCTGAAGGGCAATGTGAAGAGTGAAGTCAAGTCTGGCATTTTCTGTGGTGCAGC AAAT[C/G]CCCCCTTTATTTAAATGATTCCAGACATCTGGGCAGCATAGCT
stSG3058	81	GA	---			GTCCCAACTCCTCTCTCTTAGAGAAAAAACTGTGATTACCTCAACTTGAATATGAAACTGTGATTG AAAAAGTCAAAAC[G/A]TGAAGAAGCATCAAAAGCAAAAGGCAAAAGGCAAACTGGCTGAGGC
stSG3092	94	TG	---			CAGCATCTCCAGAACATCTCCTAGAACTGAACCATTTCTGTCACTATTGAAAAACAAGCCCAAGTTC CAATCCAAAATAATAATGAACGTGC[T/G]GATAAACATTTCTTATGTTCCAGCCCCCTACTTT AGTT
stSG3230	95	AG	---			AAGAAGTACTTTGGTAGCTATTTAAATAAGAGGGGGTGGGAATGAATGTCGAGATACGAGCACCTG CATCTTTTAGTCAATTTGTCAGTGGAGT[C/A]G/TGGGGTGTCTAAGTGTCTGAAGTGAAGTAG
stSG3245	160	GC	---			ACATCTCATACCCAGTAAGATGCAAGAAAGGAATATCTGAGAGCAAGCAGCCCTGCTCCAGGGGCC CAGGTATGTGAGAGGCCAGTGGGGGTGCCACTTGGTGTCTACACCCCCCTGCCATCCAGTCTG GCCCCAGTACCTACCTGGGAGGTT[G/C]GTACTTGGCTTAAGTACTTCATGCTTTAT

siSG3265	42 T C ---	---	AGGTGAATGAGTTACTAAATGTAGCATTATTTATAAGGAATTC/GCATTGTGAATAGTTTCTCAG TTTTCAATTATGGAAGATGATGATTTTCAGCCACATTCAGTGTATGTTTCTAAATAACACAATCGAC AGGACTGTCTGTTCAGTACAATGGAGGACAGCTTTTCAGGGCAATGGGATTTCTTGATAATGCTAA ATCTGTCTTGTGAGCTGAATTTCTTGGGCTTTATGTGGCAGTGTGGTAAAA
siSG3269 b	141 C T ---	---	TGTACTTACTGTGTCATCCTATCCATTCCCTCCCTGAGCTGGACTGCTCTCCAAGGGAGACTAGG AGTGAAGGGAGGAGTCTCCCAAAGTTACCTTTAAGCTTGATAATTAGCTCCATAGCCATGCTAAA GCATGA/C/TTGTAGATCCCAAGTCCCTGACACATTTCTCTAAGAACT
siSG3269 a	24 A G ---	---	TGTACTTACTGTGTCATCCTATCC/G/TTCCCTCCCTGAGCTGGACTGCTCTCCAAGGGAGACT AGGAGTGAAGGGAGGAGTCTCCCAAAGTTACCTTTAAGCTTGATAATTAGCTCCATAGCCATGCT AAGCATGACTGTAGATCCCAAGTCCCTGACACATTTCTCTAAGAACT
siSG3284	130 C T ---	---	TTAACTCAAGAACTTTTCAGTTACAGGAAGATTTATCTAATATTAAATGACTAAATTACAAAAAGC ATAAAATGTTGAAGCCATTTTAAAGTTGTTTGAATCCATATTAGCACTCAGACTTCCCCA/C/TT TCCCTAACTTTTGTAAATGCTGTAATGGGACATTTGTGTTTGATCTACCC
siSG3292	99 A T ---	---	GTCTCAAGTGAATCTGTAATACATTTTAAAGTCTGACTTCAATCGGTACATGAGGCTTAGACATA CACATCATGGACAAGTGAATTAATATCTAA/ATTTACAAATCAATAGCATTTTCCTAACCTCAA TAAATGTCATATCTTTAGTCTCACT/C/AJCCAGTGTATCCATTTCCCAAGCCGTAGAGCTTTCTG TTCTGTAGATTTGCCTGCTGGACATTTGATATAAATGAGTGTCTGTATCATGTTGAGCTTCTCTC ACCTAGCATGATGTTTCAAGACACATCCATGCTGTAGCATGCGTCAGTGTCTTCACTCTTTAA GATCCCAGTATTATTTCTAAATTTGAACCTTGTGTTGTGGAATAAAAAATCTGAGGACCCTCAGAG GG/C/TTATAAGGGAACCTCTTTTGTCTTAGTTCATAAGGACTTTCT
siSG3369	69 C T ---	---	CAAGACTGTAAAGACGTAGGCCCTGTGAGAGTGAAGGAGGATGCTCGAACTTGGCCAGGACTCAGG CTTCAGCTTCACAATCCCGAGGAAGGAATGACATTTCCAAACTGTCACCTTTGTAGC/G/TTCTGGGT CAAAGTCTAAGAGGACAAATAAATAGAGACT
siSG3398	125 G T ---	---	TCTTACTCTGTTAACTCAGTCTGGAGTAAAGGATGCAATCACG/G/CTCACTGTAGCCTGGACTCC TGGGTTCAAGTGATCCTCCACCTCAGCCAACTGAGTAGCTGGCCTGCAGGACAAGTCACCATGCCTA CCTAAGTTTTGTAGAGACAG
siSG3416 a	43 A G ---	---	GTAAGACAAGGTTTGTCTATGTTGACCAGGCTGGTCTTGAACCTCTGGCTTCAAGCGACCGTACCA CCTTGGCTCCCAAGTTGCTGATATTACAGGTGAGCCACTGCCCCCGGAGCTTTTAACTGAAT GTTGAAATCATTTCTGCTCTTTGCTGGGTAACTGAT/AJCAAGTTGCTTAACTTTGTGAACCCAC TTTCTCTATCTGTAAACAAATGGACAACAGAACTTTTCTCTTCTCTC
siSG3424	173 T A ---	---	GTTTCATGTTAAAGATTAGGAAGCTGTGGATGTGAGGGGTGAGGTGATGATGGAGGCTTCACAGA ATGAGTGGCAGAGAGGGCCCCCT/AJGAAATAGCTTACTCTGTGTTTCTCTATC
siSG3436	88 T A ---	---	

s1SG3463	103 C T	GATACAGAAGATAGTGGTATGGATGGATAGTGAAGGACAAAATAATACAAATATATTTATTG AAATAACAAAAATGCATACACAGCTCAATGGGTAC[C/T]TGGAAACAACTTGCCTTGACTATATTA CTGA
s1SG3491 b	71 G A	CAAGTACTTTCATTGCTCTAAGTAGTGCAGTGTGGCAAATATTTCTACGAACAAGGACGATTG AAGA[G/A]GTGGAATTAAGTGAAGGAGTACTTTACCTCCAAATAGCCTGCAATTTAGCAGTCTGA ACAACTCTTAATCTTTTACTGGCACCTGTGGATTTCTATTAACTCAATTTACTATTTTCTGTGATG ACAGAAAAATAAGTTAAC
s1SG3523	33 C T	TAGCCATCTTACTCTAGTCTTTTGGGTTT[A/C]TGCCATATATGTGTACAAACACACACACACC CCTAATCTCTCAATGCTCTGGCATAAGTTTATCTCTTACTGGTCTC
s1SG3536	213 A G	AGTACAAACACAGATTTAAAGAGCTCAGCAGTATTGACACGCTGGAAATTAATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGGTAGCCTACCTACACAGCTGCTACAAAAACCAAAATACAGAATGGCTTC TGTGATACTGGCCTTGTGAAACGCATCTCACTGCTCACTATTCTATTGTTTAAATGAGCTTG TGCACCATTAAG[G/T]CTCTGCTGGGTGTTCTCAGTCTTGCCATGAAGTATG
s1SG3583	112 G A	GAAAAAGCTTAACATACGATCCATGTGCAAAACCCCAACAGGATCTACGAACCTCTGGCATGATCCA CATCGCTACACATACCATGCTGGAAGTGCACATCCACACAGGCAC[G/A]TAACATACACAGTACTGT CTAGTTATCAACACCTAC
s1SG3586 a	60 G C	CCTAGTACATAGTGAGACCTCGTCTCTACTAAAAATTTAAAAATCAGGTGGTGGT[G/C]ACCG CCTGTAGTCCCTACTTGGGAGCTGAAGTAGGAGGACTGCTTGAACCCAGGAGATGGAGGCTACAGT GAGTTATGATGGGCCATTGCACCTCCAGCTTGAGACTGTTTCAAAA
s1SG3589	101 T C	ATATAGTGTGTAGCATTATAAAGTCTTTAAAAAGCAATCTGGCCATATCAAAAGGCAAAAAAGT GTATATACCACTGGCACAACCAACCCCAATGA[T/C]CTATTTCCAAAGATGTATCCAGATGAAA GTATCCAAACAACAAAAAGCTATATACAC
s1SG3590 a	70 A T	GAGAGATGAGCTATTTATCTTTTACTTTAATGAAGATGTAAGAAATGATCTTCTGTCTAAAAAAA AAA[A/T]TTTCTCTGATGCTCTTGACCTGTAGGAAACACATTCAGTTTCTACACT
s1SG3619	78 A C	CAGTGAGACTTCTCATTTTATAGCAAATACATTTTTCAGCTTAAATTTCTTGAATTCATACGCT TCTGTCAATTTA/CJAACAACTTCCAGAGAAAACTGGGCTCTATATTTAAG
s1SG3644	40 T C	ACATATGTAAGTCCATTAGTAGCCATATTTAGGATGAGAT[C/G]GATTGAGAGGCATGAACCAAGG ATGCGTAATAATCATTATGAATAATAAGTTATCTGGGGAACGGCCATTTGTCCAACATTTACTAA GTGCCTACTA
s1SG3646 c	70 G A	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAAATATATGATGATAACAAATAATATGCTTACT GGT[G/A]TATTAATCTTGATACTTGGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA

stSG3646 b	55 A G ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATGATAACAATA/GJ/TATGTCCTT ACTGGTGATATTAACCTTTGATACCTTGGTTAAGATGGTGCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3646 a	43 A T ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATG/A/TJTGATAACAATAATATGTCCTT ACTGGTGATATTAACCTTTGATACCTTGGTTAAGATGGTGCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3693 b	85 A C ---	---	ATTGTTTCCCTGAACATTCOCGTGGTCTCCCTCTGAAAGCCGATGACCATCCAAACCCCTGGACTCACCT GAAATATCCTACGAGGC/A/CJTGCCCTCCGAGACTGACGATTATTAACCCACCCACACGGAAAAAGG
stSG3693 a	30 C T ---	---	ATTGTTTCCCTGAACATTCOCGTGGTCTCC/C/JTJCTGAAAGCCGATGACCATCCAAACCCCTGGACTCA CCTGAAATATCCTACGAGGCATGCCCCCTCGAGACTGACGATTATTAACCCACCCACACGGAAAAAGG
stSG3698 b	145 G A ---	---	TCTGGCCCTTTGTGTTACCCCTAGAGAGATGGCACCCCAATCCCCAGGGTGTCTCTGACTTCCACCAT TCACTGACTTTTATTGCCAGAGAGCTCCACAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTAAGTCT TTATTGGG/G/AJAGAATACCCACCCACCTTCCCTCACTGCAGA
stSG3698 a	51 C G ---	---	TCTGGCCCTTTGTGTTACCCCTAGAGAGATGGCACCCCAATCCCCAGGGTGT/C/GJ/TCTGACTTCCA CCATTCACTGACTTTTATTGCCAGAGAGCTCCACAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTA AGTCTTTATTGGGGAGATACCCACCCACCTTCCCTCACTGCAGA
stSG3724	107 C T ---	---	ACCAGCTCATGTGCAGAGGGTCTCCTGCTGGATCCCCAATCGAGGCCATCCCTGGGCCCTAGACTTCT GTCTCCCTCACTTCTAAATGAGTGCTCAGTGATGTGAAG/C/JACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTGCT
stSG3725	104 G A ---	---	GCCAAAACAAAAAGATCTTTGGAGTTTACTGACGGCAGCAGTTAATAGCACAGTCAACAGCATTTAA ATCAATATATATTACCAGCCCAACAGCAACAGCCCC/G/AJAGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGGTAAATAACGGCACATTTA
stSG3751	128 G A ---	---	CGGAAGAAAGAAACACAAATCCACAGGAACAATCTATGGTTCATACCTTTTAGAAAGATGATTTTG AGGGCTTCAGTATTTAAGGGGAAAGCAGGCTGGAGGGGAAAGAGAGGATATGGTCCC/G/AJ/T GCTGACTCCATGTGTGCAAGAG
stSG3787	49 T A ---	---	TTCTGTGCAAAAAGAAATCCACATCATTTGTTGGTAGCAGAGGATCTCTTAT/AJAAAGTCCCTAAGA CACTGAGGGCATAAACCCAAACAAAATAAAATAAGGAGTATAGGCTAAAGCAGTATCTTCCCCT
stSG3880 b	115 G C ---	---	GACAAGAGGAAGAGATGCCACAGAGAGAGAGGGCTGGGGCAGCTGGGGTCCCTGAGTCCAGGGCGC CACCACAGTCTGTGGGTCAAGGCCCTCTCTGGGAGCAGGTCTA/G/CJ/GGCACGGAGGATGCAG GGCTGGAGGGGAOCCCACTCGGGGACCCAAAAGGAGTCCATTTCTGCCCT

stSG3880 a	36 G C ---	---	GACAAAGGGAGAGATGCGCCAGAGACAGGGCTG[G]GCGAGCTGGGGTCCCTGAGTGCCAGG CGCCACCACACGTCCTGTGGGTCAAGGCCCTCTCTGGGAGCAGGTCTAGGGCAGGAGGATGCAG GGCTGGAGGGGACCCACCTCGGGGACCCAAAAGGAGTCCATTTCTGCCCT
stSG3885	44 A G ---	---	AATCAGCCATTGTACACATTGCAGCTATGTATTGTAGTGTG[A/G]TTTTTTTTTCCATTAACTAA TACATGCCCTCATAGATATATTCAATTAGTGTATCACCATGGGAACAAGATGCTGATTCGTCAACTG AAAA
stSG3902	104 T C ---	---	TCTGTTGAGACTGGAGAGACAGGTACCAAGCACCGACTCTGGTGGGAACCTGGCTTCCCTGATAACA TCATCTATTTACCTAAATGTGAAGTCTTTCTTTCT[C]TCAGCTCAATAGCTTAACATCTAATTC ATGTTTGTCTCCCTTTGCTGGACAAT
stSG3935	50 G A ---	---	GGGTGTCTGACGGACAGGCACACCCAGCAGTTCACAAAGCAATTTGTCC[G]A]CTAGTGTGCAGGC TCCTCCCCAGTTTCCACAGGCTGAGTACTATGGGTCAACCTTCTCTGGACGT
stSG40	25 A G ---	---	GAGGAAGAGGTTGAAGAAAGTGTGA[A/G]AAATATATTTAAGATTTCTTTGGGAGAAATCTGTGC CCAAACCTGGTATGATGCCCTTACTATTAGATAAGGAACAAATAAACCCCTTGTGTATGTATCA CCCA
stSG4009	32 A G ---	---	GTGTGGGCTGTCTGATGATGAATGGCGCGCTC[A/G]TACTCTTTACGGTCTTACACTTTTATGCTCCT ATGAATCTCTGATGGGCTTTAAGGGCTGAACCATATCTGAAGTTTCCACACTGCTTACA
stSG4033	123 T C ---	---	AGAAGCCTTGGGACAATGGCAGTGGCCTTTCTGAGTAAGACATGAATGCCATCTGGAGGATCCATT TGAACCTACAGTGCAGTAACCAAGAACCTAATGTTTTCAAGCATAAAGGTACTTT[C]TGTGAAC AGGTGGGCAACAC
stSG4038 a	29 G A ---	---	GCTGAGAGCACGTGTACAGCCACGCCCTGT[G/A]CGGAGGCCACTCTGTGCAATAAACATGTTCTGCC CATGTTCTCAGTCAGGAGGTTCAAGGCTCCCGGAGAGCACCTGAGGGTTCCATCACT
stSG406	53 T C ---	---	ACTGTGGTTCAACAGTATTGCGTTGTCAGACTAGGAAAGCTAAACGAACAAA[A/C]GGTTTAGTT TTGCTGAAGACTGGCCTTATTAATGGACAGCTTTCCTAACAGAGATTATTAACCTTTATCAGGTGTT AACATCTGTTTCAGGAACATGGCA
stSG4095 b	55 G T ---	---	ATCTGGGCTGAATTAGTCAAGCAGGTCAAGTACTATTGTCTGCTAGATGTATTAG[G/T]ATAAAAA GTTTGCTTCTGTATACTTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGTCTTGAGAAATCAAG CCTTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
stSG4095 a	27 A C ---	---	ATCTGGGCTGAATTAGTCAAGCAGGT[C/A]GATACTATTGTCTGCTAGATGTATTAGGATAAAAA GTTTGCTTCTGTATACTTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGTCTTGAGAAATCAAG CCTTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
stSG4120	65 G A ---	---	TGCATGTTCCACATCTTTTCATAACAGCAAAATGTATAATAAACTTACGTACTTATGGATAATCAC[G/ A]CTTTTCCCTCAGAGAGCCACAGTTAAACACGTTCCAGCACACCATTAATCCACCGAGCT

stSG4128	54 A G ---	...	CTTGGCAGATAAGGACTCGTTTGCAGATATGACTTTCCTTTGTGTACATTTCT/GATATATTTT TACTTCTTGAAATGCCACATAATTTGCAATAAATGATTCACTCCTTAGCTCCAAAGCAAGTCC TTTATCAAAATGCAAAATGTTCCAGAGG
stSG4209 b	128 G A ---	...	CACGAAACAGATGCAGCCTACACAGTGTGTAGGACCGAGGCTCACAAACATCCACATGGCACAAAGC AGGCGCGCCACTCCAGCAACGAAGCCACCCCGAACCTTGACAGGGCGCACTCCCTC[G/A]GC AGGGGACCAACGGAGCGACAGGTGCTTTGATGCCCTCGAAGAGCTGAGCTCCATTCCA
stSG4209 a	65 G A ---	...	CACGAAACAGATGCAGCCTACACAGTGTGTAGGACCGAGGCTCACAAACATCCACATGGCACAA[G /A]CAGGGCCGGCCACTCCAGCAACGAAGCCACCCCGAACCTTGACAGGGCCGCACTCCCTCGGC AGGGGACCAACGGAGCGACAGGTGCTTTGATGCCCTCGAAGAGCTGAGCTCCATTCCA
stSG4254 b	31 G A ---	...	CATTACCCAGAACGCCATGGAGGACCAGAGC[G/A]CCACGGCCGGGACTCCGCGATGGCTGGGGG GCTATGGCTTGACAAGAGGATGAGCGAGGGCCGGGGCTGCTCTCCCCAGGGGCAGACGTGAC TGGGGGACCATGGCCGAAGAGAGGATGACCGGTGATG
stSG4301	81 T G ---	...	TGCAACAGCTCTGAGAGGAAATCCTTGGCAGATCAAAAGAGAGGGTAGTGGCTCCACACTTTCCAT TTAAGCAAAATAAAIT[G/AGCTTCTGAGTAGTGTCCAGTTCACCCAAACATTTTG
stSG4331 b	71 T G ---	...	CTCACAAGGCCAACACAGAAAAGATACAAATACATTCACAGCTAATATTAGTTTATGACAC AGAGT[G/JTTTCAACAAGTTTAAAGTGCACCTGAAGAGCATGTTAAAAGTTTAAAGTTATCATT GGAGAGCAGATTCTTGGCTCGCCCTTGATCTGTTGAGGGGTGTC
stSG4340	76 G A ---	...	TTTTGCAACAACATGGATGGACCTGGAGGCCATTAAGTGAAGTAAATGATACAGAAAGTCAAAAACC ACATGTTCTC[G/ATTAAGTGGGAGATAACAATGTGTACACCTGGACGTGGAGAGCAGAA
stSG4361 b	109 A C ---	...	TCCCAACCATTTGAGTGACAGAGCTCAGTCAATGCAAGAACTCAGGTTTGCATGACTCAAAATTAGGCAC AAGTCTTGGAATTTCCATAAGGGATAACTGCATCTTTTGC[C/C]CCTTCACAACTAGAAACGACTC AGCGACTTTTCTGTGAGCAAAATGTCGAGG
stSG4361 a	24 T C ---	...	TCCCAACCATTTGAGTGACAGAGCT[C/C]CAGTCAATGCAAGAACTCAGGTTTGCATGACTCAAAATTAGG CACAAGTCTTGGAATTTCCATAAGGGATAACTGCATCTTTTGCACCTTCACAACTAGAAACGACTC AGCGACTTTTCTGTGAGCAAAATGTCGAGG
stSG4376	73 A G ---	...	TTCACTGCTACTGGTTTCGGTGTCTGAGTCCCTCAAACTCTGCTTTGCAAGTGCTTCTCCAAGGGGAG AACAGI/GI/GTGAACCTCGGCTCTGCAAGAAGCCATTCTTCCAAAGCCATTCTTCTCAGCTGC
stSG4381	50 T C ---	...	GAAAGCCACAACACTCCATAGCCAGAGAATGACAACATACGATTTCTTTT[C/JT]CAGTCTTGTAGT ATCCACAGTAGTGTCTGTCCATGTACAAGTGTCTGTCCAGAACCCCATTAATTCATGCC ACCAATGGTCTGTATGTGATCCGATATTTTTCGCCGATCTGAAATACTGCAAGGGCTTAACCAT TCAACACCCG[G/JTGACAACGAACCCAGTGGACTGTGAAACTCAGGCTGCAGGAGGGTGGCTTGT CAGCTGGGT
stSG4410	79 A G ---	...	

stSG443	65	C T	---	AGCAGATCAGTCAGCCCACTTGCTCTCTCTCTTTAGGGAGAGGCTAGGCAGTGAACACATCA/C/
stSG4430	54	A G	---	TGTATGCAATGAGAAAAATAACCAACTGGTAGGATGGGGAGGGGAGGCAGGGAATAGGCAC
a				AAATGGAATCTATCCTGGCTGCTCTCTCAGGTC
stSG4448	99	G A	---	ATGCACATTAAATGAATGGCCTAACTACTGCGGAACCTTAGTAGTTCTATAAGGTJA/GJATTAACATA
stSG4449	92	T C	---	GGTAGGATCAGATTCCTATGACAGGCTGCTGAAGGAACAGATATAGGCATCAAGAGGGCCATTTT
stSG4467	42	C A	---	CCTCCCTCCCTTCCCTTCCCTTCCAGTCTTTCCATAGTGTCCCTCCGCCCCACCCAGGCTCT
stSG4475	21	A C	---	CGCTAGCCCTGCCCTCTGGGGTCACTGC/GJATGGGTTAGGCCCCCCCAAAAA
stSG4477	32	A G	---	ATTAGCCATTTCATTGGAACAATTGCTTTACTGTAACATAAGAGTACTGTACTGATGTTTACAAT
stSG4531	79	C T	---	TAACTTTGGACAACCTAAACCTTA/T/CJTAGTGACATTGCTGTCTAATAATCAAATACTTCATCATA
stSG4550	86	G A	---	GGCTGAACATAATTATAAAGAGCAAAAGTTACCCCTCCC
b				CAGACATGAGGGATGCCCTGTCTCTCTGGGACAGAGCCCTCA/CJAGATGATGTCCATGTTTGTGT
stSG4550	85	C G	---	GAATGAACTCAAACACTCTTCAGTTTTAGAGTCATTTTCTGTATCGAGCGACACACCGAGGAG
stSG4590	47	A G	---	CACACCTGCTTCCAAAGGCTGCTGCTCTGCACACAGT
stSG4623	22	T C	---	ACATGTCACTTCTGACCAGG/A/CJTATTAATAGTTTATTTAGAAGAAATGAGTTGAAGTGAGCGCA
stSG4843	102	A C	---	TTAAGAGACACAACTGGACTTTTGTTTTCTTTACTGTAGCACCCAGGTTTCATG
				GTAACTTCTGGGGTGGGGTGAGACAAACA/A/GJATGAACCAATAATTAATTACAATTATACATT
				TCAAGGAGACTTTTAACTAGGTTAATGTGAAACGCAGCCATCAATGGTTTGTGAGGAAAAAGGAGA
				TGAACTCTGCTCTGGGCAACGTTTGGCCCTCATTCGAGTCAGACTTGGC
				TGAATCAGAGCTGGGTGGGAGCTGCAGCAGGGGAGGCTGGGGCCAGATGAGCCGCCGGGGA
				CAGCAGGCGTC/CJGCCACGTCCTGGCGTTGGTAGAAGAGGACATAGGCTGCCCTTGGACTCGATCT
				GATTCATTGACAGGGGAGAGCGCTGTGTCATCAA
				TGCATTAAAGGAATGATACGGCATATTTGGGGGACAGAGAACAAGCTTGATGAGGACAGAGCTATTT
				AAAAGACAGATGGGCACC/CJACAAATGGAGGGGAAGCGGGGCAGGGTTTAGAGAAC
				TGCATTAAAGGAATGATACGGCATATTTGGGGGACAGAGAACAAGCTTGATGAGGACAGAGCTATTT
				AAAAGACAGATGGGCAC/CJ/GCAATTTGGAGGGGAAGCGGGGCAGGGTTTAGAGAAC
				AATCAGGCAAGCTCGGGAGAGAAGCCAAACAAGCTCTCTGCAC/A/GJATGGGAGGGAGACAC
				CATTGAAAAGGCGATCGTTCTCTTCTTCATGCAAGCGAGGCTGGCTCCACAGGCATGGTCTCCTTG
				AATCTGTATCACCCAGCGCTGGT/CJCAATGTACTAGTAGCTTTCCACAGGGATTTTTTATACTATTC
				CTATAAGGTTTTATCATGAATAAAAAAGCTCACAACCTCTTTTCAGCCATTGCAGATTTCACATTTATCT
				TAATATCTCTTCAAGATGCTCTGGAG
				TAAAAAAAACAACCCCCCAAAAAACACCCAGAAAGTTTTTGAGTTTTTATGTTTTTCAGATTTAAAG
				GTATTTCTTTCTAGCTTCTAAATTTTGAGTCA/TJATCAGAAAGTCTTCCCTACTCCAAGGTGA
				GAAAGGA

stSG4850	38 C T	GGAACTCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTC[CTGTGCACCTTGCAGGCCACGTCAGGAG AGCCAGCGTGCTGTGGGGAGGTTTCCAAGTGCTCCGTGAAGAGCATGGGCAAGTTGTCTGACAC TTGGTGGATTCTTGGGTCCC
stSG4879	86 A G	AACCTCTGAAGGGGGTGACCTCAACCAGCCCTTGTTCTGTGAGGTCTGCTTTTGCAGAATGGCCTG CCCTGGGACTGGAGCAG[AG]CTTGGGTGAGCTCTAGGTGAGGGTGGTGGAGGGGCATAGAAAT AAACCTTCC
stSG4885	104 G A	ACTGGACTGGCTGCTTGTGAGCCGGCTGAGCGCGTGGGACTCGGGCTGACCACCTCGCTCTTCAG AGACTGCGCCGCGGTGACCACTACGCTCTGCC[GA]GTGGGAAAGCAGAAGCAGGACC
stSG4896	112 C T	AAACAAATCAAAACCCAAATCCCCAGCAGTCTATGTACAGGGCCACTCCCTGCCTCTCTGCCATAGAGA GGTTGGGGGCAGCTGAGGAGTGGTGGGGCTGGGCACCTTTCTCTCAGCCACAGGCCCTGAGG AATTAATTGACTG
stSG4932	22 G A	ACAGTCCGATGGTTACACAA[GA]TTGTAATGTATTAATCCCACCTACGAATGATTAAAATGA TAAATCTTATGTTTATTTATCATCACTACCAAAAGGCTGTGGTGCAGGGGTCTGTTTCTGGTCT
stSG4950	24 A G	TCATGACTCCAGGAAAGGTCCT[GA]GTCTTAGCTTCTCTCCCTACTTTTCTCTACATGGTCAGC ACTGTAATGTAGCTAAGATATAGTAAGGCATTGCTCCCTACCCCTACACTTCAAGG
stSG4957	136 G A	AGATACGGGCAAAACACTGGGATGGCTTCTTGACAACCTTAAGAGGTCTCCGAGTTATATTCTGGTT GGGAAACACTGACCCAGCCCTTATTCTTCAAGGACTCTAGTCATTGGCAAGGAGGATTCATGAGCC CC[GA]GTGACACAGATGGGGCCCTGCTCTATATTCAAC
stSG4961	91 C T	GAAAGTGCTCTGAGGAGGTGTGACTCTCCCTGGCTGACAGGGGAAGGCTTAGCAGAGCTTTGTCTTAG AGGAGTAGATGAAAGGAAAGTA[CA]TTAGAGAGGGCATTGAGGCCAAGTCAGCAACACAGACAA
stSG4967	72 A G	ACTGTGCTCTCAGCAGATTACGGGTGTCAGGGCTGTTACCAACAACTCAGTAGGAGTCAA GGCT[GA]GTACCCCGGAGCTAGACAGCCTGGGTTTGAATCTCAACTTCTCCCTTTTCTGTGTGC AACCTTG
stSG4997	22 T C	CAAAGGAGTAGGAGCCCA[TC]TTTAAATGGTTTCTCTCCCTCATGCTATTGATCCAAAA CTATATACAAATTTGTAGCAGTCTCTGTATAGTTATTACACATGTTTAGAAGGGAGGAGGCAAGAA GGGATAGGGAGAATGGTGATCCAAAAT
stSG6312	37 C T	ACAGGTTCTCACACTTTGAGCCCTTAGTGCAAAAAACA[CA]TTATGCCATGCGGGAAATAAAATGCTT ATCCAGTGGAGCGCTCCCTGATGCATTGAAATATTAGGATACTCAAGCAGAAGAC
stSG6345	107 G A	GCTCTGTCGAAGAAATCTCCAGGACAGAAGCAACAGGACAGTAACACACATGTATGACCCCTTA CAAGTGCTTTAAGATTTTAAAAATGTGATGTTTTGTCCAC[GA]ATAGTTGAGGCAATTAAGAATAT GCAACCCAGAGAAATTTCTGTGAAAAACATTTTGTCTTTTGGCCTGGTGTGGACAGAAAGGTTGGCCAA ATGGATTGAGTGATGAGCAGACATG

stSG8362	88 G C ---				<p>TGTGAATGTACACTCAGGTCTAACAAATACCTATTATTTCTCTGTTAAGAAGTTTAGCAGGAGC CTCCAATGAGCACTGTATGTA[G/C]AGAAAAGGGAAGGAGCAGGAGGAGGAACACAGATCTGCACAGA AT</p>
stSG8010	62 G T ---				<p>CACATCTGTGTTTTCTGGAGCAAAAGGGAACACACAGAAGGCCAGGAGTTTGGGTGTGCACTGG[G/T] GTCCTTCAACTGGGTGGAACCAAACTGAGTCCTTGAAGTCTCGCTCCTGAGGCTGCAGAAGAATAGA TGGCTT</p>
stSG8022	53 G A ---				<p>AGCTCCTGACTCCCTGTTCAAGTGACGTCATGTTGGTAGCCCTGAATGGACCAC[G/A]GTGGGAGTTAT TTACACCATGGAAACTGGAAACTCTACAAATCAATGCGTTTATTTCTTTATTTTCAGAGGGCAGGTT TATCAGCACACGCTGTATCTCC</p>
stSG8032	67 G C ---				<p>TGATTGTTAGGATAAGTGGGCAATTGTGTTTACAAATACCTCCAAAGAATTACAGAAAATTGTGTGT G/CJTGGAGGCAGGTTAGCAAGATAAAAGAGGGAGGACAGCTGGGTTGGTAAAA</p>
stSG8064 b	46 C A ---				<p>AGCTGGCTCTTCTCTGTGCGT[G/C]TTGGGAGGCTTACGTCTCGCCGCTGGTCCCTGGGTGGCC TGCAGGACCAGGGGTGGGAACAATGCCAGGGAGAAATTCCTGTACATCAACAGGGAACA</p>
stSG8064 a	23 G C ---				<p>AGCTGGCTCTTCTCTGTGCGT[G/C]TTGGGAGGCTTACGTCTCGCCGCTGGTCCCTGGGTGGCC TGCAGGACCAGGGGTGGGAACAATGCCAGGGAGAAATTCCTGTACATCAACAGGGAACA</p>
stSG8072	59 A G ---				<p>CACCATCATCATCGAGTAGGCTGAGGAGCAGGAGGGGTGGTCTTGTCTTAGGG[G/A]GTGGC AGAGCGAGAAGGAAGTCCGAGTATTAGTGGCGCATGCAGTTCAGCCTGTGCTGTTCAAAA</p>
stSG8100	40 A G ---				<p>ATACACCCACACACCCCACTCAACCTTGATCAAAATCC[A/G]AAGTGTAACATAAGATATAAGAAT ATCATGACTAGTTAAAGATAGCAAAATACCATAAGGTACAAGTTCAAGTATTAGTATAACAAGTAT CTGAGTAACAAATGTCCTTGGAAATGGG</p>
stSG8102	138 T C ---				<p>AAGGCTCCTTGAAGCATGGTTTATTGTTCCATTTAACTTGTTCTCAGCTATACTGAAGTATGATT GACAAATAAACTTGCATATATTGAGATGTACAGTGTGATGATACATGTATGTATACAATGTGAAA TGA[T/C]TGTCAATAATCAATAATTAATGGTATATTGGTTTAGGAAATGTGATGGT</p>
stSG8105	110 A G ---				<p>CAGTGGTTCTCAAACCTCAGCGTACACGAGGATGGTCTTGCTTGTTAATACACAGATGACTAGGCC CACCTGCGGAGTTCCTGTTGGAGTCTAGGCCCTGAGAATATTC[A/G]TTTCTAACAAAGTCCCAGGTGA CCTGAGGCTCTTGGACTGGGGAACATGCTTTGAG</p>
stSG8130 b	96 T C ---				<p>GTGTGTACATCATTTGGGAATGGAGGGAATAAATGACTGGATGGTGGCTGCTTTTAAGTTTCAAAATT GACATTCAGACAAGCGGTGCCTGAGCC[T/C]GTGSCCTGTCTTCAGATCTTCACAGCACAGTTCC</p>
stSG8130 a	36 C G ---				<p>GTGTGTACATCATTTGGGAATGGAGGGAATAAATGA[C/G]TGGATGGTGGCTGCTTTTAAAGTTTCA AATTGACATTCCAGACAACGGTGCTGAGCCTGTGCTGTCTTCAGATCTTCACAGCACAGTTCC</p>
stSG8145 b	124 T A ---				<p>TTGTGGACTTCAAAATCTTTCTTCAGATTTTAAATGACATTATGCATGTACATATTTTAAAAATTT AGACACATTTTAGAGAACACAATTTGTGAACACAAAATCTAAGAAATGAATGAGATGTT[A/CT]GAAA TCTGATTCAAACACTATCTTAAACTGAC[T/C]TGCAATCTCTGTCTGTGCTGTGGAAGG</p>

stSG8145	97	C T	---			TTGTGGACTTCAAATCTTCCCTCAGATTTAAATGACATTATGTCATGTACATATTTTAAAAATTT AGACACATTTTAGAGAACACAAATTGTGAAC[C/T]ACAAAATCTAAGAAATGAATGAGATGTTCTGAAA TCTGATTCAAACACCTTATCTTAAACTGACTTCTGTCAATCCTCTGTCTGTGAAGG
stSG8150	36	A G	---			ATTGTTCTTGCAATTGCTTGGATTTTTCAGAAATAGT[AG]ATAAAATAATAACGGGAATCCTAGGCAT TCGTGTTTTTCTATGTTTTAACAGGATTTTCTCTAATGTTTGCCTATTAAATACCATGCAGGAAAT GGGAAAT
stSG8340	30	C T	---			AGAGGATTATGGAGAGAGCTGGCAGGATC[C/T]CAACATTATGACCCCTGAACCTCCAGAACCTGGAT TCACTAGAAGGAGAGAGAGAAAACGCTCATCAAAA
stSG8466	111	G A	---			TGTGTATTGGTGACTGTAGCCTAAGGATAAATGAAATAAATGACAGCAATGTTATAAGCAGTGGGA GGAGTGAACCTGGGAATACTTGGTTACAAGGTATTTGCACTACCT[G/A]TGAAGCAGCACAGCATTAT TTGAAAG
ESTD-ACE	---			GATCAAGCAGTGCACACGGGTACGATGGACCAAGCTCTCCACAGTGCACATGAGATGGCCATATA CAGTACTACCTGCAGTACAAGGATCTGCCGTCTCCCTGCGTGGGGGCCAAACCCGGCTTCCATGA GGCCATTGGGGACGTGCTGGCGCTCTGGTCTCCACTCTGCAACATCTGCACAAAATCGGCCCTGC
ESTD-ADA	---			AOCATCTTACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCAGCTCCACCCAGAGGCCCTGGGGAATCCAGGTCACCTGTTCTCTCTGCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAAGTGGACTGTGAGGACATGGAGGCCCTCGGCACCTGAGCTGCAGACCC GCAGACCAACTCTGAGCTTTCTGGCCCTCTGAGTCTTGTCCCTC
ESTD-AK-168	---			GGGAGTGACAGCTAGAGCACCAAGGGGGCTCTACAGCTGTGTTCTCATGGAGGACAGGCTTCTGCTC ATTCTGG
ESTD-ALB	---			AATCCAGCACTTTAGGAGGCTGAGGCAGGCATATCACCAGAGGTGAGGATTTGAGACCAGTCTGA CCAACATGTTGAACCCCATCTCTACTATAAAATACAAAATAGCCAGGCATGGTGTGTCATGCTGT AATCCAGGAGGCTGAGGCAGGAGAAATCGCTTGAACCTGGAGGCCGAAGGTTGTGTGAGCCGAGAT GGCAACATTGCACCTCCAGCCTGGGCAACAAGAGTAAACTCTGTCTTC
ESTD-ANT1	---			TCTCCTGTCACTTCTACTCCATTAGTTCAAGGTCAGTGAAGAACTGGGCAATTAACCAAGTAATTCA TGGACTGCCAACTCGGAACAAAGAGGGCGCAGTGGAGCAGGAGTATTGCTACGCGGTTACCTT TTTTATGGAGGACCGAACTGAGGCTGAGCTCAGATGATCCTGT
ESTD-APOA2	---			CCAGGTGTTGTGGCACGTGCCTGTAATCCAGCTACTCGGGAGACTGAGGCATGAGAATCTTTTGAAC CGGGAGCGGAGGTTGCAGTGAGCTGACATCGCGCCACTGCACCTCCAGCCTAGGTGACAGAGCAAG ACTCC
ESTD-APB3	---			GGAAGAAAATGGAGCCTGTGGGAAGGAGCGTCCGAGGGTGGGCTTTGTGGCAAGCCCTTGTGA AGCAGAAGGGCGTGAAGAACCGGAGCTCATCCACATCTCTGACTGGCTGCOCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTCGACGTGTGGAAAACCATCAGTGAA GGAAGCCCATCCCCAGAAATTGAGCTGCTGCATAATATTGACCCCAAAAC

ESTD-AT3a	..	--	---	---	AGACCTCAGTTCTCTGTATAAAGGGAAGTTTGTTCTTGGATCTCCATGGGCCAGCCAGCACTG GTGCCCTGTAGTCTGTATCAGGTAGAGGAGATGGACCAGGTGGAGGAATTTGAAAGGGCATTG GAATTCAGAGCAAGAGACAGATATTAAGAGCTGGGGAATGTGG
ESTD-B3AR	..	--	---	---	GGCTGCCAGGGTTCCGTGGAGCGGCCCTAGCCGGGGCCCTGCTGGGCTGGCGGTGCTGGCCACC GTGGAGGCAACCTGCTGTTATCCTGGCCATCGCCCGACTCCGAGACTCCAGACCATGACCAACGT GTTCTGACTTCGCTGGCCGCGCAGCCGACCTGGTGATGGGACTCTGGTGGTGCAGCGGCGCCACCTTT GGCG
ESTD-BA511	..	--	---	---	GGGCAACATAGTGAACCCCATCTCTACAAAAATACAAAAATTAGCCAGGTGTGGTAGCAAGTGC CTGTAGTCCAGCTACTTGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGAGGTGGAGGCTGCAG TGAGCCAAGATGGTCCACTGCA
ESTD-BCL2	..	--	---	---	AGCTGGATTATACTCTCTTTCTCTGGGGCCGTGGGTGGAGCTGGGGCGAGAGGTGCCGTT GGCCCCGTTGCTTTCTCTGGGAAGATGGCGCACCTGGGAGACAGGGTACGACAACCGGAG ATAGTGATGAAGTACATCCATTAAAGCTGTGCGAGAGGGGTACGAGTGGGATCGGGAGATGTGG GGCGGGGCCCCGGGGGCGGCCCCCGACCGGCATCTTCTCTCCCA
ESTD-BCR	..	--	---	---	CAGTGGCTGAGTGGACGATGACATTCAGAAACCCATAGAGCCCCGGAGACTCATCTGCGCAAGA GACCAAAGAGGTCAGCTTCTGTTGTCCGGGAAGGGAGGCGAGGTGACAAGCTAACTCTGTTCAA ATCAACCATCCGGTGGACACTGTGTGGCTGCCATCTGCCCTGGCACA
ESTD-BRCA1a	..	--	---	---	AAGAAGAGAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAGATCTCATGTTAA GTGGAGAAAGGGTTTGCAAACTGAAAGATCTGAGAGATGAGAGTATTTCACTGGTACCTGGTAC TGATTATGGCACTCAGGAAAGTATCTGTTACTGGAAAGTTAGCACTCTAGGGAAGGCCAAAAACAGAA CCAAATAAAT
ESTD-BRCA1b	..	--	---	---	ACTAATGTAAGAAAAATCTGCTAGAGGAAAACTTTGAGGAACATTCATATGTCACCTGAAAGAGAA ATGGAAATGAGAACATTCCAAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAAAATGTT TTTAAAGAAGCCAGCTCAAGCAATATTAAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTA TTAATGAAA
ESTD-BRCA1c	..	--	---	---	ATGCATCTCAGGTTGTTCTGAGACACCTGATGACCTGTAGATGATGGTGAATAAAGGAAGATAC TAGTTTTGCTGAAATGACATTAGGAAAGTTCTGCTGTTTTAGCAAAAGCGTCCAGAAAGGAGAG CTTAGCAGGAGTCTAGCCCTTTCACCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGCCAAGA AATTAGAGTCTCAGAAAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
ESTD-C1R	..	--	---	---	ACACAGGTGCTGGCACTGGGGCTGGGATCCTCTCTCCCTAAATTTGCTCGGGGAAGCACTTCATCAA CCCAGTCAGTTTGGGGACAGCCATGCACTGAGCCTCTGGTAGCCTTTCAACCATGCATTCCTCAT GCTCTGCAAAAT
ESTD-C8	..	--	---	---	

ESTD-C7	..	--	--	---	---	---	ATATCGTGGCCTTAGTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD-CB22	..	---	---	---	---	---	GGCAAGTTTTATTGATAGAGAGGAATCAAATAATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAATGGGAGTGCCAAACCCATAGGGCGGATACAAAAGAC AGGCAAGGAAGGGGTAGAACCATCAAAGAGGAATAGGCTGGTGAACCCCAAGCAAGGAGGACCTAG TAACATAATTGTCTTCATTATGGTCTTCCCGCCTTCTCTCACACAC
ESTD-CB23	..	---	---	---	---	---	TAGAACATCAAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCAATTATGGTCTTCCCGCCTTCTCTCACACATACACAGAGCCCCCTACGAGGACGACAGCT CTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAAAAGGTGTTCCCAACCCGA GGTCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAA
ESTD-CB24	..	---	---	---	---	---	ACCAGGACGACAGCTCTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAA AAAGTGTCCACCCGAGTCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAAAG GCCACTGTATGCTGGCCACAGGCTTCTACCCCGACCACTGGAGCTGGTGGTGAATGG GAAGGAGTGCACAGTGGGTGACGACAGACCCGCGCCCTCAAGGAG
ESTD-CB25	..	---	---	---	---	---	GTTTCTTTACAGACTGTGGCTTACCTCCGGTAAGTGAGTCTCTCTTTCTCTCTATCTTCGCCGTG TCTGCTCTCGAACCAAGGCATGGAGATCCACGGACACAGGGCGTGGAGGCCAGAGCCACCTG TGACAGTACCTACATGCTCTGTTCTTGTCAACAGAGCTTACCAGCAAGGGTCTGTCTGCCAAC ATCCTCTATGAGATCTTGTAGGGAAGGCCACCTTGTATGCCGTG
ESTD-CB27	..	---	---	---	---	---	TTTTCTGTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTGTTGGGCTGTTGCTTTCAGGAGTCTGTGGAGTCTGCTCATCACTGACCTATCTCTGA TTTAGGGAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCCAATGCTGCT TTCTCTGTTTCATCCTGATGGAAGTCTCTCAACACCATTTCCATACC
ESTD-COL2A1c	..	---	---	---	---	---	AGAATGTATATAGTCTCAACTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTACATACGTTGCTATTATGCTCTCTTCTCTGCTACTTCAGGGTGTCAAGGTGGAAAAGGT GAACAGGTCCCGCTGGTCTCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACAATACTGCTTTTG GTCAGCCTATTGAGCTGTAATCACCATACCGTACCT
ESTD-COL2A1d	..	---	---	---	---	---	TGAGAGAACACCTAGTCTCCATCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGTGGACCTGGAACACTGGACTTCTTCTACTGACGACAGCAAGACTTACCC AAGAGAGATTAAATGGCAAGATATACAATAACAATTTTATTGACCAAAACACTATCATGGAACAGC ATT
ESTD-CPT2	..	---	---	---	---	---	GCCGCAATGCCCGGAGTTTCTCCAATGTGTGGAGAAGGCCCTTAGAAGACATGTTTGTATGCTTAGAA GGCAATCCATCAAAAGTTAACTTCTGGGAGATGAAAAGCTACCATCACTTCTCATCATGAAAAC TGGGAGGCCGGCATAGTCTCATGCTGTAATCCAGCATTTTGAGAGGCTGAGCGGGTGGATCAC TTGAGGTGAGGAGTTTGAGACCAACCTGGCCAAACAT

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ESTD- D7S399	..	--	---	---	---	TGAATCTTAATTGCTATCTCTACAAAATGTATAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGTCTCCTACATCATCTCTTTCACAAACATTTTCATCCATGGACTCCATACCTAG AATATTTGAAGAAACAACATGACAAACATTTTC
ESTD-DM	..	--	---	---	---	GTGGGACACCGAGGGCTCCAGGCTGGCGCTTCACAGTGTGGCTCAAGCAGCTGCTCGGCCCTCCACT TCCATGGGTGTGGGCTGGACCTCACTGTCCTGGGAGAGGAGGAGGAGTGGGAGGGAGACA GAATGCTGATTATCTGGTGGAGAACCAAACTTCTGGCTGTGGGTAGGGGCAGCTGCTTCCAAGACC TCCTGATTTGAGGAAGGGGAGCAGCAGAGCGAAGAGACAGAGT
ESTD- DRD1	..	--	---	---	---	TCCCCAGCCTATCGGTGCATATTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAAOCCCATCAG ACAAACGGTCAAGCACCCAACTGAATCGCAGATGAATCCTGCCACACATGCTCATCCCCAAAAGCT AGAGGAGATTGCTCTGGGCTCGCTATTAAGAACTAAGGTAC
ESTD- DRD2	..	--	---	---	---	TCTGCTTTGTGCAGGAGGCTGCCGGCGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGGACCCGTTACAGCCCATCCACAGCCACACCAGCTGACTCTCCCCGACCCG TCCACACGGTCTCCACAGCACTCCGACAGCCCGCCAAACAGAGAAGATGGGCATGCCAAAG ACCACCCAAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	..	--	---	---	---	AAGCAGTGCCAGGATGAGCGGCAGTAGGAGAGGGCATAGAGGCATGTGGCGGGCTCGCTGG CACCTGTGGAGTTCTCTGCCCCACAGGTGAGTTCAAGTGGCCACTCAGCTGCTCAGAGATGCCATA GCCAGAGGGAGTGGTGATGCCAAGGGCTTCTGTGAGGAGA
ESTD- ERB2	..	--	---	---	---	TCTTCAGGATCCGCATCTCGGCTGGTTGGGCATCGTCCGCTAGGTGACGGGTCCACACGCTGG GGTAGGGGTGGTGCTAGTCCCGGGGGCGGTGACAGACCCACCGGGCTGGAGGACTTCAOCC CGCTCACTCCGTTTCTGCGAGCAGTCTCCGCATCGTGTACT
ESTD- ETS2	..	--	---	---	---	ACTCACAGTCTTTTAAGTGAAAATGGTCGAGAAAGAGGCCACCGAAGCCGCTCGTGGCGCTGGCA GTCCGTGGGACGGGATGTTCTGGCTGTTTGAGATTCTCAAAGGAGCGAGCATGCTGTGGACACAC AGACTATTTTAGATTTCTTTTGCCTTTTGCAACCAGGAACAGCAAAATGCAAAAACCTCTTTGAGAGG GTAGGAGGTGGGAAGGAACAACCATGTCATTTCAGAAGTTAGTTTG
ESTD-F2	..	--	---	---	---	GATAAGTACACTGAGGCCCCAGGAGTTATTGCCTAGTAGCCCCAACTGTGCTGACCGCTTAACCTCT GCACAAATGGCTCCAGGCCCCGTAGGGGAACCTGGGGGATCTAGGGGATGGGTGAGGAATGGCCC AGCCAGTCCGGCGGTGCTGGGTCCCAACAGAGGAGGCCGTGGAGGAGGAGACAGGATGGGC TGGATGAG
ESTD-F9	..	--	---	---	---	AGATCCTGATGATTTTTTCTCTATTTTTTCTAAATGTTTTACAGTTTTGAAGTTTTAGATTTATGCCCA TGCTCCATTTTGAGTTAATATTTGTGTAAAGTATGATGTTTTAAGTCAAACTTCATTTTTTTTTCCATA GGTATGTCCAATTTATCCAGCACAAATTTGTATAAACAAAAAAC

ESTD- GCH	--	--	CGCAGACCGTGTCAGTGTGGGTGGAGTGTGGAGGGAAGGAGGGAAGAACTGGGGTTAGGGACT TTCCGGGTGACTTCCCGTTCTGTGCTTGCAGAGAAAGGGGGAGAACACAGAGCCAACTGGCTAA GTGTAAGGACCTCTGTGTCGACCGTGTGTTCTGCTGCCCTGTTACGCTGTCTGTCTGCGCGAGTCGA CTCTGTCCCGGAAATTCGAGAGCT
ESTD-GCK	--	--	GTATTATGCATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCTCTGTGTACCATGAC AACACAGGCCCTCTCAGGAACACAGTAAGCCCTGGCAGGAGAAATCCCCACCCACACCTGGCTGG AGCAGGAAATGCCAGCGCGCTGAGCCCCAGGGAAGCAGGCTAGGATGTGAGAGACACAGTCACC TGCAGCCTAATTACTCAAAGCTGTCCCGAGTACAG
ESTD- GNAT2	--	--	GACCTGAGTACCTCCCTAGTGAGCAAGATGTCTCCGATCCAGGGTCAAAACCCACAGGCATCATTTG AAACCAAGTTTCCGTCAAAGACTTGAATTCAGGTAAGTGCATGGTCCCTAGG
ESTD- GPPK2L	--	--	AGTCTTCATCTGCGGTGTCAGGTAGATCCCTTTACCCGCCGAGAACTGCTCGATATC
ESTD- HRAS	--	--	CTGGGCTGCGCGCAGCAGCTGCTGGCACCTTGGACGGCGGCCAGGCTCACCTCTATAGTGGGTGG TATTGCTCCACAAATGCATCTGGATCAGCT
ESTD- HSD3B1	--	--	TTGGAAGTTCTCCACTGTTAACCCAGTCTATGTTGGCAATGTGGCTGGGCCACATTTCTGGCCTTG AGGCCCTGCAGGACCCCAAGAGCCCCCAAGCATCCGAGGACAGTTCTACTATATCTCAGATGACA CGCCTCACCAAGCTATGATAACCTTAATTACACCCCTGAGCAAGAGTTCGGCCTCCGGCTTGATTCC AGATGGAGCTTCTCTTATCCCTGATGTATTGGATTGGCTTCCCTGCTG
ESTD-HT2	--	--	GGGTAAATTTCCGAGCAACTTTGCATAGACTGTTTTATTGACTTGACAGGATTGCTAGAGATAGG CAGGAGAGGAGATGTGTACAGTTTGTACAGAGAGATAAAAGGATAACCTGGGGTTTCTGTGC TTTGCTTCTCACATCCCTGGGAGTTAATAGCTGCAATTTTCAAAGAAOGGTATACAGGGACAGCA AAGCGCAGTCTGTAAGTTTCAAACAAGACACACCTT
ESTD-HT4	--	--	ACCAACGAGCCCGGATACAGACACTCTTAAGTTTTGCCCTAAGGCTCATTCAAATCATTAGGCATTTT CTGATAAACTAGGTTCTTGGTGCTTCTATCGGCAAGAATGCGTACTTATTTGAATAGTAGAGGTAA ACCACGCGCCGAAGAGTCACTGAGACTGGCAGCTTCTGCAGCAGCGCTGAACCCCGTAGCCTAAA TGACAGCCGAAGAGGCGCCGAAGACATGCAGATGTGC
ESTD-HT5	--	--	AACACACAAGCCCGCAGGAGAAATTGAACCTCGGACCCCTGGTTTACAGACAGTGTCTTAACCCCT GAGCTATGGAGCCCTGCTGCTGTGTTGTTTCTTCTTCTCATCTTATAGATTGATGTTATGCTCCTA GCATTCGGGCTACCGAATAGGATGTAGCTTGAGTAAATCCAGGATATTCCTCACAAAATGAAA ACATTTCTGCTCTGTAATCCCTCGAAAAGTTCT
ESTD- IGFBP1	--	--	ACCCAGTGGAGCCCGCTCATTGCACGGTCTTGGCAGGAGGTGCCCTGGGAGAGAAGGAAGATGTTTC CAGGGCACACATAGCTTAGTGGAGACTC

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ESTD- IGHV4-6	TTTACTATTTCAATGGATACAGAAITGTGGGAGTCACTATATTCCTATGAACAAAAATTGAGATTT CAGTGTTAAGTAATGTTGCCTACATTTGTGTGAGTGACGGGAGTGTGGATCCGAGAGTGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGAAAGATGAGTATCTATGGATACGAACTGAAAGT ATGTAATACTTCACAAAATACTAATAAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	CAAAGTAAGCACCCCAATAAATGTTAGCTATTACTATCATTTATTATTATTATTTATTTTATTTTGG AGATGGAGTCTGGCTGTCAACCCAGGCTGGAGTGCAGTGGCACAATCTGGCTCACTGCAAGCTCTG CCTCTGGGTTTCATGCCATTTCTCTGCTCAGCCTCCGAGTAGTGGGAATACAGGCACCCGCCACT GTTCCCGGCTAATTTTGTATTTTGTAGACGAGTTCACCGT
ESTD-IL1B	CCACTACAGATGGATAAATGGGTACAATGAAGGGCCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGTCTCTACCTTGGGTGCTGTTCTCTGCTCAGGAGCTCTGTGCAATTGCAGG
ESTD- KRT10	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAAGTGTACCTTTTGGCAATATT AAAGGAAGAAAATGCAATTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTCTC TGCCAGATACATCTCCCTATATAAGTTATAACCAAGTATTGATA
ESTD- KRT8	ACCTCACCCCTCCCTAGCCGTTAGCCGTTGGGAGCAGGAAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACAGAACTTCTAGAGTT TGCTAGAGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCCCGTCTCAGGTTTACCACGTCAACATTGACACA
ESTD- LF79	GGTGATTTTGAGGCTCAGTTAATATTTCAAAATTTGAACCGTAGCAAACTGCATTGGTATTTAGA AAATAAAAATTTCCAATATGTAGTGTGTGTTATACCTGCCTCTGCCATGCAGCATCATAGCCTGT GGGAACCGAGGGCTTCCCTACCAACCCAGA
ESTD- LMP2	TACACACTTTCTTACCCATTCACTGAAAACGACTCGCAAACTGGAGCCTTGTAGGAATGGAGTTGA CCTTCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	TGTCAGTGTCCCTAGGGGCACCTCAACACTCCAGCTTCTCAGCTGTGCCCTGTCTGCTGCTGCA AGGGTTTGTCTTAATCTCAATTCAATGTCTCTTCTCATCTTTAGCAGCTGTGGGTTTTGTTGTTTC TTCTGTTTTTGTCTAGTATCTGACTACTTTTTTAATTATAAAAGAGATGTATCTAAACAAAATAGAG ATTGTTATCAGAAAGTTCACAACATTTATAAAAATTTTTTCACTG
ESTD-MOC	TTGTCAGGAGTGTGCTGATGCTGCCCTCCAGCTCTGTCCCTAGCCGAACCTTCAGGACAACGTGCAG CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTGTCTTTCCAAAGGGTTGGTCTAAGTGTCTAATACCGGATTTTCTGACGATC TTTCAACTGCTAGAGCATCTGGTCTCTGTTTAGCATGG
ESTD-NF1	ATTATCCAGATGAATTTACAAAATACTATACCAGATCCCAAGACTGATATGGCTGGT

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ESTD-RDS	..	--	---	---	---	CCCGAGGAATCTGAGAGCGAGAGCGAGGCTGGCTGTGGAGAAAGAGGTGCCGGAGACCTGGAAGG CCTTTCTGGAGAGTGTGAAGAGCTGGCAAGGCAACAGGTGGAAGCCGAGGGCGCAGACGCAGG CCAGGCCACAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCAC CCAAGAAACGTGGATCTCCCCCTCATCCAACCCGAAAGTCTGAA
ESTD- FYR1	..	--	---	---	---	CTTGTGACGGGAGGTACGTCTCCGCTCTTTTCATGGACATATGGATGAGTGTCTGACCATTTCCC CTGCTGACAGTATGACAGCGAGACTTGTCTACTATGAGAGGGAGCTGTGTGACTCATGCCCGC TCCCTCTGAGGCTGGAGCCACTGAGAAATCAGCTGGAGTGGAGCCACCTGGCTGGGGCCAGCCACT CCGAGTCCGGCATGTCACTACCGGCGAGTACCTAGCGCTCACCGAGG
ESTD- SPTB	..	--	---	---	---	TGAAACACCCTGTGGTCCGGAGCCAGGTGTGTTTCTCTCTGGAGCCTGAGGAGTTTGTGTGTGTG CAGTCCCCCGGCCACCTGCTGTTGAGCCTGGACATACACCTTACCTCTTGGCCCCGGAGAAGAC ATTACCCACCTGGCCATGTCCCTGGCCTGTTGTGCACACCCTGTGTGAAGACCCCAACCCCTGCTCC CCCACCAAGCCAGTTTCTAGCAAGGGCAGGAC
ESTD- SSA1	..	--	---	---	---	TTCACTTTGTGGATTGTTCTTTGTGTGCAGCACCTTTCAACATGATGTGATCCCATTTGTCCAAG TTTGCTTTGGCTGCTGTGCTGTGGGATATTGAAAGAGATCTTTGCCAGTCCAATGTCTAGAGAG TTTTCCCAATGTTTCTGTGTAATAGTTTCATAGTTTGGGCTTAGATTAAAGTCTTTAATCCATTTTG ATTTGATTTCTGTA
ESTD-TAT	..	--	---	---	---	AAATGGTCAGGACCCTGATCCACAAGAAAGTGGTACCATTTCATCAGGGCCATCAGTTTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTTCACTTAAATGACTTGTGGACAGGATCA ATTTCTCTCACCTAGAAGCTTTGTTTACAACCTTTCTCCAGTATGGATGGGATATGATGGGGGG GAGAAGCAAAATTTAAATAGGACCCCATGAGACACATCA
ESTD- THR8	..	--	---	---	---	TGGGGCTTTCTCCGGCAGGTAGACTTCTTACTTGGCTGTGATTTCCAAGAGAAAGAGTCCCAAG CACACGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAAATCACACAGGATCACTTCATCCA CACTGGATTGGCCCAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCTGTAGATGGG
ESTD- TNFA	..	--	---	---	---	TTCTTGATCCTGTCTGGAAGTTAGAAGGAAACAGACCACAGACCTGGTCCCCAAAGAAATGGAGG CAATAGGTTTGGAGGGCATGAGGACGGGTTTCAAGCTCCAGGTCCTACACACAAATCAGTCAGTG GCCAGAAAGACCCCCCTCAGAAATCGGAGCAGGAGGATGGGGAGTGTGAGGGGTATCCTTGATGCTT GTGTGTCCTCCCACTTTCCAAATCCCGCCCGCCGGATGG
ESTD-TYR	..	--	---	---	---	TAGTGAAGTTTTCATCTCTGTGAGCTTCTGGATTCTTTGTCCACCGCAACAAGAGAGTCTATGC CAAGGCAGAAAGCTGGTCTTCATGGGCAAAATCAATGTCTCTCCAGATTTCCAGATCCCAAGCA GTGCATCCATTGACACATAATATGATCCAGACAAAGAGGTCAATAATATTGATGTGCGTTAAACAT GGGTGTTGATCCATTTTCATTTGGCCATAGGTCCCTATGGGGATGACA

ESTD- TYRP1	---	---	AGTAGTGATGAAGCTAACAGCCTCTCTCACTGATCATCAATGCTATGCTGAAGAATATGAA AACTCCAGAATCCTAATCAAGTCTGTGGTCTACAAATGCCCTACTCTCTTATGCATTAGTATCACAA AACCACCTGTTGAATATAATAGATTGAGTTATTAAGTGATTTTCTTTCACTTTATTACCTTCCTTCT AATACAAGCATATGTTAGAAATTAAGTTCTAGGCATACTT
ESTD- VB12	--	--	--	---	---	TCCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAAGGTCACAGACAGAGAACACACCGATG ACTCTGAGATGTCACCGAGACTGAGAACCACCGTTATATGTAAGTATGATCGACAAGACCCGGGGCATG GGCTGAGGCTGATCATCTACATAT
ESTD-VWF	--	--	--	---	---	AGGTAGGAAAAGCAAGAGITGATTAGTGAAGGAGAGAATGGACCTACCTCCACACTGTCCTTTGG TCCCCTAGAGTCTG
ESTD-WT1	--	--	--	---	---	AAGACTACGTGAATGTTACATGTGCTTAAAGCCTCCCTCTCTCTCTCTGCTGCAGGATGTG CGACGTGTGCTGGAGTAGCCCGACTCTTGACGGTCGGCATCTGAGACCAGTGAGAAACGCCCTT CATGTGTGCTTACCAGGCTGCAA
ESTD- s14544	--	--	--	---	---	TTGGGAAGTTAGAGCCTATATTTAAATTACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGA TATCCCAAAGTTGAAATGTCTCAGTTGCTGTGTGGTTAGATGCAGGATTTATATGATCCGTTAACCC TCT
EST71770 6	--	--	--	---	---	AGCCACCTCTCACGTCAGCCTCAGCACCAGATGCTGTTCTATAAGGATGACGTGCTGTTTTACAA CATCTCCTCCATGAAGAGCACAGAGATTTATTTCTGGAAGTCCGGATCTATGACTCAGGGACAT ATAAATGTAAGTGTGATTGTGAACAACAAGAGAAACCACTGCAGAGTACCAAGCTGTTGGTGAAGG AGTGCCAGTCCAGGGTGACACTGGACAAGAAAGAGGCCATCCAAAG
EST52418 6	--	--	--	---	---	CAAATTACAGGGTCAACTGCTATGATGTGTTGGAGCCCAAGTCAACCTTTGGTGGCTACAAGATGTCG GGGAGTGGCCGGAGTTGGCGAGTACGGGCTGCAGGCATACACTAAAGTGAAACTGTGAGTGTGG CCCACCTCTATTTGCCAGCCCCAGGGACAGAGCTGATCCTTGAAGTCTTAAGTTCCACATTTGCCAGGA CCAGTGAGCAGCAACAGGGCCAGGGCTGCTTATCAGCCTCCAGCCAGACCCAGACCTGGCTGCAGACAT AAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGGTGCGTCTGCTGCTGCCCCCG GTCACTC
EST13586 3	--	--	--	---	---	AGGCAGAAACTGGCCCCCATGCGGGGACGTGGAAGGCCACTTGAGCTTCTCTGGAGAAGGACCTGA GGGACAAAGTGCAACTCTCTTCTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAAGACTCTCTCCCT CCCTGAGCTGGAGCAACAGCAAGAACAGCAGCAGGAGCAGCAGGAGGAGGAGGAGGAGGATGCTGGGCC CCTTTGGAGAGCTGAGCTGCCCTGGTGC
EST51976 7	--	--	--	---	---	

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EST11458 6	..	--	--	---	---	CCACTTTGGTAGTGCAGTGTGACTCATCCAAATGATTTCTCCAGTGCTCATCTTGTCTCGAGTTTT CTCTGCCATGTTGCTATTGCAGGACGGACCTGTCCCAAGCCAGATGATTTACCATTTTCCACAGTGGT CCCATTAAAAACATTCTATGAGCAGGAGAGAGATTACGTATTCTCGAAGCCGGGCTATGTGTCC CGAGGAGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC
EST39852 8	..	--	--	---	---	CGGTCTTCCTTCCAGGTATTGTGCAGAAAGCCGAGATGACCTCTATGTCTCAGATGCATTCCATAAG GCATTTCTTGAGGTGAGTACACCTTCCACACTCTCTTACGGTACAGAAAGGAGATGCATGAACAGCA GGAACACGTGGAAGGCCCTGTTTCCAGTGTTAAGGCATGCAAAAGGCCCTCCACAGGCTGCTATAAT ACAGGCCCT
EST62448 0	..	--	--	---	---	ACCTGGTGTGCTGGTGTGGGTGAACCTGGTCTCTTGGCATGCGGGCCCTCTGGGGCCCGTGG TCCTCCTGGTGTGGTAGTCTGGAGTCAACGGTGTCTCTAGTGAAGCTGGTGTGATGGCAACC CTGGAAACGATGCTGTOOCCAGGTGCGGATGGTCAACCCGGACACAAAGGAGAGCGGTTACCCCTGG CAATAT
EST38027 2	..	--	--	---	---	AGTGACTTCCAAGGAAATGGCTACCCAACTTGCCTTCATGGGCTGTGGCCAACTATGCCTCTCAGA ACATCACCTACCACTGCAAGAACAGCATTGCATACATGATGAGGAGACTGGAAACCTGAAAAAGG CTGTCACTTACAGGGCTCTAATGATGTTGAACCTGTTGCTGAGGGCAACAGCAGGTTCACTTACACT GTTCTTGTAGATGGTGTCTAAAAAGACAAATGAATGGGAAAGACAA
EST12274 0	..	--	--	---	---	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTCTTCCAAATAGAGCCCTACCAAAGTGAT TACATAAGAAAGTCAAGTGGTTTACTCCTCATGACCAAAATATTCTTCCCTCTTAGGATGAGGTGA TAGTAAATGACCGATGGGGTCAGAACTGTTCTCTGTCAACATGGAGGATACTATAACTGTGAAGATAA ATTCAAGCCACAGAGCTTGCCAGATC
EST76807 7	..	--	--	---	---	ATGCTAAGGGGATCGGACATGAAAGGACCCCTGTGAGCCGATTGTCTCTATCTCCAGGGCCCTGTCTC CAGCTCACTCATCAATGGGGCCAGTCAGGCCAGGCACTGGGCTCCGGAGGACTCAOCCACTGCCCCCT GCTGCCATGTGGACTGGTGCAAGTTGAGGACTTCTTG
EST44438 7	..	--	--	---	---	GCAGCCAGGAGCCGCTGCACATGCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGACGTCT GCTCCGACCTAAGCGGAGCAGCCCTCAAGAGCCGAGCCGAGGTGGG
EST12839 3	..	--	--	---	---	TGCAAAACACACAAAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAAATATGGTCTTTTGGCT CCTAACATCTATGTACTGGATTATCTAAATGAAACACAGCAGCTTACTCCAGAGATCAAGTCCAAGG CCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGGAACTTGAATGTTATTCAACTGG ATTTCCAGTAGTTCAGTACTTATGAATATTATGATACTAGCTTAG
EST54419 8	..	--	--	---	---	CTTCTGCCTAATTTGAATGATATTGTTGCTGTGGGACCTGAGCACTTTATGGCACAAATGATCACTA TTTTCTTGACCCCTACTTACAATCCTGGGAGATGTTATTTGGGTTTAGCGTGGTGTGTTGTTGTTACTA TAGTCCAAAGTGAA

EST10398 2	--	--	---	---	---	---	TGCTGGGTGGCAAGGCTGCAAAACAAGGAGGCAACCCAGGAGGCTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTTATCTACTTATGATGATGTTACATTTGGGGCTTGACTTTCCAACACGGAGAAG CATTTGTTCTTCGGGCCAAGAAGGTATCTACCAATAGTGCTATTAGGCATTG
EST38751 7	--	--	---	---	---	---	CCAAGTCGTTCAATTTAGCTTTGCAGGTTTAACTCGATTACTTTTCTATTCAAATCTCTGTAAAA TTGAAATATGAACCTAGTTTCTGATCTATGTTTCAAGTTAAACAG
EST40582 2	--	--	---	---	---	---	CACGTGAAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAACTGTCCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAGTTTCACTGGATGCAATTAATAACAAATATTTACCTTTTGAAGAAATAAATG AAGGATTTGACCTGCTCGCTCTGGAAGAGTATCCGTACCGTCTGACGTTTGAACAATACAGAT GCCTCCCTTGTAGCAGTTTTCAGCCTCTCTACCCCTA
EST18288 3	--	--	---	---	---	---	GCTCTATACCCCTGTGTCCTCCACGCTCTCTGGACTTCACAGAACTGGATTTGCTGCTGAGAA GATTGACAGGTTTCATGAGGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGACGGAGCCAGTGTGG ACAGCACCTGGCTTCAACACCTACGTCCACTTCCAAGGTAAAGGCAACCTCTCTGCTGGCTCTGGC CCTAGGACTTAGTATCC
EST70523 3	--	--	---	---	---	---	TTCCGCGACGCCCCCATCTTGGCACCCCTGGTCCCTCAGGGGCCACCCCGCGCACTCACCGCTCT CGCTCTCGTAACATCCGGCCGGCGCCCTCTTGACACATAGCTGGACCGTTTCCGTATAGGAGG ACCGTGTAGGCTTCTGTCCTGGGCTTGCAGGGGCCAGCCCTGCAGAGAGGGGGTCCCTGTGGT TGAGCTGAACACAGCTGTGGAGTGTCTCCACGTG
EST58707 7	--	--	---	---	---	---	CAGTGTATCTGGAAGCCTACAGGACACCAAAATAACCTTAATCATCAATTGTTACAGGAGGCTTT AAGTTCAAGCATCTTTGGCTACATGAAGGCCAAATTCGAGAGACCCTAGAAGATACAGAGACCGA ATGTATCAATGGACATTACAGCAGGAACCTTCAACGATACCTGTCTGTGGTAGGCCAGGTTTATAGCA CACTTGTCACCTACATTTCTGATTGGTGGACTCTTGTGCTAAGAACCTT
EST74167 6	--	--	---	---	---	---	AGACCATGAAGGAGTTGAAGGCTACAAATCGGAACCTGGAGGAACAACCTGACCCCGGTGGCGGAGG AGACGGGCGCACGGCTGTCCAAGGAGCTGCAGGGCGCAGGCCCGGCTGGGCGGACATGGAGGA CGTCCGGCGCCCTGGTGCACTACCGCGGCGAGGTGACGCCATGCTGGCCAGAGCACCGAGGAGC TGCGGTGGCCCTGGCTCCACCTGCGCAAGCTGCGTAAGCGGCTCTC
EST43211 8	--	--	---	---	---	---	CGCTGTGTCAGTACCGCGCGAGGTGCAGGCAATGCTCGGCCAGACACCGAGGAGCTGCGGGTGCG CCTCGCCTCCACCTGCGCAAGCTGCGTAAGCGGCTCTCCGCGATGCCGATGACCTGCAAGAGCGOC TGGCAGTGTACAGGCGGGGCGCGAGGGCGCGGAGCGGCTCAGCGCCATCCGCGAGGCGCTG GGGCCCTGGTGAACAGGGCGCGGTGGCGCGCGCACTGTGGGCTC
EST38770 4	--	--	---	---	---	---	TGTAGCCAAAGTCACTGCATCATCTTGGCTGCTGGCAGCTTGGCCAGTTGCCAGCTATAATCC ATCGAAATGATTTTCAATTGAGAACCAATAATTACAGTTTGTGCTTCCATTATGAGTCCCAAAAT TCAACCTCCGATAGGGCTGGGCTGACCAAAATACTGGGTTTCTGTTCTCTTCTGATCAT TCTTACAAGTTACTCTTATTGGAAGGCCCTAAAGAGGCTTATG

EST26021 1	..	--	---	---	---	TAATGTAAGCTCATCCACCACCAAGAGCGCTGCACCATGTTTTGAGTTGAGTGACATGTTTCGAAACCTGT CCATAAAGTAATTTGTGAAGAGGAGCAAGAGAACATTCCTCTGCAGCATTCTACTACCAATGA GCATTAGCTACTTTTCAGAAATTGAAGGAGAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAGCTTTTCTTCTTTGCAACAAGACAAAGCAAGCC
EST51212 0	..	--	---	---	---	ATCCTGAGCTCGCCAAATAGCTTCTTGTTCTACTTCTCTCTCCACAGCCCAATTTCACTTTCTCA GAGGAAATCCCAAGCTTAGGAGCCCTGAGCCCTTTGTGCTCCCACTCAATACAAAAGGCCCTCTCT ACATCT
EST20118 2	..	--	---	---	---	GTTCGAAATCCTCCTCTGAAAGTGCCGGGTTTAACTGCTCATGACGCTCGGCTGTGGTCCAGCT GAGGTGAGGGGCTTGAAGCTGGAGTGGGTTTAGGACGCGGTCTCTGCTGCATCTTAAGCTCT GAGAGCAACCTCCCTTGAAGCTGGAGTGGGTTTAGGGACGCGGTCTCTGCTGCATCTTAAGCT CTGAGA
EST53018 6	..	--	---	---	---	ACAATCCAGGTCACACATTCAGAAAGAGGGGTGTCAGTGAGCCTGGGTAGGTCCAGTAATCCA AGGATTGAGGAAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC
EST68787 5	..	--	---	---	---	CTTCTATGGGATTTGACTTTATTTTCTCCATTGCTTACCTTTACAGGTGTTAATATAGTGAAAAG GAAGCTTGACGCTCATGACAAATTTGAAGCTGACAAATACACAAGAGGAAATAAATTCACAGTCAA AGAATCAAGCACTTTTCGAAACATTGAAGTTGTTTTGAAGTGTGTACCTTTAATTACAACTAG CAGACGGAACCTGAACTCAGGGTAAGAAT
EST34088 2	..	--	---	---	---	GTGGGGCAACAGTGGGAGAGAGGGGCCAGGGTATAAAGGGGCCACAAAGAGACCGGCTCAAGG ATCCCAAGGCCCACTCCCGAACCACCTCAGGGTCTGTGGACAGCTCACCTAGCTGCAATGGCTACA GGTAAG
EST37382 5	..	--	---	---	---	CTGAGAAACAATTGGCAATAAAGGAATTTGGCACTCCCAACCCCTCTTTCTCTCTCCCTTGGA CTTTGAGTCAAAATTGGCCTGGACTTGAGTCCCTGAACCAAGCAAGAGAAAGAGACCCAGAAAT CACAGGTGGGACGTGCGTCTACCGCATCTCCCTTCTCACGGGAATTTACAGGGTAACT
EST74082	..	--	---	---	---	TCAGGGTGGCTGGACCCAGGCCCAAGCTCTGCAGCAGGAGGACGTGGCTGGCTCGTGAAGCATG TGGGGTGAGGCCAGGGGCCCAAGGAGGACCTGGCTTACGCTGCTCAGGCTGCTGCTGCTGCTG CCAGATCACTGTCTCTGCAATGGCTGTGGATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG TGGGGACCTGACCCAGCCGAGCCTTTGTGAACCAACACCTGTGG
EST45311 0	..	--	---	---	---	GCCCTCTCTCTCCAAATCTGTCCCTATAGTTTCTCTATTAAAGTGAACATGCAATCTTTTAGT GGATAGATGCACACAAACACACAGCCATTATGGGAAGGATCCAGCTGTGGCCATATTGTAAACA CATTTTCTGCAATCACCTCTTTTCATTACAGCCCTTATTCAATGGCCTTTTCTTTTTCAGTAGTA CATACACATCTGTGCTATTGTTGAAT

[illegible]

Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer
6=SNP Reverse Primer 7=Sequence

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EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that

5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the

10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

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CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,
or a portion thereof which includes a polymorphic site,
5 or the complement of the segment or portion thereof.
2. The nucleic acid segment of claim 1 that is DNA.
3. The nucleic acid segment of claim 1 that is RNA.
4. The segment of claim 1 that is less than 100 bases.
5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
7. The segment of claim 1, wherein the polymorphic site is
biallelic.
8. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is the reference base
15 for the fragment listed in the Table, column 3.
9. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is an alternative form
for the fragment listed in the Table, column 4.
10. An allele-specific oligonucleotide that hybridizes to a
20 segment of a fragment shown in the Table, column 7 or
its complement.
11. The allele-specific oligonucleotide of claim 10 that is
a probe.

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12. The allele-specific oligonucleotide of claim 10,
wherein a central position of the probe aligns with the
polymorphic site of the fragment.
13. The allele-specific oligonucleotide of claim 10 that is
5 a primer.
14. The allele-specific oligonucleotide of claim 13,
wherein the 3' end of the primer aligns with the
polymorphic site of the fragment.
15. The allele-specific oligonucleotide of Claim 10, which
10 is selected from the group consisting of the nucleotide
sequences of the Table, column 5.
16. The allele-specific oligonucleotide of Claim 10, which
is selected from the group consisting of the nucleotide
sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the
Table, column 7 or the complement thereof, wherein the
polymorphic site within the sequence or complement is
occupied by a base other than the reference base shown
in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising
obtaining the nucleic acid from an individual; and
determining a base occupying any one of the polymorphic
sites shown in the Table.
- 25 19. The method of claim 18, wherein the determining
comprises determining a set of bases occupying a set of
the polymorphic sites shown in the Table.

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20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method
5 further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.